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(54) Title: A NOVEL NUCLEIC ACID MOLECULE (57) Abstract The present invention is directed generally to an isolated nucleic acid molecule encompassing a neocentromere or a functional derivative thereof or a latent, synthetic or hybrid form thereof and its use <i>inter alia</i> in developing a range of eukaryotic artificial chromosomes including mammalian (e.g. human) and non-mammalian artificial chromosomes. Such artificial chromosomes are useful in a range of genetic therapies.		

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A NOVEL NUCLEIC ACID MOLECULE

FIELD OF THE INVENTION

5 The present invention is directed generally to an isolated nucleic acid molecule encompassing a neocentromere or a functional derivative thereof or a latent, synthetic or hybrid form thereof and its use *inter alia* in developing a range of eukaryotic artificial chromosomes including mammalian (e.g. human) and non-mammalian artificial chromosomes. Such artificial chromosomes are useful in a range of genetic therapies.

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BACKGROUND OF THE INVENTION

Bibliographic details of the publications referred to by author in this specification are collected at the end of the description.

15

The rapidly increasing sophistication of recombinant DNA technology is greatly facilitating research and development in the medical and allied health fields. A particularly important area is in mammalian including human genetics and the molecular mechanisms behind some genetic abnormalities. Progress in research in this area has been hampered by the lack of a cloned
20 nucleic acid molecule encompassing a human centromere. The identification and cloning of a human centromere will promote the development of techniques for introducing genes into eukaryotic cells and in particular mammalian including human cells and will be an important asset to gene therapy and the development of a range of genetic diagnostic tests.

25 The centromere is an essential structure for sister chromatid cohesion and proper chromosomal segregation during mitotic and meiotic cell divisions. The centromere of the budding yeast *Saccharomyces cerevisiae* has been extensively studied and shown to be contained within a relatively short DNA segment of 125 bp that is organized into an 8-bp (CDEI) and 26-bp (CDEIII) domain, separated by a 78- to 87-bp, highly AT-rich, middle (CDEII) domain (Clarke
30 and Carbon, 1985). The centromere of the fission yeast *Schizosaccharomyces pombe* is considerably larger, ranging from 40 to 100 kb, and consists of a central core DNA element of 4 to 7 kb flanked on both sides by inverted repeat units (Steiner *et al.*, 1993). Recently, the

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functional DNA components of a higher eukaryotic centromere have been characterized in a minichromosome from *Drosophila melanogaster* and shown to consist of a 220-kb essential core DNA flanked by 200 kb of highly repeated sequences on one side (Murphy and Karpen, 1995).

5 The mammalian centromere, like the centromeres of all higher eukaryotes studied to date, contains a great abundance of highly repetitive, heterochromatic DNA. For example, a typical human centromere contains 2 to 4 Mb of the 171-bp α -satellite repeat (Wevrick and Willard 1989, 1991; Trowell *et al.*, 1993), plus a smaller and more variable quantity of a 5-bp satellite III DNA (Grady *et al.*, 1992; Trowell *et al.*, 1993). The role of these satellite sequences is
10 presently unclear. Transfection of a cloned 17-kb uninterrupted α -satellite array into cultured simian cells (Haaf *et al.*, 1992) or a 120-kb α -satellite-containing YAC into human and hamster cells (Larin *et al.*, 1994) appear to confer centromere function at the sites of integration. Other workers have analyzed rearranged Y chromosomes (Tyler-Smith *et al.*, 1993), or dissected the centromere of the human Y chromosome with cloned telomeric DNA (Brown *et al.*, 1994) and
15 suggested that 150 to 200 kb of α -satellite DNA plus ~300 kb of adjacent sequences are associated with human centromere function. In addition, a human X-derived minichromosome that retained 2.5 Mb of α -satellite array has been produced by telomere-associated chromosome fragmentation (Farr *et al.*, 1995). In all these studies, it is not known whether non- α -satellite DNA sequences are embedded within the centromeric site and operate independently of, or in
20 concert with, the α -satellite DNA.

In mammals, four constitutive centromere-binding proteins, CENP-A, CENP-B, CENP-C, and CENP-D, have been characterized to varying extents and implicated to have possible direct roles in centromere function. CENP-A, a protein localized to the outer kinetochore domain, is a
25 centromere-specific core histone that shows sequence homology to the histone H3 protein and may serve to differentiate the centromere from the rest of the chromosome at the most fundamental level of chromatin structure - the nucleosome (Sullivan *et al.*, 1994). CENP-B, a protein which associates with the centromeric heterochromatin through its binding to the CENP-B box motif found in primate α -satellite and mouse minor satellite DNA, probably has a role in
30 packaging centromeric heterochromatic DNA - a role which, however, may not be indispensable since the protein is undetectable on the Y chromosome (Pluta *et al.*, 1990) and is found on the

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inactive centromeres of dicentric chromosomes (Earnshaw *et al.*, 1989). CENP-C has been shown to be located at the inner kinetochore plate and is postulated to have an essential although yet undetermined centromere function, as seen, for example, from inhibition of mitotic progression following microinjection of anti-CENP-C antibodies into cells (Bernat *et al.*, 1990; 5 Tomkiel *et al.*, 1994) and from its association with the active but not the inactive centromeres of dicentric chromosomes (Earnshaw *et al.*, 1989; Page *et al.*, 1995; Sullivan and Schwartz, 1995). Finally, CENP-D (or RCC1) is a guanine exchange factor that appears to have a general cellular role that is neither specific nor clear for the centromere (Kingwell and Rattner 1987; Bischoff *et al.*, 1990; Dasso, 1993). More recently, a new role for the mammalian centromere 10 as a "marshalling station" for a host of "passenger proteins" (such as INCENPs, MCAK, CENP-E, CENP-F, 3F3/2 antigens, and cytoplasmic dynein), has been recognized (reviewed by Earnshaw and Mackay, 1994, and Pluta *et al.*, 1995). These passenger proteins, whose appearance at the centromere is transient and tightly regulated by the cell cycle, provide vital functions that include motor movement of chromosomes, modulation of spindle dynamics, 15 nuclear organization, intercellular bridge structure and function, sister chromatid cohesion and release, and cytokinesis. At present, except for CENP-B, none of the constitutive or passenger proteins have been demonstrated to bind mammalian centromere DNA directly.

In work leading up to the present invention, the inventors identified in a patient (hereinafter 20 referred to as "BE") an unusual human marker chromosome, mardel 10, which is 100% stable in mitotic division both in patient BE and in established fibroblast and transformed lymphoblast cultures. In accordance with the present invention, a region of the mardel (10) chromosome has been cloned together with the corresponding region from a normal human subject. The nucleic acid molecules cloned contain no substantial α -satellite repeats yet are mitotically stable. The 25 nucleic acid molecules encompass therefore, a new form of centromere referred to herein as a "neocentromere". The identification and cloning of a eukaryotic neocentromere without substantial α -satellite DNA repeat sequences now provides the means of generating a range of eukaryotic artificial chromosomes such as mammalian including human artificial chromosomes with uses in genetic therapy, transgenic plant and animal production and recombinant protein 30 production. A range of diagnostic reagents is now also obtainable using the cloned neocentromere.

SUMMARY OF THE INVENTION

Sequence Identity Numbers (SEQ ID NOs.) for the nucleotide sequences referred to in the specification are defined following the bibliography.

5

Throughout this specification and the claims which follow, unless the context requires otherwise, the word "comprise", or variations such as "comprises" or "comprising", will be understood to imply the inclusion of a stated integer or group of integers but not the exclusion of any other integer or group of integers.

10

A fibroblast cell line 920158 carrying the mardel marker chromosome was deposited at the European Collection of Cell Cultures (ECACC), Centre for Applied Microbiology Research, Salisbury, Wiltshire, SP4 0JG, UK on 1 May, 1997 under Accession No. 97051716. Bacterial artificial chromosomes (BACs) carrying portions of the mardel (10) chromosome have also been

15 deposited at ECACC as follows:

BAC/E8-1: deposited on 5 May 1998 under Accession Number 980505016;

BAC/F2-14: deposited on 5 May 1998 under Accession Number 980505017.

20 A number of human fibrosarcoma cell lines carrying various neocentromeric constructs were deposited at ECACC as described hereafter by Accession Number with the date of deposit in parentheses.

	HT-38	98050704 (7 May 1998)
25	HT-47	98050705 (7 May 1998)
	HT-54	98050706 (7 May 1998)
	HT-190	98050707 (7 May 1998)
	HT-191	98050708 (7 May 1998).

30 One aspect of the present invention provides an isolated nucleic acid molecule comprising a sequence of nucleotides derived from a eukaryotic chromosome and encompassing a

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neocentromere or a functional derivative synthetic or hybrid form thereof which nucleic acid molecule or its derivatives, synthetic forms or hybrid forms when introduced into a compatible cell is capable of replicating, acting as an extra-chromosomal element and segregating with cell division.

5

Another aspect of the present invention contemplates a nucleic acid molecule or its chemical equivalent having a tertiary structure which defines a human neocentromere or a functional derivative thereof or a latent, synthetic or hybrid form thereof or its mammalian or non-mammalian homologue.

10

Yet a further aspect of the present invention is directed to an isolated nucleic acid molecule comprising a sequence of nucleotides encompassing a neocentromere derived from a eukaryotic chromosome, which nucleic acid molecule when introduced into a compatible cell is a replicating, extra-chromosomal element which segregates with cell division.

15

Still another aspect of the present invention is directed to an isolated nucleic acid molecule having a sequence of nucleotides or their chemical equivalents which directs a conformation defining a human neocentromere or a functional derivative thereof or a latent, synthetic or hybrid form thereof or a mammalian or non-mammalian homologue thereof wherein the neocentromere
20 associates with centromere binding proteins (CENP) -A and CENP-C or antibodies thereto and does not contain substantial α -satellite DNA repeat sequences.

A further aspect of the present invention is directed to an isolated nucleic acid molecule comprising a nucleotide sequence encompassing a neocentromere or a functional derivative,
25 synthetic or hybrid form thereof which when said nucleic acid molecule is in linear form and co-introduced into a cell together with a telomeric sequence, is capable of replicating, remaining as an extra-chromosomal element and segregates with cell division.

Another aspect of the present invention provides an isolated nucleic acid molecule or a
30 derivative, synthetic or hybrid form thereof comprising a sequence of nucleotides:

- (i) which directs conformation defining a human neocentromere or a functional derivative

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thereof or a latent, synthetic or hybrid form thereof or its mammalian or non-mammalian homologue wherein said neocentromere is capable of associating with CENP-A and CENP-C;

- (ii) which contains no substantial α -satellite DNA sequence repeat; and
- 5 (iii) which is capable, when introduced into compatible cells, of replication, remaining extra-chromosomal and segregating with cell division.

Even yet another aspect of the present invention is directed to a genetic construct comprising an origin of replication for a eukaryotic cell and a nucleic acid molecule encompassing a human
10 neocentromere or a functional derivative thereof or a latent, synthetic or hybrid form thereof or its mammalian or non-mammalian homologue flanked by telomeric nucleotide sequences functional in the cell in which the genetic construct is to replicate and wherein said genetic construct when introduced into a cell is a replicating, extra-chromosomal element which segregates with cell division.

15

Another aspect of the present invention is directed to a genetic construct in the form of a eukaryotic artificial chromosome such as a mammalian artificial chromosome (MAC), a human artificial chromosome (HAC) or comprising an origin of replication and a sequence of nucleotides which:

- 20 (i) directs a conformation defining a human neocentromere or a functional derivative thereof or a latent, synthetic or hybrid form thereof wherein said neocentromere is capable of associating with CENP-A and CENP-C or antibodies thereto; and
 - (ii) contains no substantial α -satellite DNA repeat sequences;
- said sequence of nucleotides flanked by eukaryotic (e.g. mammalian) telomeric sequences which
25 are in turn flanked by yeast telomeric sequences wherein a unique enzyme site is located between the human and yeast telomeric nucleotide sequences such that upon contact with said enzyme, the yeast telomeric sequences are removed and the eukaryotic (e.g. mammalian) telomeric sequences are exposed.

30 Still another aspect of the present invention provides a genetic construct comprising an origin of replication and a first nucleic acid molecule defining a human neocentromere or a functional

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derivative thereof or latent, synthetic or hybrid form thereof, a second nucleic acid molecule encoding a peptide, polypeptide or protein, wherein said first and second nucleic acid molecules are flanked by a first set of eukaryotic (e.g. mammalian, such as human) telomeric sequences which are in turn flanked by a second set of eukaryotic (e.g. yeast) telomeric sequences wherein
5 there are unique enzyme sites between the first and second telomeric sequences such that upon contact with a required enzyme, the second telomeric sequences are cleaved off to expose the first telomeric sequences.

BRIEF DESCRIPTION OF THE FIGURES

10

Figure 1 is a schematic representation showing identification of a YAC contig spanning the marker centromere region. (A) Comparison of GTL banding patterns of mardel 10 and normal chromosome 10. The pair of open arrows indicate the two breakpoints on a normal chromosome 10 in generating the marker chromosome (Voullaire *et al.*, 1993). The long and short arms of
15 the marker chromosome are designated q' and p', respectively, to distinguish them from the q and p arms of the normal chromosome 10. Asterisk denotes the position of a cosmid 10pC38 that was used to "tag" the q'-arm of stretched marker chromosomes in the ANTI-CEN/FISH experiments. (B) A 4-megabase YAC contig (#082) from 10q25.2 region that spans the marker centromere. The tilling path of YACs #0 to #23 and their corresponding CEPH library addresses
20 are shown. (C) FISH mapping of selected YAC clones from contig #082 using normal fluorescence microscopy and standard metaphase chromosomes prepared from transformed lymphoblast cells of patient BE. The distribution of FISH signals (vertical axis) is shown as a percentage of the signals on one arm of the marker chromosome that is in excess of those found on the opposite arm of the chromosome. The total number of fluorescence signals scored for
25 each of the YAC clones is indicated in brackets.

Figure 2 is a photographic representation showing ANTI-CEN/FISH analysis of the marker centromere. (A) Detection of α -satellite DNA using a mixture of α -satellite DNA probes (red signals) under low stringency conditions. Centromeres were counter-labelled with CREST#6
30 autoimmune antibody (pale blue dots; or white when superimposed on a red background). Chromosomes were prepared from transformed lymphoblast cells of patient BE. The right-hand

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panel represents green pseudo-coloring of DAPI images of chromosomes to provide a better definition of chromosome outline. Only the signal for the antibody, but not that for α -satellite, was seen on the marker centromere (arrowed). (B) Simultaneous labelling of stretched human metaphase chromosomes with CREST#6 (red) and anti-CENP-C antibody, Am-C1 (pale blue), with the white color indicating full coincidence of the two antibody signals. (C) Detection of CENP-C on the marker chromosome. Simultaneous labelling of the marker chromosome (arrowhead) with (a) Am-C1 (pale blue) and (b) CREST#6 (red). (c) Combined images of a and b, showing complete coincidence of Am-C1 and CREST#6 signals. (d) FISH analysis of the same cell as a-c using the 10pC38 cosmid probe (pale blue dots and green arrows) to identify the marker chromosome. Some loss of ANTI-CEN signal, especially for the Am-C1 antibody was seen following FISH. (e) Green pseudo-coloring of DAPI images. A colour photograph corresponding to this figure is available upon request.

Figure 3 is a photographic representation showing ANTI-CEN/FISH analysis of cosmid clones on stretched (A, a-f) and superstretched (B) metaphase chromosomes. (a-c) Examples of cosmid signals (white arrows) localized to the q'-region of the marker centromere. (d-f) Examples of cosmid signals (white arrows) localized to the p'-region of the marker centromere. Green arrows indicate positions of the 10pC38 cosmid DNA tag used to mark the q'-end of the marker chromosome. (B) Mapping of Y6C21 onto a superstretched metaphase chromosome. Not included is the 10pC38 q'-tag signal located further to the left of the chromosomal segment shown. ANTI-CEN signals are in red, FISH signals are in pale blue, and overlapping ANTI-CEN and FISH signals are in white. Each of the pictures is accompanied by DAPI images of chromosomes pseudo-coloured in green. A colour photograph corresponding to this figure is available upon request.

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Figure 4 Localization of the anti-centromere antibody-binding domain. *a*, Relative positions of different cosmid and PAC clones within the YAC #082 contig, using YAC-3 as a reference. Cosmids are designated as Yn Cm, where 'n' denotes the YAC of origin and 'm' denotes the cosmid number. PACs 1-5 are five different PAC clones isolated from a human PAC library (Genome Systems Inc). "HC-contig" represents a group of overlapping cosmids that map tightly around the marker centromere in ANTI-CEN/FISH experiments. A genomic map corresponding

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to the depicted YAC region was derived from the DNA of patient BE and shown above the YAC map. S, *SalI*; K, *KspI*; N, *NotI*; Sf, *SfiI*. **b**, Cumulative scoring of FISH signals in ANTI-CEN/FISH experiments for cosmids Y3C64, Y6C8, Y3C94, Y7C14, Y4C45, Y6C10, Y6C21, Y3C3, PAC5, Y13C1, Y13C8, and Y17C6. The distribution of FISH signals (vertical axis) is
5 those found on the opposite arm of the chromosome. The total number of fluorescence signals scored for each of the cosmid clones is indicated in brackets. **c**, Restriction mapping of the 80-kb region covered by the eight overlapping cosmids of the HC-contig. These eight cosmids were derived from four different YACs (YAC-3, YAC-4, YAC-6, and YAC-7) and provided independent confirmation of the map. Furthermore, the map agreed fully with the restriction map
10 of a 120 kb-insert PAC clone (PAC4) that spanned the entire HC-contig region. E, *EcoRI*; R, *EcoRV*; N, *NotI*.

Figure 5 is a representation showing restriction analysis of genomic DNA of patient BE and those of his normal parents using Y6C10 as probe. DNA was resolved on a PFGE (A) or
15 standard agarose gel (B and C). Samples 1, 2 and 3 were fibroblast cultures of mother of BE, father of BE, and patient BE, respectively. Sample 4 was a somatic hybrid cell line BE2C1-18-5F containing the marker chromosome. Fragment sizes are in kilobases.

Figure 6 is a representation of the full nucleotide sequence of the HC-contig DNA derived from
20 normal human chromosome 10q 25.2 region.

Figure 7 is a diagrammatic representation of the method used to retrofit YAC3 and YAC5.

Figures 8A to J are diagrammatic representations of the different vectors used for cloning
25 DNA as YACs by the conventional restriction/ligation methods.

Figures 9 is a diagrammatic representation of circular TAR summarising the recombination process.

30 **Figure 10** is a diagrammatic representation showing modification of TAR vector.

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Figure 11 is a diagrammatic representation of the cloning of 10q25 human neocentromere DNA from mardel (10) chromosome. This DNA is designated NC-contig DNA to distinguish it from the HC-contig derived from the corresponding region of the normal chromosome 10. (A) Structural map of the NC-contig region and flanking DNA. Arrows indicate the relative positions and directions of primers used in PCR analyses (Table 3). The restriction sites *EcoRI*, *EcoRV*, *SrfI*, and *SfiI* are indicated by E, R, Sr and Sf, respectively. The position of the TAR "hook" CE-F2 is represented by the solid box. The hatched bar represents HC- or NC-contig. p' and q' refer to the short and long arms of mardel (10), respectively. (B) Circular TAR strategy using the vectors pVC39-Alu/C3-F2(+) and pVC39-Alu/C3-F2(-) for the direct cloning of the neocentromere DNA from mardel (10). The position of the Alu consensus sequence hook is represented by the white box. Crosses denote the sites of recombination between the TAR vector and the genomic DNA at the Alu and C3-F2 hooks during cloning. (C) Structural maps of the resulting circular YACs 5f-52-E8 and 5f-38-F2 containing the neocentromere DNA of the mardel (10) chromosome. The DNA flanking the NC-contig is represented by stippled bars. (D) Structural maps of BAC/E8-1 and BAC/F2-14. Nt represents *NotI* and URA-BAC-neo represents the retrofitting vector BRV1 (Larionov *et al.*, 1997).

Figure 12 is a diagrammatic representation showing specific TAR of HC-region from mardel 10.

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The method was as follows: (1) Co-transformation into YPH857; (2) Select HIS^+ colonies; (3) screen for HC-region by PCR; (4) Prepare high-MW DNA; (5) Digest with *I-SceI* to expose hTELS; (6) Transfect HT 1080 cells; (7) Select for G418^R; and (8) analyse by PFGE and FISH.

25 **Figure 13** is a diagrammatic representation showing cloning in yeast as YAC/HAC.

Figure 14 is a diagrammatic representation outlining TACT procedure.

Figure 15 is a diagrammatic representation of TACT constructs.

30

Figure 16A is a representation of the full nucleotide sequence of the NC-contig DNA derived

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from mardel (10) and corresponds to the HC-contig DNA region of the normal chromosome 10.

Figure 16B is a representation of the partial nucleotide sequence of the BAC/F2-14 clone that is derived from a region immediately p' of the NC-contig DNA (see Fig. 11D).

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SUMMARY OF SEQ ID NOs.

	SEQ ID NO.	DESCRIPTION
	1	DNA primer
5	2	DNA primer
	3	Nucleotide sequence of HC-contig
	4	Nucleotide sequence of NC-contig
	5	BAC-F2 contig 1
	6	BAC-F2 contig 2
10	7	BAC-F2 contig 3
	8	BAC-F2 contig 4
	9	BAC-F2 contig 5
	10	BAC-F2 contig 6
	11	BAC-F2 contig 7
15	12	BAC-F2 contig 8
	13	BAC-F2 contig 9
	14	BAC-F2 contig 15
	15	BAC-F2 contig 33
	16	BAC-F2 contig 39
20	17	BAC-F2 contig 41
	18	BAC-F2 contig 42
	19	BAC-F2 contig 44
	20	BAC-F2 contig 47
	21	BAC-F2 contig 47 fragment 1
25	22	BAC-F2 contig 47 fragment 2
	23	BAC-F2 contig 47 fragment 3
	24	BAC-F2 contig 47 fragment 4
	25	BAC-F2 contig 47 fragment 5
	26	BAC-F2 contig 47 fragment 6

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27	BAC-F2 contig 47 fragment 7
28	BAC-F2 contig 47 fragment 8
29	BAC-F2 contig 47 fragment 9

5 ABBREVIATIONS USED IN THE SUBJECT SPECIFICATION

	mardel (10):	Marker chromosome from patient BE; comprises a rearrangement of chromosome 10.
	HAC:	Human artificial chromosome
	YAC:	Yeast artificial chromosome
10	MAC:	Bacterial artificial chromosome
	PLAC:	Plant artificial chromosome
	neocentromere:	A centromere containing no substantial α -satellite DNA
	CENP:	Centromere binding protein
	HC-contig:	Region of normal chromosome 10 comprising neocentromere
15	E8:	q' end/region of mardel (10) neocentromere
	F2:	p' end/region of mardel (10) neocentromere
	BE:	Patient from which mardel (10) identified
	TAR:	Transformation-associated recombinant
	PCR:	Polymerase chain reaction
20	Marker neocentromere:	neocentromere on mardel (10).
	NC-contig	region of mardel (10) chromosome comprising neocentromere

DETAILED DESCRIPTION OF PREFERRED EMBODIMENTS

- 25 The present invention is predicated in part on the identification and isolation of nucleic acid molecules exhibiting neocentromeric properties. In accordance with the present invention, a neocentromere is considered a centromere which does not contain substantial α -satellite DNA repeat sequences and, when activated, is capable of functioning as a centromere. The term

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"substantial" in this context means that the nucleic acid molecule does not contain detectable α -satellite by FISH analysis under medium stringency conditions. The neocentromere may contain a small number of highly diversified α -satellite DNA. In primates, α -satellite DNA is considered 171bp in length. A nucleic acid molecule containing an activated neocentromere
5 or a neocentromere otherwise functioning as a centromere facilitates in accordance with the present invention, the nucleic acid molecule replicating, remaining extra-chromosomal and segregating with cell division. Reference herein to "neocentromere" is taken to mean a centromere substantially devoid of α -satellite DNA repeat sequences.

10 Accordingly, one aspect of the present invention provides an isolated nucleic acid molecule comprising a sequence of nucleotides which defines an eukaryotic neocentromere.

More particularly the present invention provides an isolated nucleic acid molecule comprising a sequence of nucleotides derived from a eukaryotic chromosome and encompassing a
15 neocentromere which nucleic acid molecule when introduced into a compatible cell is capable of replicating, acting as an extra-chromosomal element and segregating with cell division.

The present invention is exemplified herein by the identification and cloning of a human neocentromere. This is done, however, with the understanding that the present invention extends
20 to all eukaryotic neocentromeres such as from mammalian, plant, avian, insect, fungal, yeast and reptilian chromosomes. The most preferred neocentromere, however, is from human chromosomes and their mammalian homologues.

The present invention is predicated in part on the identification of an unusual chromosomal
25 marker in a patient designated "BE". The chromosomal marker is referred to as "mardel (10)" and results from a rearrangement of human chromosome 10. The mardel (10) marker is mitotically stable and, in accordance with the present invention, contains a functional neocentromere at a location regarded as non-centromeric. The neocentromere at mardel (10) is located between q24 and q26 on chromosome 10 and more particularly around q25. Even
30 more particularly, the neocentromere maps to q25.2 on chromosome 10. The present invention is exemplified by DNA cloned from the q24-q26 region of the mardel (10) chromosome as well

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as the corresponding region on normal human chromosome 10. These DNA molecules contain a functional neocentromere. The present invention extends, however, to any neocentromere or any chromosome in mammalian and non-mammalian animals as well as plants, yeasts and fungi.

5

For convenience, the DNA clones from the mardel (10) chromosome as well as from normal human chromosome 10 are summarised in Figure 11. The neocentromere located at or around 10q25 is located on a clone designated the "HC-contig". DNA clones from mardel (10) are referred to as "E8" or the "NC-contig" which extends from the long arm (q') of mardel (10) towards the short arm (p'). Clone F2 extends further p' from E8 (see Figure 11). It is emphasised, however, that the present invention extends to any neocentromere on any human chromosome as well as neocentromeres on other mammalian and non-mammalian chromosomes including chromosomes from plants, insects, reptiles, yeast and fungi.

15 The present invention further contemplates a nucleic acid molecule or its chemical equivalent having a tertiary structure which defines a human neocentromere or a functional derivative thereof or a latent, synthetic or hybrid form thereof or its mammalian or non-mammalian homologue.

20 Even more particularly, the present invention is directed to an isolated nucleic acid molecule having a sequence of nucleotides or their chemical equivalents which directs a conformation defining a human neocentromere or a functional derivative thereof or a latent, synthetic or hybrid form thereof or its mammalian or non-mammalian homologue wherein the centromere associates with centromere binding proteins (CENP) -A and CENP-C or antibodies thereto.

25

Reference herein to "latent" in relation to a centromere includes reference to a centromere not normally functional but nevertheless activatable under certain conditions. A latent centromere may also be considered as a neocentromere provided it has no substantial α -satellite DNA repeat sequences.

30

The size of the neocentromere in accordance with the present invention may range from about

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50 bp to about 1500 kbp, from about 70 bp to about 1000 kbp, from about 75bp to about 800 kpb, from about 80 bp to about 500 kbp, from about 85 bp to about 200 kbp, from about 90 bp to about 100 kbp, from about 100 bp to about 1 kbp, about 120 bp to about 500 bp, about 180 bp to about 300 bp. In one particular embodiment, the centromere is approximately 60-100 kbp.

5 In another embodiment, the centromere is about 80 kbp.

The nucleic acid molecule encompassing the HC-contig for human chromosome 10 of the present invention set forth in Figure 6 (SEQ ID NO: 3). The nucleic acid molecule encompassing the NC-contig (part of E8) from mardel (10) is set forth in Figure 16A (SEQ ID NO: 4). The nucleic acid molecule encompassing F2 of mardel (10) is set forth in Figure 16B as separate contigs (SEQ ID NOs: 5-29). The nucleic acid molecules have a tertiary structure and the neocentromere is a conformation of nucleotides within this tertiary structure. Accordingly, the neocentromere is not defined by a linear sequence of nucleotides although this linear sequence directs the conformation which in turn defines the neocentromere. Although this aspect of the present invention is exemplified using the nucleotide sequence set forth in Figure 6, 16A and 16B, the subject invention extends to any sequence directing a conformation defining a centromere and hybridising to the sequence set forth in one or more of Figures 6, 16A and/or 16B under low stringency conditions at 42°C and/or which comprises a nucleotide sequence having at least about 40% nucleotide similarity to one or more sequences set forth in Figures 6, 16A and/or 16B. Preferably, the percentage similarity is at least about 50%, more preferably at least about 60%, still more preferably at least about 70%, even more preferably at least about 80-90% or above such as 95%, 97%, 98% and 99%.

Another embodiment of the present invention is directed to YAC 3 and YAC 5 encompassing the HC contig and flanking sequence as well as nucleotide sequences related to YAC 3 and/or YAC 5 at the homology, similarity or hybridization levels.

Reference herein to a low stringency at 42°C includes and encompasses from at least about 1% v/v to at least about 15% v/v formamide and from at least about 1M to at least about 2M salt for hybridisation, and at least about 1M to at least about 2M salt for washing conditions. Alternative stringency conditions may be applied where necessary, such as medium stringency, which

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includes and encompasses from at least about 16% v/v to at least about 30% v/v formamide and from at least about 0.5M to at least about 0.9M salt for hybridisation, and at least about 0.5M to at least about 0.9M salt for washing conditions, or high stringency, which includes and encompasses from at least about 31% v/v to at least about 50% v/v formamide and from at least
5 about 0.01M to at least about 0.15M salt for hybridisation, and at least about 0.01M to at least about 0.15M salt for washing conditions. These stringency conditions may be altered dependent on the source of DNA and other factors.

The term "similarity" as used herein includes exact identity between compared sequences at the
10 nucleotide level. Where there is non-identity at the nucleotide level, "similarity" includes differences between sequences which nevertheless result in conformation defining a functional neocentromere.

The nucleic acid molecule of the present invention may comprise a naturally occurring nucleotide
15 sequence from a healthy human subject or may comprise the nucleotide sequence from a human subject exhibiting one or more chromosomal-dependent conditions such as a subject carrying mardel 10 chromosome or a chromosome conferring an equivalent or similar condition or may carry one or more nucleotide substitutions, deletions and/or additions relative to the naturally or non-naturally occurring sequence. Such modifications are referred to herein as "derivatives" and
20 include mutants, fragments, parts, homologues and analogues of the naturally occurring nucleotide sequence. Preferably, the derivatives of the present invention still define a functional neocentromere.

Reference herein to a "neocentromere" includes reference to a functional neocentromere or a
25 functional derivative thereof meaning that it is capable of facilitating sister chromatid cohesion and chromosomal segregation during mitotic cell divisions and/or is capable of associating with CENP-A and/or CENP-C and/or is capable of interacting with anti-CENP-A antibodies or anti-CENP-C antibodies. Generally, and preferably, the neocentromere is incapable of interacting with CENP-B or anti-CEP-B antibodies. Alternatively, the neocentromere may be a latent
30 centromere capable of activation by epigenetic mechanisms. The neocentromere may also be a hybrid of other human, mammalian, plant or yeast neocentromeres. Synthetic neocentromeres

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provided by, for example, polymeric techniques to arrive at the correct conformation are also contemplated by the present invention. All such forms and definitions of neocentromere are encompassed by use of this term.

5 Another aspect of the present invention provides an isolated nucleic acid molecule or chemical equivalent having the following characteristics:

- (i) comprises a nucleotide sequence or chemical equivalent directing a conformation which defines a neocentromere or a functional derivative thereof or a latent, synthetic or hybrid form thereof or;
- 10 (ii) comprises a nucleotide sequence or chemical equivalent substantially as set forth in one or more of Figures 6, 16A and/ or 16B or having at least about 40% similarity thereto or capable of hybridising thereto under low stringency conditions at 42°C; and
- (iii) comprises a neocentromere capable of associating with CENP-A or CENP-C or antibodies thereto.

15

Preferably, the neocentromere is incapable of interacting with CENP-B or antibodies thereto.

In a particularly preferred embodiment, the centromere corresponds to a human genomic region which maps between q24 and q26 on chromosome 10, and in particular q25 on chromosome 10.

20

The nucleic acid molecule or its chemical equivalent of the present invention defining a conformational neocentromere or functional derivative thereof or latent, synthetic or hybrid form thereof is useful *inter alia* for the generation of artificial chromosomes such as human artificial chromosomes (HACs), mammalian artificial chromosomes (MACs), yeast artificial chromosomes
25 (YACs) and plant artificial chromosomes (PLACs). HACs are particularly useful since they are capable of accommodating large amounts of DNA and are capable of propagation in human cells. The HACs are non-viral in origin and, hence, are more suitable for gene therapy by, for example, introducing therapeutic genes. Furthermore, the HACs remain extra-chromosomal and, hence, have no insertional/substitutional mutagenic potential. The essence of a HAC is the presence of
30 a neocentromere or latent, synthetic or hybrid form thereof which enables stable segregation during cell division. The HAC also remains extra-chromosomal and, hence, is more suitable for

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gene therapy. Reference to "extra-chromosomal" means that it does not integrate into the main chromosome and, in effect, is episomal.

Accordingly, the present invention provides a genetic construct comprising an origin of
5 replication for a eukaryotic cell and a nucleic acid molecule encompassing a eukaryotic
neocentromere or a functional derivative thereof or a latent, synthetic, hybrid form thereof or its
mammalian or non-mammalian homologue flanked by telomeric nucleotide sequences functional
in the cell in which the genetic construct is to replicate and wherein said genetic construct when
introduced into a cell is a replicating, extra-chromosomal element which segregates with cell
10 division.

More particularly, the present invention further contemplates a genetic construct in the form of
an artificial chromosome comprising an origin of replication for a mammalian, human, plant or
yeast cell and a nucleic acid molecule encompassing a human neocentromere or a functional
15 derivative thereof or a latent, synthetic or hybrid form thereof or its mammalian or
non-mammalian homologue flanked by telomeric nucleotide sequences functional in the cell in
which the artificial chromosome is to replicate.

Another embodiment provides a genetic construct in the form of an artificial chromosome
20 comprising an origin of replication for a mammalian, human, plant or yeast cell and a nucleic acid
molecule having a tertiary structure which defines a human neocentromere or a functional
derivative thereof or a latent, synthetic or hybrid form thereof or its mammalian homologue
flanked by telomeric sequences functional in the cell in which the artificial chromosome is to
replicate.

25

Yet another embodiment is directed to a genetic construct in the form of an artificial
chromosome comprising an origin of replication for a mammalian, human, plant or yeast cell and
a nucleic acid molecule having a sequence of nucleotides which directs a conformation defining
a human neocentromere wherein the centromere associates with CENP-A and/or CENP-C or
30 antibodies thereto and does not contain substantial α -satellite DNA repeat sequences, said
nucleic acid molecule flanked by telomeric nucleotide sequences functional in the cell which the

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artificial chromosome is to replicate.

Still yet another aspect of the present invention relates to a genetic construct in the form of an artificial chromosome comprising an origin of replication for a mammalian, human, plant or yeast
5 cell and a nucleic acid molecule comprising a sequence of nucleotides which:

- (i) directs a conformation which defines a neocentromere or a functional form thereof or a latent, synthetic or hybrid form thereof;
- (ii) comprises a nucleotide sequence substantially as set forth in one or more of Figures 6, 16A and/or 16B or having at least about 40% similarity to the nucleotide sequences set
10 forth in Figures 6, 16A and/or 16B or is capable of hybridising to one or more of these sequences under low stringency conditions at 42°C;

wherein the neocentromere is capable of associating with CENP-A and/or CENP-C or antibodies thereto and wherein said nucleic acid molecule is flanked by telomeric nucleotide sequences functional in the cell in which the artificial chromosome replicates.

15

In a preferred embodiment, the genetic construct is a HAC and comprises human telomeric sequences. In a particularly preferred embodiment, the HAC further comprises yeast artificial chromosome (YAC) arms and, hence, becomes a HAC/YAC shuttle vector capable of propagation in human and yeast cells. Preferably, the HAC/YAC contains a unique enzyme site
20 between yeast telomeric sequences and human telomeric sequences such that upon contact with the particular enzyme, the yeast telomeric sequences are removed leaving the human telomeric sequences. Preferably, the unique enzyme site is a yeast specific enzyme site such as I-SceI.

According to this embodiment, there is provided a genetic construct defining a HAC/YAC
25 comprising an origin of replication and a nucleic acid molecule encompassing a human neocentromere or a functional derivative thereof or a latent, synthetic or hybrid form thereof or a mammalian or non-mammalian homologue thereof, said nucleic acid molecule flanked by human telomeric sequences which are in turn flanked by yeast telomeric sequences wherein a unique enzyme site is located between the human and yeast telomeric nucleotide sequences such
30 that upon contact with the enzyme, the yeast telomeric sequences are removed and the human telomeric sequences are exposed.

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More particularly, the present invention is directed to a genetic construct defining a HAC/YAC comprising an origin of replication and a nucleic acid molecule encompassing a human centromere or a functional derivative thereof or a latent, synthetic or hybrid form thereof or a mammalian or non-mammalian homologue thereof wherein the neocentromere associates with
5 CENP-A and/or -C or antibodies thereto and does not contain substantial α -satellite DNA sequences wherein said nucleic acid molecule is flanked by human telomeric sequences which are in turn flanked by yeast telomeric sequences wherein a unique enzyme site is located between the human and yeast telomeric nucleotide sequences such that upon contact with said enzyme, the yeast telomeric sequences are removed and the human telomeric sequences are exposed.

10

Even more particularly, the present invention is directed to a genetic construct in the form of a HAC/YAC comprising an origin of replication and a sequence of nucleotides which directs a conformation defining a human neocentromere or a functional derivative thereof or a latent, synthetic or hybrid form thereof or a mammalian or non-mammalian homologue thereof wherein
15 said neocentromere is capable of associating with CENP-A and/or CENP-C or antibodies thereto, said sequence of nucleotides flanked by human telomeric sequences which are in turn flanked by yeast telomeric sequences wherein a unique enzyme site is located between the human and yeast telomeric nucleotide sequences such that upon contact with said enzyme, the yeast telomeric sequences are removed and the human telomeric sequences are exposed.

20

Preferably, the length of the nucleotide sequence is between about 30 kpb and 1500 kpb, and more preferably between 60 kbp and 1000 kpb.

In a particularly preferred embodiment, the unique enzyme site is a yeast specific enzyme site
25 such as I-SceI.

The present invention extends to yeast cells and human cells carrying the genetic constructs of the present invention and to proteins produced therefrom.

30 The genetic constructs may also comprise marker genes and other unique restriction sites to facilitate insertion of adventitious DNA. Accordingly, the genetic constructs of the present

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invention may further comprise adventitious or heterologous DNA encoding a product of interest. Preferred products of interest include pharmaceutically useful genes such as genes encoding cytokines, receptors, growth regulators and the like. Endogenous genes may also be replaced by wild-type genes or modified genes.

5

The adventitious or heterologous DNA may also encode a molecule not synthesised in a sufficient amount in a particular subject and hence the increased copy number permits greater amounts of the molecule being synthesised.

10 Accordingly, the present invention contemplates a genetic construct comprising an origin of replication and a first nucleic acid molecule defining a human neocentromere or a functional derivative thereof or latent, synthetic or hybrid form thereof or a mammalian or non-mammalian homologue, a second nucleic acid molecule encoding a peptide, polypeptide or protein, wherein
15 said first and second nucleic acid molecules are flanked by a first set of human telomeric sequences which are in turn flanked by a second set of yeast telomeric sequences wherein there are unique enzyme sites between the human and yeast telomeric sequences such that upon contact with said enzyme, the yeast telomeric sequences are cleaved off to expose the human telomeric sequences.

20 Reference herein to segregate preferably means mitotically stable segregation. Conveniently, stable segregation may be determined as the presence of an artificial chromosome in 40-60% of daughter cells after 4-6 months of continuous passage.

The present invention extends to other artificial chromosome analogues to the HACs and
25 HAC/YACs described above such as MACs and PLACs.

Another aspect of the present invention relates to peptides, polypeptides and proteins which bind, interact or otherwise associate with the human neocentromere of the present invention or its mammalian and non-mammalian homologue. Preferably, the molecules are proteins, referred to
30 as primary (1°) proteins. The 1° proteins bind to the neocentromere and secondary (2°) proteins bind to the 1° proteins before or after association with the neocentromere. The identification

of the human neocentromere in accordance with the present invention provides a mechanism for assaying 1° proteins and 2° proteins which may be important for screening chromosomes in, for example, genetic disorders. This is particularly the use in Down's Syndrome which results from defective chromosome segregation.

5

The 1° proteins are readily detected by, for example, a gel shift assay. The nucleic acid molecule of the present invention defining the human neocentromere is digested, labelled and contacted with nuclear extract putatively containing the 1° proteins and resolved on a gel. When a 1° protein binds to a fragment carrying a binding portion of the neocentromere, the DNA fragment
10 migrates in the gel at a slower rate due to the bound protein.

The present invention extends to purified 1° proteins capable of association with the subject centromere and to genetic sequences encoding same and to antibodies thereto.

15 The neocentromeres of the present invention are readily identified and characterised using, for example, human fibrosarcoma cell lines. For example, DNA suspect of carrying a neocentromere, is introduced into fibrosarcoma cells in a linear form, generally together with a telomeric sequence. The cells are then screened for the presence of replicating, extra-chromosomal and segregating elements, referred to as mini chromosomes.

20

The present invention further encompasses eukaryotic cells carrying replicating, extrachromosomal and segregation nucleic acid molecules. Preferably the eukaryotic cells are mammalian cells and most preferably human cells. The nucleic acid molecules according to this aspect of the present invention are preferably as herein described. Particularly preferred cells are
25 HT-38, HT-47, HT-54, HT-190, HT-191, BAC/E8-1, and BAC/F2-14.

The present invention is further described by the following non-limiting Figures and Examples.

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EXAMPLE 1

YAC and Cosmid Probes for FISH

YACs carrying specific STSs were identified (Moir *et al.*, 1994) by PCR-based screening of
5 YAC libraries prepared in pYAC4 vector at the Center for Genetics in Medicine at Washington
University (Brownstein *et al.*, 1989) and at the CEPH (Albertsen *et al.*, 1990). Cosmid DNA
inserts (35-40 kb) were ligated to SuperCos I vector (Stratagene) and packaged with Gigapack
III Gold extract (Stratagene) according to the manufacturer's instructions. YAC probes were
prepared by Alu-PCR of total yeast genomic DNA using primers 5'-
10 GGATTACAGG(C/T)(A/G)TGAGCCA-3' [SEQ ID NO:1] and 5'-
(A/G)CCA(C/T)TGCACTGCAGCCTG-3' [SEQ ID NO:2] according to published method
(Archidiacono *et al.*, 1994). For probe labelling, 1 µg of the YAC PCR products or whole
cosmid DNA isolated by CsCl centrifugation or Qiagen column was used. The DNA was
labelled with Biotin-16-dUTP (Boehringer Mannheim) using a NICK translation kit (Boehringer
15 Mannheim). A probe mix of 6-10 µg/ml of biotinylated probe DNA, 300 µg/ml of COT-1 DNA
(Boehringer Mannheim), 500 µg/ml of carrier salmon sperm DNA and, where indicated, 10
µg/ml of biotinylated 10pC38 tag DNA was ethanol precipitated, resuspended in a hybridization
mix of 50% v/v formamide in 2 x SSC and 10% w/v dextran sulphate, denatured at 95°C for
5 min, preannealed for 30-60 min at 37°C to suppress repetitive sequences, before adding to
20 slides. FISH of α -satellite and satellite III probes was performed under low stringency as
previously described (Voullaire *et al.*, 1993).

EXAMPLE 2

Somatic Cell Hybrids and Other Cell Lines

25

Skin fibroblasts and transformed lymphoblast cell lines were established from patient BE
(Voullaire *et al.*, 1993) and from his normal parents. The presence of the mardel 10 chromosome
in the patient cell lines was confirmed by FISH. In addition to these cell lines, two somatic cell
hybrids were produced by fusing cultured fibroblast cells derived from patient BE with the
30 Chinese hamster ovary cell line CHO-K1 using polyethylene glycol. Hybrid cells were selected
in a proline-free medium for the glutamic oxaloacetic transaminase-1 (GOT-1) gene located in

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10q24-q25 region. One of the hybrid cell lines, designated BE2C1-18-1f, was shown to contain the normal chromosome 10 but not the marker chromosome, while another hybrid cell line, designated BE2C1-18-5F, contained the marker chromosome but not the normal chromosome 10 of patient BE. The presence or absence of these chromosomes was established by karyotyping and ANTI-CEN/FISH probing. In addition, PCR analysis of an STS (sequence tagged site) marker, AFM259xg5, which resided on YAC-3, confirmed the status of these chromosomes in the hybrids and excluded the presence of submicroscopic fragments of the marker centromere region within the genome of BE2C1-18-1f, or the presence of the corresponding region of normal chromosome 10 within the genome of BE2C1-18-5f. Use of this STS marker also demonstrated that the marker 10 chromosome has originated from the patient's father.

EXAMPLE 3

Antisera

15 Antiserum CREST #6 was from a patient with calcinosis, Raynaud's phenomenon, esophageal dysmotility, sclerodactyly and telangiectasia (a constellation of symptoms commonly referred to as "CREST"; Moroi *et al.*, 1981; Fritzler and Kinsella, 1980; Brenner *et al.*, 1981). Western blot analysis of this antiserum indicated that the primary antigens detected were human CENP-A and CENP-B. A specific anti-CENP-C polyclonal antibody, designated Am-C1, was produced by the
20 inventors by expressing a partial mouse CENP-C polypeptide (amino acid #41 to 345) as a GST-fusion product in *E. coli*, followed by gel purification of the product and its use as an antigen for antibody production in rabbit.

EXAMPLE 4

25 Preparation of Standard Metaphase Chromosomes for FISH analysis

Actively replicating transformed lymphoblasts were incubated at 37°C for 17 h in the presence of 0.1M final concentration of thymidine before they were centrifuged at 2000 rpm for 10 min, washed with pre-warmed RPMI, and incubated for a further 5-6 h. 15 min before harvesting, colcemid (10µg/ml) was added. Cells were harvested according to standard cytogenetic
30 techniques using 0.075M KCl hypotonic solution for 15 min at 37°C, followed by three fixative

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washes in ice cold methanol/acetic acid 3:1, dropped onto clean glass slides, and stored dessicated at -20°C until required.

EXAMPLE 5

5 Preparation of Mechanically Stretched Chromosomes for ANTI-CEN/FISH Mapping METHOD - I

This is an adaptation of the method described by Page *et al.* (1995). Colcemid (10 μ g/ml) was added to actively dividing transformed lymphoblasts for 2-3 h, before the cells were centrifuged
10 at 1500 rpm for 10 min, washed in PBS, and resuspended in 0.075M KCl hypotonic solution for 10 min at RT at a concentration of approximately 5 x 10⁴ cells/ml; the use of fewer cells here gave better stretching of the chromosomes. 200-300 μ l of this suspension were then cytocentrifuged onto clean microscope slides using a Cytospin 2 (Shandon) at 1000 rpm for 5 min at high acceleration. The slides were immediately removed, placed flat in a shallow dish
15 and very gently flooded with KCM (Potassium Chromosome Medium: 120 mM KCl, 20mM NaCl, 10mM Tris-HCl, 0.5mM Na₂EDTA, 0.1% v/v Triton X-100) (Jeppesen *et al.*, 1992). After 10 min at RT, immunofluorescence was performed without fixation (Earnshaw and Migeon, 1985; Earnshaw *et al.*, 1989; Jeppesen *et al.*, 1992; Jeppesen and Turner, 1993). KCM buffer was gently aspirated and 50 μ l of CREST#6 serum [diluted 1:50 in 1 x TEEN (1mM
20 Triethanolamine HCl, 0.2 mM Na₂EDTA, 25 mM NaCl), 0.1% v/v Triton X-100, 0.1% w/v BSA] was added to the cell area of the slide and covered with a parafilm coverslip. The slides were incubated for 30 min at 37°C, then washed very gently by flooding in 1 x KB⁻ [10 mM Tris-HCl (pH7.7), 0.15M NaCl, 0.1% w/v BSA), three rinses of 3 min each at RT. The primary antibody was detected with Texas Red-conjugated Affini-pure Rabbit anti-Human IgG (H&L)
25 (Jackson Laboratories) diluted 1:50 in 1 x KB⁻. 50 μ l was added to each slide, covered with a parafilm coverslip, and incubated for 30 min at 37°C. The slides were again gently washed by flooding in 1 x KB⁻ for 2 min at RT, before they were fixed by flooding in 10% v/v formalin in KCM for 10 min at RT, followed by three rinses of 3 min each in distilled water. If FISH was not performed the slides were rinsed in PBS and mounted in DAPI (0.25 μ g/ml) in
30 DABCO antifade mountant. [In experiments where CREST#6 and Am-C1 antisera were simultaneously used to label the centromere (Figs. 2B and C), the above procedure was

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followed except for the addition of Am-C1 diluted 1:100 together with CREST#6, and the Am-C1 antibody was detected using 1:100 diluted Donkey anti-Rabbit DTAF (Jackson Laboratories)].

5 If FISH was to be performed on the slides, they were then given a second fix in 3:1 methanol/acetic acid for 15 min at RT. The slides were air dried for at least 5 min and either processed for FISH or stored at -20°C for up to several days before continuing. For FISH, the slides were dehydrated at RT in 70%, 90%, 100% v/v ethanol (2 min each) and air dried. Chromosomal DNA was denaturated in deionised 70% v/v formamide/2xSSC, pH 7.0 at 82°C
10 for 8 min followed by immediate dehydration in 70%, 90% and 100% v/v ethanol at -20°C for 2 min each, then air dried for at least 10 min. (This high temperature of denaturation was critical to obtain maximum FISH signals). An amount of 15 µl of the prepared probe was added to each slide, covered with a 22mm² coverslip, and sealed with rubber cement. Slides were hybridized overnight in a humid chamber at 37°C, then rinsed in 2 x SSC at RT, followed
15 by 3 washes of 0.1 x SSC at 60°C for 5 min each, rinsed again in 2 x SSC, and immersed in a blocking agent of 5% non fat milk in 4 x SSC for 10 min at RT. Probe hybridization was detected by incubation with FITC-conjugated avidin at 37°C for 30 min, followed by three washes of 5 min each at RT in wash buffer (4 x SSC, 0.05% v/v Tween-20). Signals were amplified by incubating with goat anti-avidin D antibodies for 30 min at 37°C, followed by
20 three washes of 5 min each at RT in wash buffer, then with another layer of avidin-FITC for 30 min at 37°C, before the slides were washed in wash buffer, rinsed in PBS, and counter-stained with DAPI (0.25 µg/ml) in DABCO mountant.

METHOD - II

25

The following method was modified from that of Haaf and Ward, (1994). Actively dividing lymphoblast cells were treated with 10µg/ml colcemid for 2-3h, washed in PBS and resuspended in a hypotonic solution consisting of 10mM Hepes (pH7.3), 30mM glycerol, 1.0mM CaCl₂ and 0.8mM MgCl₂, at a cell density of approx. 2.5 x 10²/ml. After 10 min of
30 hypotonic treatment at RT, 300 µl were cytocentrifuged (Shandon - Cytospin 2) onto glass slides at 800 rpm for 4 min. The slides were immediately removed from the centrifuge, dried

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for 15 sec, fixed in methanol at -20°C for 20-30 min, rinsed in acetone at -20°C for a few sec, then washed in 3 rinses of PBS at RT. Immunofluorescence staining was done using CREST#6 at a dilution of 1:50 in PBS. After incubation at 37°C for 30 min, the slides were washed three times in PBS for 2 min each. This primary antibody was then detected by a further incubation
5 for 30 min at 37°C with Texas Red-conjugated Rabbit anti-Human IgG diluted at 1:50 in PBS. The slides were fixed in 10% v/v formalin in KCM for 10 min at RT, then washed in 3 rinses of distilled water and drained. Before FISH was performed, slides were fixed in methanol/acetic acid 3:1 for 15 min at RT and air dried. Chromosomal DNA was denatured in 70% v/v deionised formamide (pH7.0) in 2 x SSC at 82°C for 4-6 min. After dehydration in an ice cold
10 ethanol series the slides were air dried, and used for FISH as described for Method I. Slides could be stored covered in foil at RT after methanol/acetic acid fix for up to several weeks before FISH.

Both methods I and II were used to obtain the results shown in Figs. 2B, 2C, 3 and 4B.

15

EXAMPLE 6

Image Analysis

Hybridization signals for YAC mapping on standard metaphase preparations utilized a normal
20 fluorescence microscope. Images for the ANTI-CEN/FISH experiments were analyzed on a Zeiss Axiolab fluorescence microscope equipped with a 100x objective and a cooled CCD camera (Photometrics Image Point) controlled by a Power Mac computer. Gray scale images were captured separately using a LUDL filter wheel and controller for Texas Red, FITC and DAPI. These images were pseudocoloured and merged using IPlab Spectrum software from
25 Signal Analytics Corporation. A number of difficulties were commonly associated with the ANTI-CEN/FISH technique: (a) the deliberate "stretching" of the chromosomes, whilst increasing the resolution of mapping, sometimes caused serious distortion to the chromosomes, often making them quite dysmorphic; (b) FISH treatment following the ANTI-CEN-labelling often significantly reduced the ANTI-CEN signals; (c) more highly stretched chromosomes
30 (which would potentially give better mapping resolution) generally gave weaker ANTI-CEN signals; and (d) the ANTI-CEN signal on the mardel 10 centromere was usually weaker than

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those of the other human chromosomes. Thus, a cell would only be considered informative and used for scoring if both the p'- and q'-arms of the mardel 10 chromosome were discernible and separated by a discrete ANTI-CEN signal. In addition, FISH signals for both the test probe and the 10pC38 cosmid tag (used to identify the q'-arm of, and thus orientate, the marker
5 chromosome) must be clearly present. Using these criteria, the overall frequency of informative cells was found to be approximately 1 in every 20-30 metaphases analyzed.

EXAMPLE 7

Restriction Analysis of Patient DNA

10

High-molecular weight genomic DNA was extracted from cultured fibroblast cell lines of patient BE and those of his parents and digested with different enzymes to generate restriction fragments ranging from <1kb up to ~1 Mb. The digested DNA was resolved either on a standard agarose gel or by pulsed-field gel electrophoresis (PFGE) using a Bio-Rad CHEF-XA
15 Mapper. For filter hybridization, 50-100 ng of whole cosmid or PAC DNA was labelled by random priming. The labelled probe was then added to 2 ml of hybridization buffer (0.5M Na₂HPO₄, 7% w/v SDS, 1% w/v BSA, 1mM EDTA, pH. 7.0) containing 500 µg of human placental DNA (Sigma). The mixture was boiled for 5 min, then placed in a 65°C water bath for preannealing of repetitive DNA for 90 min. The preannealed probe mix was then added to
20 prehybridizing filters and hybridized overnight at 65°C. Post-hybridization washes were at a final stringency of 0.1 x SSC, 0.1% w/v SDS at 68°C.

EXAMPLE 8

Identification of a YAC region spanning the marker centromere

25

The initial search for DNA sequences spanning the centromere of the mardel 10 chromosome was based on fluorescence in situ hybridization (FISH) of existing cosmid and YAC clones (Moir *et al.*, 1994; Zheng *et al.*, 1994) that have been mapped to the q24 - q26 region of the normal human chromosome 10 where the new marker centromere was formed (Voullaire *et al.*,
30 1993) (Fig. 1A). This search led to the identification of a 4 megabase YAC contig (designated #082) that spanned the marker centromere region (Fig 1B). Fig. 1C graphically presents the

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FISH mapping results with selected YACs from this contig. As can be seen, two of the YACs (YACs-1 and YAC-2) mapped to the q'-side of the marker centromere, whereas the remaining YACs mapped to the p'-side of the centromere. The low signal level observed for YAC-3 was due to a large proportion of this probe hybridising directly on the centromere itself. These results, therefore, provided evidence that YAC contig #082 spanned the marker centromere, and that the centromere region was likely to be within YAC-3, where the "cross-over" between the q' and p' signals occurred.

10

EXAMPLE 9

Development of Improved ANTI-CEN/FISH Methods for the Simultaneous Detection of Marker Centromere and Single-copy Cosmid DNA Probes

Although normal fluorescence microscopy and FISH analysis of standard metaphase chromosomes were adequate for the initial identification of the YAC contig spanning the marker centromere, methods with significantly higher sensitivity and resolution were needed to allow further walking into the marker centromere DNA. Three requirements have to be satisfied by these methods: (a) the metaphase chromosomes have to be extended to offer much greater mapping resolution, (b) the centromeres have to be more precisely defined than that offered by a cytogenetic constriction, and (c) the methods should allow simultaneous visualization of both the centromere antibody and FISH signal. Two published methods were explored (designated here as ANTI-CEN/FISH methods) based on extending metaphase chromosomes by mechanical stretching and labelling of the neocentromere by autoimmune antibodies (Haaf and Ward, 1994; Page *et al.*, 1995). Since these methods were originally established for the labelling of normal centromeres and for FISH analysis of highly repeated DNA, they were modified (see Example 4) to allow detection of the generally reduced ANTI-CEN signal of the subject marker neocentromere and the lower FISH signals resulting from the use of single-copy cosmid DNA probes.

30 With the improved detection methods, the status of α -satellite and satellite III DNA on the marker neocentromere was reassessed, since this was previously determined using standard

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microscopy and FISH (Voullaire *et al.*, 1993). Fig. 2A shows the result of antibody labelling using CREST#6 and FISH using α -satellite DNA, and indicated the absence of detectable signal on the marker centromere. The same result was obtained when the experiments were repeated without ANTI-CEN-labelling, ruling out the possibility that the anti-centromere antibody might have obscured any weak FISH signals. Similar results were obtained with satellite III DNA. Since in separate reconstruction experiments, it was possible to demonstrate the sensitivity of the procedure in detecting a single-copy DNA probe of less than 1.5 kb, and making the reasonable assumption that the low-stringency hybridization conditions used for the α -satellite and satellite III DNA which, by virtue of the use of >100-fold excess of probes and the strong hybridisation of these probes to all the other centromeres, would have allowed the detection of any related sequences, it can be concluded that these satellite are absent.

EXAMPLE 10

Co-localization of CENP-C and CENP-A on the Marker neocentromere

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To test if CENP-C is present on the marker centromere, a specific rabbit polyclonal antibody was prepared against a recombinant product of mouse CENP-C. This antibody, designated Am-C1, reacted strongly with the centromeres of rodent and human chromosomes. Fig. 2B shows results for the labelling of stretched human metaphase chromosomes using this antibody simultaneously with the CREST#6 autoimmune antibody. As can be seen, irrespective of the degree of chromosome stretching, the signals for the two antibodies coincided fully on all the centromeres. The localization of these two antibodies on the marker chromosome was further determined by employing the 10pC38 cosmid tag in an ANTI-CEN/FISH experiment to identify the marker chromosome. The results indicated that both the antibody signals were clearly present and again coincided completely on the marker centromere (Fig. 2C, a-e). Although CREST #6 was known to bind CENP-A and CENP-B, indirect evidence suggests that binding to the marker centromere presumably occurred *via* CENP-A since the presence of the marker centromere was previously demonstrated not to bind CENP-B (Voullaire *et al.*, 1993). The above results, therefore, established the localization of CENP-C, and probably CENP-A, on the marker centromere.

30

EXAMPLE 11

Localization of the anti-centromere antibody-binding domain

For further walking into the marker centromere region, cosmid libraries were prepared from total
5 yeast genomic DNA containing YACs-2, -3, -4, -6, -7, -13, and -17. Cosmid clones containing
human DNA inserts were isolated by hybridization with human COT-1 DNA using low
stringency. All resulting cosmids were screened by standard FISH to confirm their localization
to the expected marker centromere and normal chromosome 10 regions, and to eliminate clones
that might have originated from other genomic sites due to chimeric YACs. Positive clones were
10 then analyzed further with the ANTI-CEN/FISH methods, using CREST#6 to label the
centromere. Fig. 3a (I and II) show examples of cosmid signals that mapped to the q'- and p'-
side, respectively, of the marker centromere in the ANTI-CEN/FISH experiments. The cosmid
tag (clone 10pC38) was used in these experiments to define the q' arm of the marker
chromosome. For cosmid walking, we concentrated on clones derived from YAC-3 since FISH
15 mapping of YAC contig #082 indicated that the marker centromere region was likely to be within
this YAC. Fig. 4a shows a restriction map of the region covered by this and surrounding YACs
and compares this map with a genomic map derived from patient BE. The relative positions of
a series of cosmid clones (including five independent PACs) were also determined and placed on
the YAC map. Fig. 4b presents the ANTI-CEN/FISH results obtained with a number of the
20 cosmid clones and one of the PAC clones. Clones Y3C64, Y6C8, and Y3C94 localized
preferentially to the q'-side, while Y13C1+C8 and Y17C6 localized preferentially to the p'-side
of the marker centromere, suggesting that the nucleus of the antibody-binding domain is situated
between these two cosmid clusters. Within this central region, a group of cosmid clones
comprising the HC-contig (Fig. 4a) was found to map closely around the ANTI-CEN signal. Fig.
25 4c shows a restriction map for eight different overlapping clones from this HC-contig. The
chromosomal positions of five of these overlapping clones were analyzed in detail using ANTI-
CEN/FISH. Fig. 4b shows the cumulative results for more than 60 informative chromosomes for
each of these five probes. The results indicated that Y7C14 mapped preferentially q'- of the
antibody-binding domain, while the remaining four clones (Y4C45, Y6C10, Y6C21 and Y3C3)
30 mapped preferentially to the p'-side. In addition, the results for PAC5 (a 75 kb-insert PAC clone
that overlapped with the p'-end of PAC4 by approximately 5 kb; see Fig. 4a) provided further

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evidence for the emergence of the HC-contig region onto the p'-arm. Based on these results, we conclude that the eight contiguous cosmid clones within the HC-contig shown in Fig. 4c, which together constitute ~80 kbp of DNA, have defined the nucleus of the antibody-binding domain of the marker centromere.

5

From the above ANTI-CEN/FISH results, it was difficult to determine if the sequences of the HC-contig and its surrounding DNA, both originally derived from a normal individual, were part of the marker centromere DNA, or whether these sequences simply flanked a transposed centromere DNA with an unrelated nucleotide composition. However, supporting evidence from the ANTI-CEN/FISH experiments suggested that the DNA of the HC-contig region appeared to be a part of the marker centromere. This came from the mapping of Y6C10 and Y6C21 onto superstretched chromosomes that were occasionally detected in the slide preparations. An example of such mapping is shown in Fig. 3b using Y6C21. As can be seen, whilst a significant portion of Y6C21 hybridized to the p'-side of the CREST signal on the highly extended chromosome, a substantial portion of the cosmid DNA also overlapped directly with the CREST signal. This suggests that at least part of the HC-contig region actually comprises the same DNA sequence as the marker centromere. This possibility was further investigated by detailed genomic mapping.

20

EXAMPLE 12

The Marker Centromere DNA has a Similar or Identical Sequence

Organization as the HC-Contig

The genomic organization of the HC-contig region was compared with that of the corresponding DNA region of the mardel (10) chromosome. Three overlapping cosmids (Y7C14, Y6C10, and Y4C7, the latter being essentially the same as Y6C21; Fig. 4C) from the HC-contig were used as probes to analyze the restriction patterns of genomic DNA prepared from patient BE and those of his karyotypically normal parents. Fig. 5 shows examples of the band patterns obtained with Y6C10, while Table 1 summarizes the results for all the enzymes tested with Y7C14, Y6C10 and Y4C7. The detection of a single band on PFGE gels with a number of the enzymes indicated that the cosmid DNA sequences were unique within the

30

human genome (*SfiI*, *SalI*, *KspI*, *KpnI* and *BclI* in Fig. 5A; Table 1). The detection of a single on PFGE gels with a number of the enzymes (*ClaI* in Fig. 5A; Table 1) could be explained by differential methylation of different restriction sites found in this region (Nelson and McClelland, 1991); the reproducibility of these multiple band patterns ruled out incomplete
5 digestion as a possible cause. The multiple bands detected with the more frequent cutting enzymes on a standard gel (Fig. 5B and Table 1) were a result of the presence of cleavage sites present within the probe DNA, since similarly digested cosmid DNA electrophoresed next to the genomic DNA yielded identical patterns for all the bands not containing cosmid vector sequences. In all, 37 enzymes were used to generate more than 160 different fragments for the
10 three cosmid probes (Table 1). The results indicated that, except for a polymorphic fragment found in one of the parents, an identical banding pattern was present in the genomic DNA of patient BE and those of his parents. Furthermore, when the restriction patterns obtained for the genomic DNA of patient BE were compared with those of the smatic hybrid cell line BE2C1-18-5F, which contained the marker chromosome but not the normal chromosome 10, no
15 detectable difference was seen between the two DNA preparations within the HC-contig region (Fig. 5C).

In addition to Y7C14, Y6C10 and Y4C7, a host of other probes from within or surrounding the HC-contig have been tested, each with an average of 12 different informative enzymes. These
20 probes included PAC4 (which spanned the entire HC-contig region shown in Fig. 4C), Y3C64, Y3C109, Y6C6, Y6C8, Y3C94, PAC1, Y3C90, Y4C4, Y4C8, Y4C13, and Y3C33. The results again indicated identical restriction enzyme patterns between patient BE and normal DNA. Thus, through the analysis of a relatively large number of probes covering about 500 kb of YAC-3 around the HC-contig region, and the use of a high density of restriction enzymes that
25 generated a range of fragments from <1 kb to ~1 Mb, it was evident that the marker centromere DNA and a substantial stretch of its adjoining regions showed no detectable difference against the corresponding genomic region of the normal chromosome 10.

Since a potential limitation of the above Southern blot analyses was that highly repeated
30 sequences were not detected because of the preannealing step used in the hybridisation procedure, a different approach was employed to compare the DNA of the marker chromosome

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and that of the normal chromosome 10. In this approach, oligonucleotide primers from different regions of the HC-contig were used to prepare a series of PCR fragments from the BE2C1-18-5F and BE2C1-18-1F hybrid cell lines. Electrophoretic comparison of such fragments, which randomly covered approximately 40 kb of the HC-contig, indicated no detectable difference between the two chromosomes and provided independent support for the results obtained in the Southern blot analyses. Thus, it can be concluded that the sequence organization of the marker centromere region is similar, if not identical, to that found in the HC-contig region of the normal chromosome 10.

10

EXAMPLE 13

Implications for Centromere Study and Mammalian Artificial Chromosome Construction

15 The mammalian centromere has been difficult to study due to the massive amount of repetitive DNA normally associated with it. By avoiding such repetitive DNA and analyzing the unusual centromere found in the present marker chromosome, the inventors have created a much more tractable system for centromere studies. The present analysis has already shed some light on the important question of DNA sequence versus conformational requirement of a centromere, and on the intriguing concepts of latent centromeres and epigenetic mechanisms. One urgent application of this DNA is to use it to identify the primary protein(s) which binds to the centromeric DNA. Another important application of the marker centromere DNA is in the construction of mammalian artificial chromosomes. Such artificial chromosomes offer a potentially powerful vehicle for the structural and functional analysis of chromosomes, for the genetic manipulation of plants and animals, and for the stable transmission of therapeutic genes in human gene therapy. The artificial chromosomes require a functional mammalian centromere, and the marker centromere DNA element of the present invention now provides a suitable centromere especially because of its relatively small size in the absence of α -satellite DNA and its cloning stability, as indicated by the cosmid, YAK and BAC clones of the HC-contig and NC-
30 contig.

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EXAMPLE 14

Sequence analysis

Figures 6, 16A and 16B show partial nucleotide sequences for the HC-contig (SEQ ID NO: 3)
5 NC-contig [SEQ ID NO: 4] and F2 (BAC/F2-14) [SEQ ID NO: 5-29] regions, respectively.

EXAMPLE 15

Human Artificial Chromosome (HAC)

10 The following are examples of the different approaches being used in the inventors' laboratory for the production of a HAC:

Retrofitting of HC-contig DNA from normal chromosome 10

15 This procedure aims to produce HACs of 100 kb to >1Mb using the region of the normal chromosome 10 containing and surrounding the HC-contig DNA. The generation of a HAC by this approach will provide crucial proof that this normal DNA region can be reactivated to form a functional centromere.

20 A retrofitting procedure suitable for introducing human telomeres to both ends of any YAC prepared in the pYAC4 vector in the yeast host strain AB1380 has been previously described (Larin *et al.*, 1994; Taylor *et al.*, 1994, 1996). YACs (in particular YAC-3 and YAC-5) spanning the normal HC-contig region are used for retrofitting by plasmid constructs designed to recombine with their pYAC4 vector arms (Figure 7). The construct pLGTEL 1 is used to target
25 the left arms of the YACs. This serves to add a LYS2 yeast selectable marker, gpt element for ultimate selection in mammalian and avian cell culture, and a human telomere. The right arm of the YACs are targeted by homologous recombination with pRANT 11 to produce a final construct where additional markers are introduced along with a second human telomere to cap the construct. Specifically, an ADE2 yeast marker is added and the URA3 gene of the YAC is
30 disrupted, serving a useful role in negative selection of the construct. A neomycin (neo) resistance gene shown to function in mammalian and avian cells is also introduced. The finished

constructs are transfected into different cultured cell lines, including HT1080 (of human sarcoma origin) (Larin *et al.*, 1994; Rasheed *et al.*, 1974), DT40 (a recombination-proficient chicken cell line) (Dieken *et al.*, 1996), and BE2CI-18-5f (a human/hamster somatic hybrid cell line containing the mardel (10) chromosome but not the normal chromosome 10).

5

In vitro cloning of HC-region into YAC/HAC vectors

The different vectors used for the cloning of the normal and mardel (10) centromeric DNA in the preparation of HACs are summarised in Table 2.

10

A number of different YAC cloning strategies are employed:

Conventional YAC cloning approach. Figures 8A-D show the different vectors used for cloning DNA as YACs by the conventional restriction/ligation methods. These YACs can then
15 be shuttled into mammalian cells and tested for HAC function.

ALU-ALU circular TAR cloning approach. Transformation-associated recombination (TAR) in the yeast *S. cerevisiae*, is a method for constructing linear and circular YACs from mammalian DNA (Larionov *et al.*, 1996a, 1996b). The recombination process is shown in Figure 9. Briefly,
20 the technique involves the use of a vector (pVC39-AAH2, Fig. 8E) lacking an autonomous replicating sequence (ARS) but containing a functional yeast centromere (e.g. CEN6) and selectable marker (e.g. HIS3), and two ALU DNA hooks to trap mammalian DNA by recombination at ALU sequences after co-transformation of linearized vector and high molecular weight DNA into yeast spheroplasts and followed by selection on medium lacking histidine. The
25 key to the process is that the mammalian DNA provides an ARS (11-bp sequence found frequently in mammalian DNA) which allows the HIS⁺/CEN vector to replicate as a circular YAC. These YACs are very stable and range in size from 100 kb to greater than 600 kb (Larionov *et al.*, 1996b).

30 pVC39-AAH2 vector is used to clone DNA from hybrid BE2CI-18-5f to make YACs with an average insert of 250 kb. This TAR vector is further modified to create pAAH-TCNa (Fig. 8G)

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so that it has the ability to shuttle between yeast and mammalian cells (as outlined in Figure 10), including the potential to expose human telomeres (TEL) at each end of a cloned fragment using a unique restriction site I-SceI.

5 ***Semi-specific and specific circular TAR.*** A modified circular TAR method utilising two specific 5'C and 3'C DNA hooks (300-700 bp in size) may be used to clone a specific human DNA at a frequency of 3/1000 HIS⁺ transformants. The inventors prepared the vectors pVC39-ALU/C3-F2(+/-) and pTCN-TCS (Table 2) to perform semi-specific and specific TAR cloning, respectively.

10

The Semi-specific TAR methodology is a modification of a specific circular TAR strategy which permits the site directed isolation of target chromosomal DNA. Furthermore, in accordance with the present invention, the methodology described herein enables the site-specific cloning of target chromosomal DNA from total genomic DNA as a circular YAC at relatively high frequencies and
15 without the need for the construction and extensive screening of complex libraries made from genomic DNA.

In a preferred embodiment of the present invention, the methodology employs a single specific DNA hook which flanks the mardel (10) chromosome and a less specific Alu-hook to trap the
20 other side of the target DNA.

In initial experiments, a unique repeat DNA-free, 1.4kb *EcoRI* fragment (designated C3-F2) was identified from the p' side of the 80-kb HC-contig (Fig. 11A) (du Sart *et al.*, 1997). This fragment was subcloned into the centromere-based yeast circular TAR vector, pVC39-AAH2,
25 by replacing the existing BLUR13 *Alu* (Larionov *et al.*, 1996b) to create the pVC39-ALU/C3-F2 constructs. As the specific orientation of the C3-F2 sequence on the chromosome was not known, the fragment was cloned in two different orientations, for which the (+) orientation (Fig. 11B) was expected to trap the genomic region to the left of C3-F2, while the (-) orientation was expected to trap the region to the right. Both constructs were used in yeast transformation.

30

As a source of genomic DNA containing the neo-centromere, a somatic hybrid cell line, BE2C1-

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18-5f (du Sart *et al.*, 1997), containing the mardel 10 chromosome but not the normal human chromosome 10 was used. 5µg of high-molecular-weight DNA from this cell line and 1µg of pVC39-ALU/C3-F2(+) or pVC39-Alu/C3-F2(-) (linearized with *Sma*I to expose the 0.21-kb *Alu* and 1.4-kb C3-F2 hooks) were co-transformed into 10⁹ (previously prepared and stored frozen) spheroplasts of *S. cerevisiae* YPH857 which carries a *HIS3* gene deletion, (Sikorski and Hieter, 1989) and grown on SD, without *HIS* medium, (Larionov *et al.*, 1996a;b) to yield between 10 and 100 *HIS*⁺ colonies. Control experiments in which YPH857 was transformed with vector alone did not produce any colonies, indicating that the C3-F2 fragment lacked ARS-like sequences. Twenty TAR experiments were performed and *HIS*⁺ colonies were picked into 96-well trays containing YPD medium (supplemented with 50µg/ml ampicillin and 15µg/ml tetracycline), grown at 30°C with aeration for 24h and stored in 20% (v/v) glycerol at -70°C. Total yeast DNA was prepared in pools of 48 (Kwiatkowski jr *et al.*, 1990) and screened by PCR with the primers norm 5 and norm 7 (Table 3) which are located 30-kb q' of C3-F2 (Fig. 11A). Two desired positive clones, designated 5f-52-E8 and 5f-38-F2, which contained the neocentromere DNA derived from mardel 10 and mardel (10) and the DNA immediately p' of the neocentromeric DNA, respectively, were identified. For subsequent studies, these clones were grown on SD without *HIS* medium and single colonies were re-isolated for characterization.

Initially, the sequence nature and sizes of the 5f-52-E8 and 5f-38-F2 insert DNA were determined. High-molecular-weight DNA was prepared in agarose blocks and digested with an enzyme (*Srf*I) that linearized with YAC (Fig. 11A). The linearized DNA, as well as uncut intact DNA, were resolved by pulsed-field gel electrophoresis (PFGE), transferred onto a nylon membrane and probed with radiolabelled PAC4, a P1-derived artificial chromosome clone containing a 120-kb insert that spans the entire HC-contig from normal chromosome 10, (du Sart *et al.*, 1997) following preannealing with human placental DNA to suppress repetitive DNA. The intact 5f-52-E8 and 5f-38-F2 remained trapped in the electrophoretic wells and the linearized DNA migrated into the gel and demonstrated a size of approximately 110 kbp and 80 kbp, suggesting insert sizes of about 105 kbp and 75 kbp, respectively (given that the vector size is 5.9 kb).

30

Despite the use of a genomic DNA source previously shown by sequence-tag-site (STS) analysis

- 40 -

to be free from normal chromosome 10 material, it is desirable to independently confirm the mardel (10) -origin of the 5f-52-E8 YAC clone. This was achieved using a set of primers (norm 17 and 18; Fig. 11A) that detected a variable-number-tandem repeat (VNTR) region within the HC-contig/neocentromere region. The results clearly indicated the presence of a 1.4-kb PCR
5 product that was specific for the mardel (10) chromosome (Table 3).

PCR was used to further compare the 5f-52-E8 DNA with the previously cloned HC-contig sequence derived from normal chromosome 10. PCR products with sizes ranging between 0.2 and 15.9 kb were generated by standard PCR or with the Expand Long Template PCR system
10 (Boehringer-Mannheim). Products greater than 1 kb were digested with frequent cutting enzymes, *RsaI* and *BsiXI*, and their fingerprints were compared by agarose gel electrophoresis. The results, shown in Table 3, indicated the absence of any detectable difference between the 5f-52-E8 DNA and those of the corresponding regions of the normal chromosome 10 (in somatic cell hybrid BE2C1-18-1f) and the neocentromere region of mardel (10) (in somatic cell hybrid
15 BE2C1-18-5f). These results also demonstrated that the YAC 5f-52-E8 spanned at least 75 kb of the HC-contig region (Fig. 11C), consistent with the size determined by PFGE. Furthermore, the ability of all the internal primers to amplify DNA from 5f-52-E8 strongly suggested that the YAC was not chimeric. This result was confirmed by isolating DNA from four single-colony isolates of 5f-52-E8, digesting these with *EcoRI* and *EcoRV*, and probing with radiolabelled
20 PAC4. The hybridization patterns obtained with these enzymes were consistent with those established in the previous study (du Sart *et al.*, 1997). Thus, this analysis, based on cloned DNA derived directly from mardel 10, has provided confirmation that the neocentromere DNA region is structurally identical to that of the corresponding HC-contig region of the normal chromosome 10 (du Sart *et al.*, 1997).

25

The circular YACs 5f-52-E8 and 5f-38-F2 were further retrofitted with the yeast-bacterial-mammalian cells shuttle vector BRV1 as previously described (Larionov *et al.*, 1997). The resulting BAC clones were designated BAC/E8-1 and BAC/F2-14, respectively (Fig. 11D).

30 The specific TAR strategy is outlined in Figure 12 and uses unique fragments from the HC-contig region, such as the ends of PAC4 (a 120 kb-insert PAC clone containing the HC-region)

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to create the YAC/HAC shuttle vector pTCN-TCS. An example of a YAC/HAC construct containing the HC-contig region of normal chromosome 10 is shown in Fig 13.

Completed constructs are transfected into different cultured mammalian or chicken cells (see
5 above) by lipofection using Transfectam or DOSPER.

In vivo "cloning" of HC-region into HAC vectors

This strategy employs a technique known as Telomere Associated Chromosomal Truncation
10 (TACT) (Fig. 14). The technique is based on the principle that cloned mammalian telomeric
DNA when reintroduced into a mammalian cell can seed the formation of a new telomere at an
intrachromosomal location. If the introduced telomeric DNA is targeted to a known site through
homologous recombination, integration at that location and subsequent truncation of distal
sequences on the original chromosomal arm can result (Brown *et al.*, 1994; Farr *et al.*, 1995).
15 This technique is employed in our own study to truncate the mardel 10 chromosome on either
side of the HC-contig/core centromeric DNA element to produce *in vivo* a stable HAC of
minimal size.

Figure 15A shows an example of TACT-construct used in our study. Key features of this
20 construct are: (a) Cloning of the pericentric human genomic DNA in both orientations (+/-). This
is necessary since we do not know the chromosomal orientation of this DNA. This DNA is used
to target the human telomeric sequences to locations on either side of the HC-contig region on
mardel 10. Genomic DNA is derived from several different sources including Y2C24, Y3C64,
Y3C109, Y3C94, Y13C12, Y13C15, Y17C6, Y17C8. The resulting truncation derivatives
25 produced using these genomic DNAs will vary in size accordingly. (b) The termini contain 2.4
kilobases of tandem repeat human telomeric DNA (htel). This DNA has been shown previously
to act as a substrate for mammalian telomerase to allow seeding of a complete telomere tens of
kilobases in length. (c) The hygromycin (Hyg) resistance gene allows for positive selection of
mammalian cell lines containing construct sequences integrated into the genome. This is the
30 initial screening procedure. In addition, some constructs contain the neomycin
phosphotransferase gene (Neo) rather than Hyg. (c) The Herpes simplex thymidine kinase (TK)

gene is used for negative selection against non homologous integration events into the genome. Those cell lines containing the TK gene can be selected against by adding the nucleoside analogue gancyclovir.

- 5 Figure 15B shows another example of TACT-construct used in our study. In addition to the features of the linearised construct shown in Fig. 15A, specific additional features are: (a) The incorporation of tandem telomeric blocks (htel.htel) since others have shown these to have the highest seeding efficiency of new telomeres in mammalian cells. (b) The incorporation of yeast selectable marker (eg. URA3), DNA origin of replication (eg. ARS), and centromere (eg.
- 10 CEN6), to allow transfer and maintenance of the resulting truncation derivatives into yeast. This should facilitate further characterisation and manipulation, such as the introduction of therapeutic genes for gene therapy purposes. (c) The relocation of the TK gene adjacent to the genomic DNA to increase the effectiveness of the negative selection system. (d) The human growth hormone (GH) gene has been included to allow proof of principle that human genes can be
- 15 introduced into a HAC and expressed under the control of endogenous regulatory elements. This is essential for gene therapy applications of the resulting HAC. (e) A CMV promoter upstream of a P1 phage loxP site (CMV/loxP) has been included to allow introduction of large human genes into a HAC *in vivo*. A plasmid containing a gene of interest, a second loxP site and a promoterless selectable marker gene is introduced into a mammalian cell line containing the
- 20 HAC. Transient expression of CRE recombinase results in recombination between the two loxP sites within the cell, thereby integrating the introduced plasmid into the HAC and placing the selectable marker gene next to the CMV promoter to allow for marker selection.

For chromosomal truncation, the above TACT-constructs are transfected into a somatic cell

25 hybrid line BE2CI-18-5f containing the mardel (10) chromosome. Positive selection is applied for Hygromycin or Geneticin resistance whereas negative selection is applied against the Thymidine Kinase Gene. Resulting colonies are further screened with distal p' and q' DNA fragments to ascertain the presence or absence of the two mardel 10 chromosome arms. In addition to the BE2CI-18-5f cell line, a human/chicken somatic cell hybrid line (derived from the

30 recombination-proficient DT40 chicken cell line; Dieken *et al.*, 1996) containing the mardel (10) chromosome will also be generated and used.

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EXAMPLE 16**Analysis of HAC**

Irrespective of which of the approaches described above is used, the presence of a new product
5 in a mammalian cell line as an extrachromosomal, artificial chromosome, will be assessed by
fluorescence in situ hybridisation (FISH) analysis, as well as tested by extracting high molecular
weight DNA to determine independently existing chromosomal entity on pulsed field gel. The
stability of the construct through successive cell division, both in the presence and absence of
drug-resistance selection, will be determined. The presence of the construct, in all or a high
10 percentage of the original transfected cells indicates stability. Demonstration of this stability
indicates the successful creation of a HAC.

EXAMPLE 17**Production of HAC**

15

This example describes the use of the neocentromere as a source of centromeric DNA in the
"bottom-up" approach to produce HACs in human cell culture. Bacterial artificial chromosomes
(BACs) containing cloned neocentromeric DNA and a selectable marker were co-transfected
with human telomeric DNA into human HT1080 cells to yield independent HACs that were
20 single-copy and stable in the absence of selection. The properties of these HACs, and their
potential utility as a new, improved vector system for gene therapy are described.

EXPERIMENTAL PROTOCOL

25 **Preparation of DNA.** Highly-purified BAC DNA was prepared using Qiagen columns according
to the manufacturer's instructions. Prior to transfection, BACs were linearized with *SgrAI* in the
presence of 2.5 mM spermidine and examined by pulsed-field gel electrophoresis. Human
telomeric DNA was gel-purified as a 1.6-kb *BamHI/BglII* fragment from pSXneo270T2AG3
(Bianchi *et al.*, 1997). High-molecular-weight genomic DNA was prepared from cultured cell
30 lines using standard methods (du Sart *et al.*, 1997).

Transfection of HT1080 cells. Transfection of human fibrosarcoma cell line HT1080 (Rasheed *et al.*, 1974) was performed using the DOPSER liposomal transfection reagent (Boehringer-Mannheim). The day before transfection, 6-well trays (each well is 962 mm²) were seeded with 3×10^5 HT1080 cells per well and grown at 37°C, 5% CO₂. Different combinations containing
5 1-2 µg of each BAC, 50 ng of telomeric DNA, 100 ng of each PAC-1, 4 and 5 (du Sart *et al.*, 1997) and 50 ng of human genomic DNA were prepared in 50 µl of HBS (20 mM HEPES, 150 mM NaCl) supplemented with 0.075 mM spermidine and 0.030 mM spermine. These DNA cocktails were mixed with 50 µl of 0.4 µg/µl DOPSER (diluted in HBS) and left at room temperature for 15 to 20 min. The HT1080 cells were washed with PBS (phosphate buffered
10 saline) and 1 ml of serum-free DMEM (Dulbecco's modified Eagles medium) was placed in each well. The DNA-DOPSER mixture was then added dropwise with swirling and the cells were incubated for 6 h. 1 ml of DMEM and 20% v/v fetal calf serum (FCS) was then added and the cells left for 24 h at 37°C, 5% v/v CO₂. The cells were harvested and seeded into 48-well cluster trays (each well is 100 mm²) containing DMEM-10% v/v FCS supplemented with Geneticin
15 (G418, Gibco-BRL) at 250 µg/ml. The media was changed every 3 to 4 days. G418-resistant colonies normally appeared 10 to 14 days after transfection. These colonies were expanded into duplicate 6-well trays, where the cells of one tray were stored frozen in liquid N₂, and the remaining cells were analysed by fluorescence *in situ* hybridization (FISH).

20 **Cell culture and mitotic stability.** HT1080 cells were grown in DMEM supplemented with 10% v/v FCS, penicillin/streptomycin, and glutamine. The mitotic stability of HAC containing clones was determined by growth in 25 cm² flasks in the presence (200-250 µg/ml) or absence of G418 selection, and grown to confluency (3-4 days) and split 1/5 and 1/10, respectively. Aliquots of each culture were harvested fortnightly and analysed by FISH (20-50 metaphases)
25 with BAC/E8 and/or BAC/F2 probes.

FISH, ANTI-CEN/FISH and PRINS/FISH. Fluorescence *in situ* hybridization (FISH) analysis of HT1080 clones was performed with BAC/E8, BAC/F2, and/or α-satellite DNA probes. Hybridization using the BAC probes were performed under high stringency whereas the α-
30 satellite DNA probes were used in low stringency conditions (du Sart *et al.*, 1997). ANTI-

CEN/FISH analyses involved an initial immunofluorescence staining step using a CREST antibody or specific antibodies against CENP-B, CENP-C, or CENP-E, followed by FISH using the probes described above, essentially as previously described (du Sart *et al.*, 1997).

5 Results

HAC construction strategy. The basic strategy involved the co-transfection of the 10q25.2 neocentromere DNA with human telomeric DNA into human cells. The neocentromere region is cloned as two, circular YACs in *Saccharomyces cerevisiae*. To facilitate handling and
10 purification of the cloned DNA in large quantities, these YACs are retrofitted into BACs and maintained episomally in *E. coli* as circular molecules. One of the BAC clones, BAC/E8, is 120 kb in size and has an insert of 105 kb that encompassed 70 kb of the 80-kb core NC-DNA region (Fig. 16). The second BAC clone, BAC/F2, has an insert size of 75 kb that overlapped BAC/E8 by 1.4 kb, and contains ~10 kb of the core NC-DNA while extending ~65 kb into the p'-side of
15 the mardel (10) chromosome (Fig. 16). The BAC vector backbone further contains the neomycin-resistance (Neo^R) gene to allow selection in mammalian cells. BAC/E8 and BAC/F2, used either on their own, in combination with each other or with additional DNA are used in the following transfection experiments.

20 Transfection of HT1080 cells. The human cell line HT1080 (Rasheed *et al.*, 1974) is chosen for the transfection experiments because of its near-diploid karyotype, its high level of telomerase activity (Holt *et al.*, 1997), and its demonstrated ability to form microchromosomes containing *de novo* centromeres from transfected arrays of α -satellite DNA and human telomeric DNA (Harrington *et al.*, 1997; Ikeno *et al.*, 1998). The resulting G418-resistant clones are analyzed
25 by FISH and classified into different categories of events.

Transfected cell lines are designated HT-38, HT-47, HT-54, HT-190, and HT-191.

Those skilled in the art will appreciate that the invention described herein is susceptible to
30 variation and modifications other than those specifically described. It is to be understood that the invention includes all such variations and modifications. The invention also includes all of the

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steps, features, compositions and compounds referred to or indicated in this specification, individually or collectively, and any and all combinations of any two or more said steps or features.

TABLE 1

Restriction analysis of the genomic DNA of patient BE and those of his parents using three overlapping cosmids that span the marker centromere.

	Y7C14	Y6C10	Y4C7
NotI	n.a.	910	910
BssHII	n.a.	815, 340	n.a.
BsiWI	n.a.	740	740
SalI	410	410	410, 540
Clal	315, 145, 110, 80	315, 145, 110, 80	315, 145, 110, 80
SnaBI	n.a.	250, 148	n.a.
NaeI	240, 210, 155, 120	240, 210, 155, 120	240, 210, 155, 120
NarI	222, 108, 70	222, 108	222, 200, 108, 70
EclXI	180	180	180
SfiI	170	170	170
KspI	168	168	168
AatII	165, 146	165, 146	165, 146
NheI	38	38	38
BstBI	n.a.	35	35
SmaI	n.a.	90, 40, 22	90, 40, 22
BglI	25	25, 7.2, 6.2	25
PacI	n.a.	25	n.a.
BamHI	24, 19, 15	24, 22*	24, 22*
KpnI	23	23	23, 19
BclI	21	21	21
PstI	9.4, 5.9, 5.1, 4.2, 3.8, 3.3, 2.9, 2.4	9.4, 3.8, 2.9, 2.7, 2.4, 1.5, 1.1	9.4, 7.1, 4.2, 3.3, 2.9, 2.7, 1.9, 1.5, 1.1
XbaI	14	14, 10	10
EaeI	n.a.	15, 12, 8, 6	n.a.
SphI	16, 7.5	16	16, 9
PvuII	14, 7.5	7.5, 6	7.5, 6
HindII	8.6, 6.9, 6.2, 2.7, 1.8, 1.2	6.9, 6.2, 5.6, 5.2, 5, 2.7, 1.9, 1.8, 1.7, 1.2, 0.6	6.2, 5.6, 5.2, 4.3, 2.9, 1.7, 1.2
ApaI	15, 8.5 11, 4.3, 3.9, 1.9, 1.5	15 11, 4, 3, 2, 1.9, 1.7, 1.5	15 10.2, 7.6, 3, 2, 1.9, 1.7,
EcoRI			1.5
HpaII	5.5, 4.3, 3.6, 1.6	6.9, 3.6, 2.8, 1.6, 1.2	3.6, 2.8, 2.5, 1.6, 1.2

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MspI	3.9, 3.0, 2.8, 2.5, 2, 1.6, 1.2	3.9, 3.6, 2.8, 2.5, 2.2, 1.6, 1.5, 1.3, 1.2, 0.9	3.6, 3.2, 2.8, 2.5, 2.2, 1.6, 1.5, 1.2, 1
SspI	n.a.	10	n.a.
XhoII	7.5	n.a.	n.a.
DraI	7.5	7.5	7.5
BglII	8.5, 6, 5, 4.7, 3.5, 2.5	6, 5, 4.7, 2.5, 1.6, 1.5, 1	7, 6, 5, 4.7, 2.5, 1.6, 1.5, 1.1, 1
AvaII	7.4, 3.7, 3.4, 2.8, 2.6, 1.8, 1.7, 1.4, 1.2, 1.1	3.7, 2.8, 2.6, 1.8, 1.7, 1.4, 1.2, 1.1, 0.9, 0.8, 0.5	4.3, 3.7, 2.8, 2.6, 1.8, 1.7, 1.4, 1.2
StuI	12.5, 8, 7.5	12.5, 9, 8.5	9, 8.5
HindIII	6.6, 5.4, 4.7, 4.4, 2.9, 2.5	5, 4.7, 4.4, 4.1, 2.9, 2.5, 0.7	5, 4.7, 4.1, 3.1, 2.5, 2.3, 1.9

n.a.= data not available. The values represent restriction fragment lengths in kilobases. Multiple values for an enzyme denote different bands detected by a cosmid probe on a gel lane. Since there were no detectable differences between the DNA of patient BE and those of his parents in any of the fragments (except for a BamHI polymorphic band found in one of the parents, indicated by an asterisk), only one set of values is shown for all three genomic DNA.

TABLE 2

Table 2. Vectors for cloning centromeric regions from normal chromosome 10 or mardel (10) DNA into yeast artificial chromosomes (YACs). These YACs can be shuttled into mammalian cells to test for function as HACs.

Vector:	Key Feature(s)	Map
pJS97ARTi	hTEL/I-SceI/yTEL, DHFR	Fig.8A
pJS98ANTI	hTEL/I-SceI/yTEL, neo	Fig.8B
Fragmentation 1	hTEL/I-SceI/yTEL, hyg	Fig.8C
Fragmentation 2 (-/+ hGH)	hTEL/I-SceI/yTEL, neo, hGH	Fig.8D
pVC39-AAH2	ALU-ALU TAR vector	Fig.8E
pTEL/CAT/TEL	hTEL/I-SceI/hTEL/neo	Fig.8F
pAAH/TCNa	TAR vector with hTEL/I-SceI/hTEL/neo	Fig.8G
pVC39-ALU/C3-F2(+/-)	ALU-specific TAR vectors	Fig.8H
pTCS	ends of PAC4 in pBS	Fig.8I
pTCN-TCS	specific TAR vector hTEL/I-SceI/hTEL/neo	Fig.8J

TABLE 3

PCR analysis of YAC 5f-52-E8 clone and comparison with the HC-contig/neo-centromere region from normal chromosome 10 and mar del (10)

Primer-Pairs ^a	<u>Genomic DNA used in PCR (product size in kb)</u>		
	BE2C1-18-1f ^b	BE2C1-18-5f ^b	YAC 5f-52-E8
norm: 141 + 55	1.80	1.80	not present
norm: 32 + 30	0.90	0.90	0.90
norm: 28 + 29	1.00	1.00	1.00
norm: 1 + 3	2.90	2.90	2.90
norm: 39 + 52	1.20	1.20	1.20
norm: 5 + 7	0.23	0.23	0.23
norm: 16 + 5	3.50	3.50	3.50
norm: 9+ 14	0.90	0.90	0.90
norm: 36 + 37	2.00	2.00	2.00
norm: 168 + 71	4.00	4.00	4.00
norm: 27 + 10	15.90	15.90	15.90
norm: 18 + 17 (VNTR) ^c	1.20	1.40	1.40
norm: 68 + 17	8.00	8.00	8.00
norm: 34 + 47	3.00	3.00	3.00
PAC4t7: a + b	0.30	0.30	not present
AFM259xg5: ca + gt ^c	0.21	0.19	not present

^a Refer to Fig. 1a for the relative positions of each primer-pair.

^b BE2C1-18-1f and BE2C1-18-5f are somatic hybrid cell lines containing the normal human chromosome 10 and mar del (10), respectively (2).

^c The 'norm: 18 + 17' and 'AFM259xg5: ca and gt' primer sets allow distinction between the normal human chromosome 10 and mar del (10) by detecting a VNTR and a microsatellite, respectively.

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SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: (US ONLY) CHOO, Kong-Hong Andy, DU SART, Desirée and
CANCILLA, Michael Robert
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(ii) TITLE OF INVENTION: A NOVEL NUCLEIC ACID MOLECULE

(iii) NUMBER OF SEQUENCES: 29

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGATTACAGG (C/T) (A/G)TGAGCCA

19

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

(A/G)CCA(C/T)TGCAC TGCAGCCTG

19

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(2) INFORMATION FOR SEQ ID NO:3a:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40917 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3a:

GAATTCTCCT GCCTCAGCCT CCCAAGTAGC TGAGGTTACA GGTGCCAGCC ACCACGTCCA	60
GCTAATTTTT GTATTTTAGT AGAGACGGGG TTTCACCGTG TTTGCCAGGC TGGTATCAAA	120
CTCCTGACCT CAAGTGATCT GCCTGCCTCA GCCTCCCAA ATGCTAGGAT TACAGGTGTG	180
AGTCACCGCA CCCAGCCCTT CTTTCAGTTC TATCACCTCT TTTTGCTATA TTTGTATGAG	240
AGCTTTATTA TTAGGGGCAC ATACATTTAA AATTGTTATG TCTTATTGAT AGATTGATCT	300
GTCATTATGA ATGTCTGTAT TCATTCCCTG ATAGTATTTT TTTTCTAAA TATTTTCTG	360
AATGTGTCTG CTATTAACAT AGCCACTCTG GCTTTTTTAAA ATTAGTATTT TTATGGTATA	420
TATTTTTCCT TTTTTTTTTT TTTAAGTTT AGATGTTATG TTTCTTATA CTAAAGTGG	480
GTGTCTTATA GGCAGCATAT ATCTGGGTCT TGATGTATTA TTTAATCTGA TAATCTCAAC	540
CTTTTGTGTT GAGTGTTTAG GCCATTTACA TTTAGTGTA TTATAGACAT GGTGTTGATTT	600
GCTATACCAT CTTTTCATTT GTTTTATATG TGAGCCATCT TTTCATTGTT CTTTTTTCAT	660
CTTTGACCAT TTTCTTTAGT ACTGAATACT TTTTTTGTAT TTCATTATAT CTATTGGCTT	720
TTTAGTTATA CCTCTTAAAA TTTTTTTTTT TGTTTTATGT AGGATTTATA ATATACATCT	780
TTAACTTATC ACAGATTACC TTCAAATAGT ATTTTACCAG CTCAAGTGTA ATGTAGAAAC	840
CTTACAAGAG TATATTTTCA TTTCTGTCTC CTAATTTTTA TGCTATGTCT ATAATACATT	900
AGGTTTGTG TTGTTTGTTT TTACCTTATT GCTGTTGGCT GGGGTCAGCA AACATTTTCT	960

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GTAAAGGGCT AGATAGTACA GGCATACCTT GGAGATACTG TGGGTTTGGT TCCATACCAC	1020
CACAATAATA CAAATATGCA AGAAGTGGAT ATCACAATAA AGTGAGTCAC ACAAGTCTTT	1080
TGGCTTCCCA GTGCATATAA AAGTTTGTCT TATACTACAC TGTAAGTCTGT TAAGTGTGCA	1140
ATAGTGTTAT GTCTAAAAA ACACATACCT TAATTTTAAA ATGCTTTATT ACTAAAAAT	1200
GCTAACAATC ATTTGAGCAT TCAGTGAGTT GTAATCTTTT TGCTGGTGGA AGGTCTTTTC	1260
TTATTGATGA CTGATCGGGG GTCAGGTGCT GAAGCTTAGG GTGGCTGTGG CAGTTTCTTA	1320
AAACAACAGT GAAGATTGCA ATATCAGTTG ACTCTTCCTT TCATGAAAGA TTTCTCTCTA	1380
GTGTGTGATG CTTTTTGATA GCATTTTATG CACAGTAGAA CTTCTTTGAA AATTGGATCA	1440
ATCCTCTCAA ACCCTGCTCT GCTTTAACAA CCTAAGTTAA TATAATATTC TGAATCCATT	1500
GTTGTCATTT CAACAATTTT CACAGTGCTT TCACCAGGAG TAGATTCCAT CTCATTTCTT	1560
GAGATGGAAT CTTTGCTCAT CCATAAGAAG AAATTCCTCA TCTGTTCAAG TTTTATCATG	1620
AGATTGCAGC AATACAGTCA TGTCTTCAGG CCTCACTTCA CTTTAAATTC CAGTTCTCTT	1680
GCTGTTTCTA CCACATCTGT GGTTCCTTCC TCCATTGAAG TCTTGAACCT CTCCAAGTCA	1740
TCCATGAGGG TTGGAATCGA CTTCTTCCAA ATTCCTGTTA ATATTTATAT TTTGACCTCC	1800
CATGAATCAT GAATGTTCTT AATGGCACCT GGAATGGTGA ATCCTTTCCA AAAGGTTTTTC	1860
AATTTACTTA GTCCAGATCC ATCCATCCAG AGGATCCACT TTCAATGCCA GTTATAGCCT	1920
TATGGAATGT ATTTCTTCAA TAATAAGGCT TGAAAGTTGA AATTACTCCT TGATCCATTT	1980
TCTGCAAAAT AGATGTTGTG TTAGCAGGCA TGAAAGCAAC ATTAATCTTT TTGTACATGT	2040
CCATCAGAGC TCTTGGGTGA CCAGGTATAT TGCCAGTGAG CAGTAATACT TTGAAAGGAA	2100
TTATTTTCT TAGCAGTAGG TCTCAACAAT GGGCTTAAAA TATTTGGTCC ACCATTCTGT	2160
AAACTGATGT GCTGTCATCT AAACTTTGTA GTTTCATTTA TAGAGCACAG GCAGAGTAGA	2220
TGTAGCATAA TTCTTAAGGG ACTTAGGATT TTCAGAATGG TAAATGAACA TTGGCATCAA	2280
TTTAAATCAC TAGCTGTATT AGCCCCAAC AAGAGAGTCA GCCTATTTTT TGAAGCTTTG	2340

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AAGCCAAGCG TCGACTTCTC CTCCTGGTT AAAAAAGTCC TAAATGGCAT CTTCTTCCAA	2400
TATAAGGCTG TTTTATCTAC ATTGAAAATC TGTTGTTTAG TGTAGCCACC TTCATCAATG	2460
ATACTATCTA GATCTCTTGG ATAAC TTGTG CAGCTTCTAC ATCAGCATTT GCTACTTCAC	2520
CTTG TACTCT TATGTAATGG AGTGGCATCT TTCCTCGTAC CTCATGAACC AACCTCTGCT	2580
AGCTTCCAAC TTTTCTTCTG TAGTTTCCTC GCCTCTCTCA GCCTTCATAG ACTTGAGGAT	2640
AGTTAGAGAC TTGCTTTGGA TTAGATTTTG GCTTCAGGAA ATGTTGTGGC TGGTTTGATC	2700
TTCTATCCAG ACCACTAAAA CTTTATCCAT ATCAGCAATA AGGCTGTTTT GCTTTCTTAT	2760
TATTTGTGTG TTTACTGGAG TAGCACTTTT AATTTGCTTC AAGATATATT TCTTTGCATT	2820
CACAACTTGG CTGACTGGTG CAAGAGGCCT AGCTTTCAGA CTATCTTGGC TTTTGACATG	2880
CCTTCCTCAC TAAGCTTAAT CATTTCTAGC TTTTGATTTA AAATGAGAGA TGTAGGCCAG	2940
GCACAGTGGC AGGCACAGTG GCATATGCCT GTAATTCCAA CACATTAAGA GGCCAAGGTG	3000
GGAGGATTGC TTGAACCCAG GAGGTGGAGG TTGTAGAGAT CACACCACTG CATTCCGTCC	3060
TGGATGACAG AGCAAGACCT TTCTCAAAAT AAAATGAGAG GTGTGCTTCT TCTTTTTGTT	3120
TGAGCCCATA GAAGCCATAG TATGATTTTT AATTGGCCTA ATTTCAATAC TGTTGTGTCT	3180
CAGAGAATAG GGAGGTCTGA AGAGAGGGAG AGAGGTGGGG GAATGGCTGG TCAGTGGAGC	3240
AGTCAGAACA CACATAACAC TAATAAATTG TTTGCTGTCT TATATGGATG TGGTTTGTGA	3300
TGCCCCCAA CAATTACAAT AGTTACAGCA AATATCACTG ATCACAGATC ACCATAACAG	3360
ATATAAGAAT CATGGCAAAG TTTGAAATAT TCTTGAGAAT TAGCAAAGTG TGACACAGAG	3420
AAACAAAGTG AGCACATGCC GTTGGAAAAA ATTGGTGTG ATAGACTTGC TCCATCGCAA	3480
GTTTGCCATA CGCCTTCAAT TTATAAAAAA CACAATATCT AGGAAGTTCA ATAAAGTGAA	3540
GTGCAATAAG ATGAAGTATG CCTGTAAATA TTTCAGGCTT TCCAGACCAT AGGGTTTCTG	3600
TTGCAACTGC TCACCTCTGC CATTATAGCA TGAAAGCAGC TATAGAAAAT ATACATAAAT	3660
GAGGCCTGTA ATCCCAACAC TTTGGGAGCC CAAGGTGGAT GGATCACTTG AGGTCAGGAA	3720

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TTTCGAGACCA	GCTTGGCCAA	CATGGCAAAA	CCCCGTCTCT	ACTAAAAATA	CAAAAATGAG	3780
CCAGGACTAC	GCATGCCTGT	AGTCCCAGCT	ACTTGGGAGG	CTGAGGCAGG	AGAATCTCTT	3840
GAACCCGGGA	AGGGGAGGTT	ACAGTGAGCC	AAGATTGTGC	CACTGCACTC	CAGCCTGGGC	3900
AACAGAGTGA	GACTGTCTCA	CAAAAAAAAA	AAAAGGAAAA	GAAAATACAC	ATAAATGAAT	3960
GTATGTGGCT	GTGTACCAGT	ATATCCTCAT	GCTCTAGCTT	GCCAACCCTT	GCTTTACACT	4020
GTCAGTTACC	TTCTAAAGAG	ATTAAAAATC	ATAACAATAT	CTATTACGTT	TATTCACATC	4080
CTAGTGTCAT	TTCTTCCTTA	TGTAGAATCA	AATTTTCATC	TGGTATCATA	TTTCTTCTTT	4140
CTAAATAATT	TCCTTTAATA	TTTTTTTATAG	CACAGGTCTA	ATAGCAATGC	ATTATGCAAT	4200
TCATTGCTAT	TAGACCTGTG	CTATAAAATA	GCAATGAATT	ATGTCAGTTT	TTATTGTCT	4260
GAAAAAGTTT	TTTGTTTTTG	AAATATACTT	TTGCTGGGTA	TATAAATCCA	TGTTGCATAA	4320
CTTCTCTTTT	CTTCAGCACT	TTAATGAAGT	CACTCAGTTA	TCTTCTGGCT	TGTATAGTTT	4380
CTCTGGCTGC	CTTCAAGATT	TTTTTCATTGT	CTTTAATTTT	TAGCAGTTTG	ATGTGTCTAG	4440
GAGTGATTTT	CTTTGTATTT	ATCCTTTTGG	GGGCCTCTTA	ATTTCTTTGA	TCCTTTTTTT	4500
CTTTTTTTTT	TTTTTTTAAT	CAGTTTTGGT	CTGTCTCCTC	AAGTGGGCTG	AAAAAAAAAG	4560
AAAAATAAAA	TCATAGTTTA	AAAAACTAAT	TTTGGAAT	TTTCAGCTAT	CATTTCTTCA	4620
AATATTTATC	CTACTCTATG	CTCCCCCTCCT	CCCCTTTCCCT	TCTGTGACTC	AAATTACAGG	4680
TATATTTAAC	CATTTTATTT	GTTACGGCA	CTTGATGCT	CTGCTTTCTT	ATTTTTTGTC	4740
TTTCATTTTG	GATAATTTCT	ACTGACCTAT	CTTCAAGTTC	ACTGATTCTT	TTCTCAGTCA	4800
TATCTAGTGT	GCTCAACGCC	TGTTGAAGAA	ATCCTTTGTC	TTAATATCA	TGTTTTTTAT	4860
TTCTAGCATT	TTCATGTAAC	TCTTTGTTCT	GGTTTCCATC	TCTCTACTCA	CTTTTTTTTT	4920
TTTTTTTTTT	TTTTTTTGAG	ACAGAGTCTC	GCTCTGTCAC	CCAGGCTGGA	GTGTAGTGGC	4980
GCGATCTCGG	CTCACTGCAA	CTCCCGTCCC	CTGGGTTCAA	GTGATTCTCC	TGCCTCATCC	5040
TCCCGAGTAG	TTGGAATTAC	AGGTGCCCAC	CACCGTGGCT	GGCTAATTTT	TGTATTTTTT	5100

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TAGTGAAAC	AGGGTTTCAC	CATGTTGGCC	AGGCTGGTCT	TGAATTCCTG	ACCTCAGGTG	5160
ATCCACCTGC	CTCAGCCTCC	CCAATTGCTG	AAATTACTGG	CATGAGGCAC	TGCACCCAGC	5220
TCTGCTGACA	TTTTTTATCT	TTTGCTGCAT	TTTGTCTACC	TTTTCCATGA	AATCCTTTAA	5280
CATAGTAGTC	ATAGTTACTT	TCAATTCCTT	GTCTGACAGT	TCTGACATTC	AAGTCTAGGT	5340
CTGTTAATAG	CTTTGTGAGT	CTGTTAACAG	CTTTTTTTTCA	TTCTTGCTCG	TGTGTTTTGT	5400
ATTTCTTGAT	TGTATGCCAA	ATATTGCCTG	TAAAATAAAC	TTAGATAAGT	CATACTTCTA	5460
TCCAGAAATA	GGCACATTTT	TTGTGTCCAG	TCATTAGTGT	GGAGGGAGGT	TGGGGCAGTC	5520
TAGTCAGTGG	CTGAAGTAGG	TTTGGATTTG	TTGATGCTAT	ACTTAGAATG	CACCAGACTT	5580
CCATTCACTG	CAAGAGTGGG	CTGCTGCGCT	TTGTGATTCA	TGTGAGGCCT	GAATTGTGGG	5640
TTTTTCCTTA	GTGTGTCCCT	CCATGCTCAG	ATTTTCAGCAA	GTCTTCATAT	CTGTGCCACA	5700
GAAGGAATCT	GACCCATGCT	CTTTTGTACC	TCCCCAAGTG	ATCAACTGTT	GCTTGTTATA	5760
GCTTGTCATG	GAGTAAGAGG	GTGTTTTTTT	AGTTTTTCATC	CTCCAGCCTT	GGTCTTGGGC	5820
CCTGAGCTCC	TAGACTCCAG	GAGTGGATGG	AATCCAGTGA	TTTCTCAGTA	ATTCAGCCCC	5880
TTCTCCAGTA	GTGGCAGATC	TCTGCTTTGT	ATCAGTGCAA	GATCCTGGGC	TGAGCTCATT	5940
TTCTGCCCTT	CCTCGAGTGG	CAGACAGCTC	TTGCTTTCAC	CCTTCTACCA	AAGGCAGTGC	6000
ATCTTTTCTT	GGGCCTCTCC	CCATTGAACT	TATGACTTTC	ACATAAGAGA	AGGGCTCATG	6060
TATCAGAGAA	TTCTGTGACT	TTGTGCCACA	TACAGAGTCT	CTCAGTTCTC	TTGCCCTGCC	6120
CCAGTCTTTT	TTGTGAGCAC	CTAGTAGAGA	CCCTTGAGGA	AGAGCAAGGA	AGCGAGTATG	6180
GACTTCTTTT	GTGTCTGTCT	ATTGCTTTGT	TTCTCAACTG	CTACTCTTGG	ACTTTAAGAA	6240
TTTCAATAAAA	TTTCAGCTGT	TTTCTTTTAT	TCTTTTTTGT	TTTCTTTTTT	TTTTTTTTTT	6300
TTTTTAGATG	GAGTCTTGCT	CTGTTGCCCA	GGCTGGAGTG	CAGTGGTGTG	ATCTTGGCTT	6360
GCTGCAACCT	CCGCCTCCCG	GGTTCAAGCG	ATTCTCCTGC	CTCAGCCTCC	CAAGTAGTTG	6420
GGATTACAGG	TGCCCCACCAC	CACACCTGGC	TAATTTTTGT	ATTTTATAGTA	GACACAGGGT	6480

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TTCACCATTT	TGGTCAGGCT	TGTCCTCAAAC	TCCTGACCTC	ATGATCTGCC	CGCCTCAGCC	6540
TCCCAAAGTG	CTGGGATTAC	AGGCATGAGC	CACCGCGCCA	GGCCTCAGCT	GTTCTCTTTT	6600
TACCTGCTGG	GATGGCTAGT	TTTCTGTGTC	AACTTGACTG	GGCCATGGGA	TGTCCAGATA	6660
TGTAATTAAA	CAGTATTTCT	GGGTGTTTCT	GTGAGGGTGT	CTTCAGAAGA	GATTTGCATT	6720
TGAATTGGTG	AACTAAGTAA	AGCAGAGGGC	CCTGTCTAGT	AGGGGTAGGC	ATCATCCAGT	6780
CTGTTGAGGA	CTTGAATAGA	ACAAAAGGCA	GGGGAAGGTT	GGAATTGCCC	CCTCTCTGCT	6840
TGAGCTGAGA	CATCTATCCT	GCCCTTGGCA	CTCCTGGTTC	TCAGGGGTTC	AGACCTGGAT	6900
TCCTGGTCTC	CACCTTGCCC	ATGGCAGACT	GTGGGACTTC	TCAGCCTCCT	ATCTAATTAA	6960
TAAATCTCTT	CATACACACA	CACACACACA	CACACACACA	CACACACACA	CACACACACA	7020
CCCTATGTAT	CCTTCTGTTT	CTCTGCAGAA	CCATATCTAA	TACACCTGCT	TTTATGACGA	7080
TTACCTATCG	ATTCTGTATT	CTGCCAAAAC	TGAAAACAGT	TCATTTTTCC	ATCTCTTCTC	7140
AGAGAGGCTT	GTCAGCCATT	AGTTCTCTGA	TGGGCTCAAG	AAGTTATGCA	GTTTTTTTTT	7200
TCTCACTGTT	AGGATGGAAT	TGATATTCTG	TTGAACTTTT	CTATACCTAA	GTGGAACTT	7260
GTTTTGAGGT	TATTTTCTCT	ACTTACTTTT	GCTGGAAATG	GAACACTCTG	TATCTAGTTA	7320
AGACACATAA	ACTGACTTGT	GATACCATAA	TGTTGTGTTG	AATTTTATAT	TCTTAGAAAA	7380
TCATCTGTCA	AGGTGTTAAC	TAATGGCAAA	GCATTTAATA	AATCAGCATT	CATGTATTCA	7440
GGTGCTCTGA	ATTATCTGAC	TTTTAAATTC	TTACTTTATA	AATGAGAAAA	TTGGGGCATG	7500
GAAAAGTTAA	CTCTCCTAAC	CCCGAATTAT	TACATTATTA	AGGACAGGAC	TTAGAGGCCA	7560
GATATCTTAA	GTCATTAATA	TTCTTTGGCT	CACAGAATTG	GCAGTATAAC	CTAAAGGTAA	7620
TAAC TAGGTG	ATTTTCTTTT	ATATCAATTA	AATATGTCAG	TTTTCAAATA	TTCATAAGTA	7680
CCTACTGTGC	AGGGAAAGAA	CATGCCATAC	AAAAGATGTA	GTCCAGGCCT	TTAAGAAACT	7740
TTCATTTAAT	GGGAAC TCAA	GAAGTG TACA	TATAAGGAGG	GAAGTAGCAG	TATGGTACAA	7800
GATAATACAT	ACATATCAGT	GAATGATATT	GCCAAAAAGT	GCTATTGATA	GAGAAATAAT	7860

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TCATTTCTGC AACAGCTGC TGATCTCCTA CTGAAAACAG AGGAGGGAGA ACAGGACGCC	7920
TCGTGGTCAG GATAGAAGAG AAAGACCTTG AGTTGAGCCT TGAACAGTAT TTAATATTCA	7980
AAAGGTTAAG AGAGGAGAGC AATTGAGGAG GGGAGAATAG TTCCAGCACA AATGATGGTG	8040
TACAAGATGA ACACAGTCAG TAAAGAGCAG ACTGGTCTGG ATGGAGAGGA GGATTTGCAT	8100
CATTTGGGAT TACGTCATTT AGACCCTTGA AAGCCAGGAT TGAGTAAAGC CACAGTGAAG	8160
CGACTGGCTC GTATGGAAGC TTTATTTTAA GAAGATTAAT CTGGTAGTGA CATGTGCCAA	8220
AAACTGAATA GGTAGAAATG AGATGCAGAG AGCCAGTTA GAACTAAGTC TGGTGCAGTA	8280
ATGCAGGATT GAGGCAATAA ACACCAAAT ACAGTATCAC CAGATAATGG ATGTTTGAAC	8340
GGACGGTTTA AAGGAAAATT GATGGTATTT GGTAATTTAT TAGATAATCC AGGGCCATGG	8400
AATGAGAGGG GAAAATGACT AACCATAGTC ATCAATGGT TTTTCTTAAT GAATCTGAAT	8460
TTTGGTGTA GAGCAACATT TTCTTAGGCC TTGCCTAGTT GGTACAGCTG ACTATGATAA	8520
TGACTGCTAC CATGCTTGTT CCTCTTTTAG CAGCTGTGAG TCCCCACCA GCCAAACAAT	8580
GAGCCTCTTG AAAAGGACGA TGCCTTTTCA CTTCTCTCCA AGTGCTTGGC AAATAGGAGG	8640
CCTTTTGAAG TTACTTTATA GTTAGGGGTT CCCAGTGAGT ATTTGAAATA TTAAGTCATG	8700
CCCGTGGTTG ACAGCATGGC CCTACTGCTC ATCATCAGCT ATTAACCTTA GGCAAGTTAA	8760
TGAACTTTTC TAAGCCCCAG TCTACTCATT TATAAAGTGG GATTATTAAT AATGTCTACT	8820
TCATAAAATT ATGAAGCCTG AGTTAGGTCA TTCAGATAGT GTTTAGTCTG ATTCTTCGAA	8880
CCTAGTAAAC AGTCAGTAAA CAGAAGCAA TGCCACATGC CTGATTTATA TCCAAGGGGA	8940
GAAAGGTAAA AGTGAAATTT TCATGATTTA TGGATTCAAA TTATACATTT CAAAGATGCT	9000
TTATAAGCTA TTGTTTTGGT AAGAAGAATT GAGCTGAAAC AGAATTTTCT GACAGCAGTG	9060
ATTATTAAAT GGTGAAATAG GCTATTGATG TCTTTAGAGG ATATAGATGT TCACCTTTTG	9120
CATATAAGTG CACAAAAATT CACTAAGTAG ATATGTCGTG CTACACAGAG AGAGAGAGCG	9180
TGAGAGCATT AAAGTTAGTA AACATCCCCC TCGCTTTTTT TTTTGTGAGA CAGGGTCTTA	9240

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CTCTGTTGCC TAGGCTGGAG TGCAGTGGTG CAATCGTGGC TCACTGCAGT CTCAACATCC	9300
TGGGCTCAAG CGATCCTCTC GCTCAGCCTC CTGAGTAGCT GAGGTGTGCA CCACCACACC	9360
CGGCTAATTT TTAAATTTTT TTATTGTAAA GGTGAGGTTT CACCATGTTG CCCAGGTCTC	9420
AAACTCCTGA GCTCAAGCAA TCTGCTCACT TCAGCCTCCA AAAATGCTGG GATTACAGGC	9480
GTGAGCCACC ACGCCTGGCC AGTAAACCCC ATTCATTTAC ATCATCTTAC TTGTCCCTCC	9540
AAAATCCTGC AAAGTAGGTA GGTTCGTCTT TTATTTGTTA TTTAGGTGAA GAACTTGAAG	9600
TGGTGTGAG GAATAGGTGT TTTGCCAAGA GTCACGCAGC TGGAGTGGCA GAGCTGTATA	9660
CTCTTCTGAT TCCACCAACG CTGTTTACAT CACATCTGGA GAAAAGTGCT CTGAGGCACA	9720
GATGTTTAGT GGGAGGGATG AGACACAGGC TGCAATGCCT AAAGATAATC GGAATAAAAA	9780
GCAGAAAACA AGACGTTTGT TTCTGTAAAA ATGAGACAGA AAATAAGGCG TTTGTTGTTT	9840
GGGATTGAGC ACTTGAGAGAA GTGGGGAGCG ATTTGATTTG GGTGAGACTG CTCCTGGAAT	9900
GCTGCATCTG GTTCTGGACT ACTCATTACT AGGCTTATAG AAAC TAGCTG GAGGAGGTTT	9960
AAAGAAAAGC TCCAAAATGA TTAGCGGGCT GACGGGATTG ATTTATAAGA AATATTAAAA	10020
GAATTAAATG TGTATAGCTC AGCTAAGCAA AGATGAAAGA GACCAGCTAA ATGTATACAA	10080
ATATCTGAAA CGTGCAAAC TTA AAAAGAG AGATTAATTA TTTAACATGA TACACGGGGG	10140
CACAATATGC AGTCACAGGA TGAAAATTTT AGCTGAGTAT CTAGAAGAAT TCCCCGATAG	10200
TGAATCTGTT AAGGCTGTCT GTAGTGTGGC CTTTCCCTGG AGAGGCAATA GAAATTTC	10260
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ACAGTAAGGA AAGAAAGGAA GGAGGAAGAA AAGAAAGGAA GGGGAAGAAA GGGAAAAAGA	10500
GGCAAAGAAG GAAGAGAAGG TAAGAGAAAG AAAAAGAATG AAGGAAGAAG GCTGGGCACT	10560
GTGGCTCATG CCTATAATCC CAGCATTTAG GAGGCCAAGT TGGGAGGATC ACTTAATTAA	10620

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GCCCAGGAGT TCAAGGCTGC AGTGAGCTGT GATTGCGCCA CTGCACTCCA GCCTGGGTGG	10680
CAGAGTGAAG CCCTGTCTCT AAAAAAAAAA AATAAGTTAA AAAGAAAGAA AAGGATAGAT	10740
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TCCTCTTCAG TCTTCTTTAT GTATGTTTGC CAACTTTCAT AATAACAAT TTAAATTATA	10860
TTTTCCTGAT CAAAACCTAG TAGCAGTATT AATCCCTGGG CTTCTGACT AGAACAGCCT	10920
CATTACCACA TGGGCAGAGT TCTGGCCGAC CAGGGACCAC GTAGTGGTTC ACCATCTTGC	10980
TCTGGTAATG TGGTCTGGGC TGAAGGGCCC TTTCTAAGGT TGTAGATAGA AATCCAGGAA	11040
ACTTGTTAGA ACTGCAGACC TATCAGGGTA CCTGCAGGAG GTGAGTCTAC TAAGGTGAAA	11100
AAGCAGAGGG CAGAGGTCGT GATTAGCAGC TGACCGCCCC CTGCTTTTCT GTCCCTCATT	11160
CGTGGAAAAT TGAGTGAGC TCAATTTTGA GTGGAGCTCT AAGTAGCTCC ACTTGTAGAC	11220
ATTGAGTGGA GCTCTAAGTG TCTTCAGAAT AGCAAAACAC TAGTTTTCTT TTTCTTTTCT	11280
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GATCTCCGCT CACTGAACTC TGCCTCCCGG GTTCAAGCGA CTCTCCTGCC TCAGCCTCCC	11400
GAGTAGCTGG GATTACAGGT GCCCACCACC ACGCCAGCT AATTTTCCTA TTTTGTAGTAG	11460
AGATGAGGTT TCACCGTGTT GGCCAGGCTG GTCTCAAACCT CCTGGCCTCA AGTGATCCGC	11520
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ACCCTATTTT TCTTGAATGG AGAAACACTT TCCCCTTATT TATTGAGTTT GGGAAGCAAG	11640
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GCTTAATTTT TTTAAGGAAG AATTTTTTAA ACTATCTTCT TTTGAGCCTC TTTAGGAAGA	11760
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CTTATGTCTG CTTTTTGTG TGTTAGAGAA ATATAAATAT TTTATCTAGG TTTTGCTGAT	11880
GGCAGTCAAG CATGAACACA ACCCACTGTT TGAGAAGCTG TAATTTCTGA ATTTCTGCAG	11940
AGTGACATC TAGGCCAGCA AATGGCAGTA AGAGTGAGGT GGATTTAGCT CAGTGTAAGG	12000

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ATGAACTCCA GAACCATCGG CTCTGACTGA AAGTGAAGCG GCAGCCGCGT TGTGGGAAAG 12060
CTGGCTGGAG TCTCTCTCAT AAGCAGGCAT TCTTTTTCTC CAGCCCGTCA CTGTGTTGGT 12120
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GCACCTACAG GGACTCCATC CCTTGTGCCC CACATACCTC ACACGTAGAC ATTCTTAATG 12300
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ATCAAGCAAT CCTCCACCT CAGCCTCCCG AGGAGCTGGG ACCATAGGCA CGTGCCATAT 12540
GCCCCGTTAA TTTATTGTAA TTTTGTAGA GATGGGGTTT CATCGTGTG CCCAGGCTAG 12600
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GCTTTCCAC CAGACTGCGG GCTCTTCAAG AGTAAATGCC ATGTTTTAC CTTTATTTCC 12780
CCAGTTTGTG GCACATTCTA GGCACTCGCC ATCATGAAAT AAACCTCTGG AGCTGTGATA 12840
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ATTCAGCATG ATTTATTGAC TGCCCAAATC TGGGCTGCTT CCTGTCTGTG GTTCAAGGAG 12960
AGCATAGTCT ACAGAACCAG AGACCTGGCT ACTCTGGAAG TTAGACTTAA GCCACCCCG 13020
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AATCCATGAA AGAAACAAGA TGGTATATAA CTTTTCTAA TTTGTGATGC CTTTGTTTAT 13200
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AATAAGAAGC ATCTTAATAT AACTAGACTG GACATCTGTC CCATTTTCAA AAATTACAAG 13320
TTTCGATCAT TGCTAAATTG TACAGATCCC AATCTGTCTG CTCTGCATAC ATTTGCATTT 13380

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ATAAAAGCAG AAGCAGACTA GCAGTCTTTC TAATGCAATC CCCCAAATGC ATGAAGTATT	13440
AGATTGCTTC TCCCTATTGG TTCATGCATT GCTAAAGGCT TAAAAGGATC ATTGATTTTA	13500
ATTATTTAAT GTGTACAGCA GGCTGAGCTT CCTTCTTTT TTAAGGGAAG AACCTTCAGG	13560
GGCATTGCTT TAGTTTTTTA ATGTTAAATC TCATTTTCTT TTGAAAATAA GAAGTTAAAG	13620
CTGTATTAC ACAAGCTCTC AAAGTGCCAG ATTTTCATTG TGTTTTTAAA CCATCTAGGA	13680
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ATATTGTTAT AACTTCACAT GATTCCAGTG TTGTATTATT ATTTTTTCTT TTTCTTTTTT	13800
TGACCCGATA TAGATGAAGC GAAGAGACAA GGAGCAATCC CATGTGTAAT AGAAAAAGGC	13860
AGCCTGAATT GTTGTGCTG TTTTGAAT TTAAGCTGGT TTTCGATTAA ATTCAGTAAA	13920
TGGTCCAGGA CTATAAATGT TGAACATTTT TTACCGTGTG ATTTAAATTT TAGTCTTATT	13980
GTTTTTTTTT TTTTGATGG TTTACATTTT CCCCATGGGA AGCAGCTATG TCATGTCGGC	14040
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TGCCAAAAAT AAAGAGTGGT TTGTGATGTC TAGTGTGTCT TCCTTTAACA AATCAAAGGC	14160
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AGAAGGCAGG TACTATGATG TAAAAAGTTT AGGTGGGGGA TTAATAGAGT GATCATATAA	14280
TTTATGAGCT AAACCGGAGG CACTTTTTTT TTTGAGATCG AGTCTCACTG TTGCCTAGGC	14340
TGGAGTGCAG TGACGTGATC ACAGCTCACT GCAACCTCCG CCTCCCGGT TCAAGCGATT	14400
CTCATGCCTC AGCCTCCTGA GTAGCTGGGA CTATAGGCGC CCACCACCAT GCCCAGCTAA	14460
TTTTTGTTT TTTGTAGAG ATGGGGTTTC ACCATGTTGG CCAGGCTTGT CTCAAACCTCC	14520
TGACCTCAGG TGATCCGCCC ACCTCGACCT CCTAAACTGC TGGGATTACA GGCCTAAGCC	14580
ACCATGCCTG GCCCAGAGAC ACTTTTGAGA GTGAAGAGGA AGCTGAGAAT AATTCCTGA	14640
TCTACAACTG GGACCATCCA GGGCAAGCCA GATGCCATTA CCACTAGCTA GAAAGCTTGC	14700
CAAGGTCTCA TTTACCTTGG TATATAGCAA ATTCTTCTTT TGAATTCTGG AAATCTGGT	14760

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AAGTCATTGA GGTAGCTCTG TGCCAAGGAG CAATATGGTA GAATTCTAAT ATTTCAGGCA	14820
GACAACACTT TCCTGCATTT GTAGCAGGTA AAGGGAGGTC AGGGCAGAAG ACAAACCAC	14880
TGGGACTCGA CAAAGGGCAT AAACGTCTAA TGCACCTGAT GTAGCTGATG GTAAATTGTT	14940
ATCAGCTAAA GATCTTTCAT AATAAATAAA CTTATCATTT GTAGGAGGGC ACAGAAATCG	15000
TGGAAAGCTG GGATTCAGGT TGCCTGTGGC TTTAATTCTG GAATCAGAAA TATTAGTCAA	15060
GGATATCAGT CTATGAAGTA AGTTTTCAAT GTTATATGCC ACAAGATGCA GCTGTCCTAT	15120
TTTCACTTCC AGTAATTCCT TCTGAATTAA TACACCTTAA AAATAGCTGC AGCTTCTCAA	15180
ATCTGTGAGA ATCGTATGTG CTGCTTGCTA CACTTTCTTT TTCCTGAAGG CTCTTTGAGG	15240
TCTTTCAAGA ACTCAATTCA ATTCAGCAAC AATTAGGGGG TCTAAGGTAT ACAGACGCTG	15300
TGCAAGATGC TCCTGAGACA CAAAGAGGAG GTCAAGCCCC TGCCTTCAGG CACCTCTCTA	15360
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TACATACATT AAAGCCAGGT GGTAGGTGTA AGAAGATTTG TAACATGAGA ATTTTCTGCA	15480
TGTTTGAAAT ATCTTATAAT TTTTAAAAAT TAAATGGGA GATACATATA TATGTATTTA	15540
TGTATGTATA TATGTATGTA CATATACACA CATATATACA TAAATATATA CATAAATATG	15600
TATATATGTG TATATAGACA TAAATATGTA TATATGTGTA TATATACATA AATATGTATA	15660
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TATAGACATA AATATGTATA TATGTGTATA TAGACATAAA TATGTATATA TGTGTATATA	15840
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TATGTATATA TGTGTATATA GACATAAATA TGTATATATG TGTATATAGA CATAAATATG	16020
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TATACACACA TATATACATA CATAAACATT CTGCATTATA CCATTCACTT TGTAACCCAT	16140

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CTTCCCTAAA AACTGTCTCA TAAAGAGTCT TCTTTTCCCT GTACCTATGC AATGGTAAGT	16200
AGCAAAACAC ACATTCTTTT GGGTCCCCAT AACATTCCCT GTAGTTTGCC CTTAACAGTC	16260
TTTGATGTGA AATTTACTGT TTCTGTCTTA ACCTTGCCCTG TCTCGCGTAC ATGGAGTTTT	16320
GGCTCCTGGC TCCTAGTCTG CATCTTCACC CCATCCCTTG CCCAAAGAAT CTGGTTATGT	16380
GACCACTGCT CATCTTTTCT GCTGCCACAA CTCCAGTCCA AGCCACAAAC CTCTCTCTCC	16440
TGGACTCCTG CGGGGAGTTC CTTTCTCTCC CTGCATGAGT CTATTCTCCG CACAACGGC	16500
ATAGGTAAGT GAGACTGCGG AAGAGGCAAG TTTGCAAGTC CAGAGGAAAT GAAGACTCTG	16560
CTTGTCACA TGCTGGGTTT GACGGGTGCT GGATATCCGA TGGATGGCCC TTAAGGTGAG	16620
CTCAAGGCTT AAGGGAGAGA TAGGGGCTGA TGATCTGAGA TTCATCAGTG TGTGGCTGAT	16680
GTTTAAACCC AGGGGACAGG ATAAGAAGGT TATTCCAGGG AGAGCGTAGA TAAAGAAGCT	16740
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GAAAGAGTAG ATTCTGGGA CTCACGGGAT AAAGACTTTC AAAAAGTGGG GGCTGGCCAG	16860
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AATACTTACT GAACAGTTAC TGCATGCCTG GCACTGTAAC ACCCTGTTTA ATTCTCACGG	17100
CAACCCATA GAGTAGGTGT CATCATCCCC ATCTTACAGA TGAGGATATG AGGTGCAGCT	17160
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CGGATGGGCT GATCCCAGAG CTCATGCTTT AAATCGCTAG ACTGGTGCTC ACAGAAGACT	17280
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GACCCATGAC AGCAGAGACA GTGAGCTGGT AAAGTGGCTG GCGATCTAGC CCCTGAAAAT	17460
ACCTCCAGAG AGGCAGGCTC ACGCCTGTAA TCCCAGCACT TTGGGAGGCC GAGGTGGGCA	17520

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AAAAATACAA	AAATTAGCCG	AGCATGGTGA	CAGGCACCTG	TAATCCCAGC	TGTTTCAGTTG	17640
GCTGAGTCAG	GAGAATAGCC	TGGATCCGGG	AAGTGGAGGT	TGTAGTAAGC	CAAGATTGCG	17700
CCACTGTCATG	CCAGCCTGGG	CGACAGAGCA	AGACTTTTCT	TAAAACAAAC	AAACAAAAAA	17760
GAAAAAAGAA	AAGGAAAGAA	GAAAGAGACA	AAGAAAGAAA	GAGAGAAGGA	AAGAAAGGAA	17820
GGAAGGAAGA	GAAGGAAGGA	AGGAAAGAAA	GAAAAGGAAA	GAAAGAAAAA	GAAAGAAGAA	17880
AGAAAGGAAA	GAAAAGAAAG	AAAAAGAAAG	AAAGAAAATA	CCTCCAGAGA	GCCAGGTCTC	17940
TTAGGCCTTC	TGAGAAACTC	ACATCCCTTT	TGATGAACAC	AAATGCTTCA	CACTCTCAAT	18000
GTTATTGGTA	ATCCAAGTTA	TCAATATACC	TAAATCACTT	AGTACTGAAT	CTGGCATATA	18060
GTAATCACCT	AATGAAGAGA	TAAGAGTCAT	GGAGTATTCT	GAAGCAATTA	GAATCAATAG	18120
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GTAAGAACAC	ATACAAATAG	ATACATGTAT	ATTAAATATA	CTCGAACGGT	TACCTATGGG	18300
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CGTAGGTCTT	CCACTTGCAC	TCAGCTTTAC	AATGTTGGAC	TATCCTTCAG	ATGGCACCTT	18540
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CAGGGAATAA	GTATAAAAAA	AGGCACGGTG	CTCCCTGGGT	AGCCTTTCTG	GACTTCAGAG	18660
CTAAATTGCA	AAGTCAGTTT	TACACATGTG	ATTTTCATCTA	TGAAATTAGG	GCAAGGTAGA	18720
AAACTGGCAC	AGAAAAAATG	TGATTTATTA	TGGTGTTACT	ATCCCTTACA	AGCGGAGTGT	18780
CAGCTGCCTC	TTTTTGTTCA	CTGATTTAAG	GCAAGATGAA	CTGAAAGTGG	CTATGATCAC	18840
GTCTTCAAAA	GCACACTCTG	GCCCCTCGGC	TGCAGGCGCC	CTGCACATTC	CCCAGCTGCG	18900

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TGTCGGTGG	TGACACAGTG	CATAATTGTG	GCGCCTTCCT	GGTGCAAAC	GTCTCACTTA	18960
GCTCCGTCTT	GCTGGCACAG	CAGAAAGGAA	GAAATCGAAA	ATGTTTGGAT	TTCAAAGGTA	19020
ACAAGAAGCT	GGAAAACAAC	TACTGGCCGA	GTCTGAGAGT	TTCAGCGGAG	ACTGGTGCAG	19080
CCTTGTTGTTT	TTCCACTGAC	AGCTGAAAAT	GAGCCCAGCT	TCAGTGAAGC	TTGTTTCCTT	19140
CCCTCCTCAA	GGTTACCCAC	AATTCTCAGT	TCTCTCAGGA	AAGCCAAAAA	ATGAATTTGA	19200
GGGTTTAGGA	TTGTGGTTCT	TTTATCTATT	ACAGGATTGA	TAATATGTTT	CTCCACCAGA	19260
TGTTCTGCTT	GTAACAATAC	TCACCTCCTG	ACACTACTGC	ATATGCAGGA	GTGTTACTAC	19320
CAAGGTAAAC	ACAGAATTGG	CTGCCCAATT	CCAAATCCCT	GAACTGAGTG	AGAGAAATCA	19380
GAATTATAAT	AGGGGATTCA	ACAGAGCTGG	CTACGGATGT	GCCAGTGGTC	AGATACTTTG	19440
CTCATCATAC	GCAGGTGCTG	CTGCTCTAGC	AACTGCTCAC	TGCTTCATTT	CCTGCCTTGG	19500
TCTTTAAATA	CTGCTTTTCT	CAGCTCAATT	GGCTTTCTTC	CCTCTGGCAG	TCACGTTTCT	19560
TTGGGTCAAA	CAGCAAATGA	TTCTTTAGAA	TCACCTGGTA	CTCAAAGGAG	CTACAAGACA	19620
TTGGGCATCC	ACTTCCACTC	TCTTGGAATA	ACAATTTTAT	GGAAGCCAAG	GTTGCCATAG	19680
TGCCTCTTGA	GGTTGTTTGC	TCAGCCAAGG	CCCAAGCTTT	GTGCTTCAAA	CATGAAATTA	19740
GAGAGCTTCA	GAACAAGATC	CACATTTTCA	ATGGCCTCAC	CCAACTGGAT	AAAAGAACAA	19800
TTGCCATATC	TCAATGACCA	CCTTTTTCAG	GTGGGATGGT	AGATGCTGGA	ATGGGTCACA	19860
GCATTGCCCA	ACCAAACCTT	GCAAAAAAGG	CTGGAAGCTC	TGACTGGGGA	CCCTAAATAT	19920
GCAAAAGTTG	ATAGGCTCTT	CATGCAGAAT	ATGAACCCCG	TGTATGGATA	TAGCTAAAGG	19980
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TTAAAAATG	TCAACAATTG	CATTTATGAT	GCTGTGTATA	GTAACCTACA	GATCATGCTC	20100
CATGAAAATG	CTTCAGAACC	CAATATAAGG	AGATTTTTTA	GCCATGTGTG	ACAAAAGAGA	20160
GGCCATTTCA	GTGTTGAAAT	TGTTTCAGAG	AGTATTTGAT	TATGTTTTCT	CAGATCTTTT	20220
TATTTTTATT	TTTTTTGAAA	CAGAGTCTCA	CTTGTGCACC	CAGGCTGGAG	TACAGTGGCT	20280

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GTGGTCTCGG	CTCACTGCAA	CCTCTGCCTC	CCAGGTTCAA	GCGATTCTCC	TGTCAGCTTC	20340
CCGAATAGCT	GGGATTACAG	GCGCATGCAC	CACCATGCCT	AATTTTGTGA	TTTTTAGTAG	20400
AGACAGAGTT	TCGCCATGTT	GACCAGGCTT	GCCTTGAAC	CCTGACTTCA	GGTGATCCAC	20460
CCACCTCAGC	CTCCCAAAGC	ACTGGGATTA	CAGGCATGAG	CCACCGTGCC	CAGCCTGTTT	20520
TCTCAGATCC	TGTATTTGTT	TCTGAAGCCT	TCATTTCTAT	CTTCTTATTC	ATTTTGGAAG	20580
TAGTACACCT	AAGTAAGGTT	TTTAACAATC	AAATATCTTT	GGAAAATTCC	CTGGTTCCTT	20640
TCTTATTCCT	ACAAAAATAT	GTTCAGTATA	GCTGATGTTA	TGTTTCTTTC	AAATTATTCA	20700
TTTCTCTATC	TCAGAATTTA	TCTCATGCCT	AATTGTTATT	GAATAGTCTT	CACTTCTTGT	20760
CATCCAGTTT	CTGGTCTCTT	ATTTCACTCT	AAGTCTAAGT	GGCTATTAGA	ATAAAGAGCT	20820
TGTAACAGAT	TCTTCTCCA	ATATGTCTTA	TCTTTTGACT	GCATGCCAGT	GACAACTGT	20880
TAAGTGTGTT	GATTCTTCAT	AACATTCAC	AGAACATGCT	GACTCCTCTC	TTCCTGAAAG	20940
CAATGCCCAA	GCACAGCATT	GTTAGATAGT	ATGTACGCAA	CAGGGACATG	GGTGCATAGC	21000
AAAAACTAGA	AGGAAGGAGG	ACCTTCCTTA	GCAATGGGTG	ATATGGTCCC	TGGACTTAGA	21060
CTCCAAAGGG	TCGTGAGGTG	AAACACACAT	CGTCCATACC	CAGGAAGCAC	ACAGGTGGGA	21120
TGGAAGAGCT	GTGCCTAATG	AACTTCATC	CACGTGGAGG	TGGAGGAGGC	TGCAGCTGCA	21180
AGAACTCAGA	GCTGCCTTAC	CCAGACCAGG	GACCAGGGAG	GGCTTTCTGG	AGGAAACAGC	21240
CTCTGAACTG	CCAGCTGATA	GAGGAGCTCT	ACCTCAACTC	TTCTGGTTCC	CCAGGGCTGC	21300
TTTCCACGT	CCATTTATTG	GCACTGAAAGT	TTGAATACCT	TCAGGGGCCC	GAAAGCCTGC	21360
CAGGTCTCT	TCTCTGCAGA	GCAATCACAC	CAACCTGCAA	AGGGCTAGGA	AAGGGCTGTC	21420
ATCATCTCCT	ACTCAGAAAC	TGGTTCACTG	GAAGGACTCA	GGGGCCACTG	AATACATCCT	21480
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TTTCTCCTTC	TCTTAGAGTT	TGGAGGACGC	AAATGTGCTG	AGAAGTCAAC	CTTCTCTGCA	21600
AGGTGAGACA	CAAGGGCCTT	TCCCAGCAGA	AAGAAGAGAG	CAAATGGAAG	GTCTTCTTTC	21660

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CTCCAGTAGA	GGATGGACTC	TGTCTGGCAG	CCACCCAACA	GGAAAAGCAC	AATGCATGCC	21720
TGCCTGCTTC	CCTCCCTCCC	TCCGTTTCTC	CCTCCCTCCC	TCCTTCCTCC	CTTCCATTCT	21780
CTTCCCTTCC	CCTCCCTTCC	CTTCCCTTCC	CTTCCCTTCC	CCTCCCTTCC	CCTTCCCTTC	21840
TCCCTCTCCT	TCCCTTCCTC	TTCCCTTCCT	TCCTCTTCCC	TTCTTTTCCC	CTCCCTTCC	21900
TTTCCCTTCC	TCCCTCCCTT	CCTCCCTTCT	TTCTTTCCCT	TCTTTCCCTC	CTCATTTCCCT	21960
CCCTTCCTTC	CTTCCTTCCT	TCCTTTCTTC	CTACTTTCCT	ACCTTTAGGG	CTCTGTGTCT	22020
TTGGAGTCCA	TTCTGATTAT	GCTGTAATGT	CTGCCCTTTC	CTCTTCTCTG	TCAAAAAATG	22080
AAAGACATGG	AAGCCACTTG	CCTTTTACTG	AATTAAAAAT	TAGTAAAAGA	GCTAAAAATT	22140
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TCTTAATTAA	AAGCTGACAG	GGAGGGAAAC	AAGAAAAGAG	AAACACAAAA	CAATAATCTA	22260
AATGACCTAT	TAGTTGGAAG	AACAACATCA	GAGAAAATAG	ATACTGTGTA	TAGTCATGTG	22320
TATGTCTATG	GAATAACATT	TGTAGAGAAA	TCTGGACTGA	TCCTTTCTGA	GTAAAGAGAG	22380
CTGTGGGTAC	AATTAAGGGG	AGATTGAAAG	GAATCCAAAA	GCATAGCAGA	TGCTGTGCCT	22440
CACTGGAATG	GTTGCCGATC	TCCTCCAAAC	TATGAAGTGT	TTGAGGCTCA	ACTTTAATAT	22500
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CTTCTCTGTT	AAAAAAGGAG	CTTGTGCTAT	AGGAGGTTTA	AAATATACTT	CTGACCCATC	22680
TCCAACATTC	TAAATCCTTC	CCAGAAAAGT	ATGCCAATCC	CAAGAAATAT	TCAATCAAAT	22740
TGCTGGAAAG	AAAAATACAA	AATATTAAAA	TGTATTAGGA	AGCGACAGTA	ATTAAATCAG	22800
AACTGGAGCA	GGAATAGACC	AGCAGATCAA	TGAGACAGAC	ATCAAGTCCC	GGAATGTGGA	22860
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AAAAATTAAT	CTTATAATAA	TTGATATTGC	AATAATTGTC	TAGTAATTGG	GGGAAGAAAT	22980
AAGCTTATTC	CTTATCTCAT	TTCTTTTTTT	CTTTTTTGAGA	CAGAGTCTCA	CTCTGGTAGC	23040

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CCAGGCTGGA GTGCAGCGAT GCGATCTCTG CCCACTGCAA CCTTGCTCTC CCGGGCTCAG 23100
GCGATTCTCC CACCTCAGCC TCCCGAGCAG CTGAACTACA GGCCTGTGCC ACCACTCCCC 23160
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TGAACCTCTG GGCTCAGGCA ATCCACCCGC CTTGGCCTCC CAAAGTGCTA GCATTACAGG 23280
CATGAGCCAC CGCGCCTGGC AGCTCATTTT TTAGACTAAA TAAATTGGAG ATGGCTAAAA 23340
GATTTCTATG TAGGCCAACT ATGTTTTTAA AAAGTTTTTT TTTTAAGGAT ATCTGCTGGA 23400
ACCAATCATG CCACCAACCA AAGATGCAAG ACTATAAAAC ATACCCAGTT TTTCAAAGCA 23460
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CTCATTTTCAT CCTCAAGGAA CCATCTGAGG CAGGCACTGT TATCATCTCC ATTTTACAGA 24360
TAAGGAATAG ACCCAGAGAG GCTGAGCAAC TGGGCCTATT CCACAGCTAC TATGGTGGAG 24420

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ATGAGATTTA AATCTAATCA TTGGCTCCAG AGCCCATGCA CCCAATGGCT GCACTAAGTG	24480
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GGTGGTATCA GGCAGCAAAC AGGCTGCTAG TCGAAATCCC ACTTCTTCTC TGAGTGGTCC	24660
ATACAGTTTT ACTCTACTTG CTTACAGAAT GAAAATAGCT GGAGTTCAGG TGCGCTTTCA	24720
ATGCCCTGTT GTCAGGATTG GGCTTTTCAA GTTTATTTTT TGTGTGTGTT TTTAATAGAC	24780
TGTACTTTTT AGAAAATTTT TAGATTTACA GAAAGATTGA GAGGATAGTA CAGAGAGTTC	24840
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CTGTATTCCC AGATACTCAG GAGGCTGAGG CACAAGAATT GCTTGAACCA GGGAGGCGGA	25140
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TGCTTAGGCT CCTCTTGGCT AGACTGAGTT TTAATCTACT TTCTGCAGAG CCTGAGAACT	25440
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CCATTTACAA GACTTATGTT CGAATTTTCA GCACTCTGTT TTCACTAACC ATATCCTTCA	25740
ACTTTGATAA GTACTGCTTT AATCAACTCA GAAAATTTAA CTTGACTAAT TTTTTTTCAC	25800

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CATCAGTTTT	TTTTCTGTTG	ACTCTTTCTC	CTTTTCTGT	TTGCCAGAA	ACATGCTCAG	25860
GATTCTCTCA	GGCTTTAAAA	AATGAAAAAA	TGTTTCCTGC	AATCTAGTTA	CTCCTTGATT	25920
CTCTTGTTCT	GTTTATCGCT	GGAATTCCTG	AAAGCTTGGT	GTATTAGTCT	TTTTTCATGC	25980
TGCTGATAAA	GATATACCTG	AGACTGGATA	ATTTATAAAG	AAAAAGAGGT	TTAATGGACT	26040
CACAGTTCCA	CGTGGCTGAG	GAAGCCTCAC	AATCATGGTG	GAAGGCAAAA	GGCATGTCTT	26100
ACATGGCAGC	AGACAAGAGA	GAATGAGAAC	CAAGGGATTT	CCCCTTATAA	AACCATCAGA	26160
TCTTGTGAGA	CTTATTCACT	ACCACAAGAA	CAATATGGGG	TAAACCGCCC	CCATGATTCA	26220
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TGACATTTGG	GTGGGGACAT	GGCCAAACCA	TATCACCTGG	CCTATAGCAT	TATTTCCATT	26340
TCTTCCCCAT	CCTTTTATTC	CTCAAACCGG	TACAACCAGA	CCTCTTTTTT	TTTTTTTCTA	26400
CCTGAAACTG	CTCTTTTGAG	GGTAGCTGAT	AAGTCCAAAA	TACTGTCACC	TTTTCTCAAT	26460
TCCGTTCCCT	CTTATGCCTT	TGGAGCAATT	GACTGTGTTG	GTTGCCCCCT	CCTTTAAAGT	26520
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ATCTTTTATG	CTTCCCTTCC	CCCTCCCATC	CCCTAAATGT	CCTTGTTTCC	CAGAATCTGC	26640
CTCACCTCTT	TGACTTCTCT	ATGCCCTGTC	ATTCACTCAT	GGGTCTTTAT	TACATTATTG	26700
CATCTGTGTC	AATAACTCTG	GTCTTCTGT	TAAGTCCAG	TCTCCCATTT	TCAAATGTCC	26760
CCAGACATTT	CCAATTGAGT	ATCTCTCCAA	TGTATTTAAC	CTGCTAAATA	TCTAACACAT	26820
AATCTTTCCC	ATCAAATCGT	TTCTCTTAA	GCTTTTCGTT	ATTCCTATT	AGACTCCTGC	26880
ACTTCTCCCA	GGAGCCCAGA	CTTAAACCT	TGAATTTCTC	ACCATAACCT	CTCTTTTGTC	26940
TCCCATAATC	AATTAGTAGC	AAGTGTTATC	AATGATTACT	TGACAATATC	TTTTTCTATT	27000
TCCCTCCCTG	CTATGATCAT	TCATCTAGCA	AGAAGAGTTG	GCCCTTTGTA	TCTGTGGTTT	27060
CTGCATCCCT	GGATTCAACC	AACTGTAGAT	GGAAAATATT	TGAAGAAAAA	AGCGTCTATA	27120
CTGAGTATGA	AAAAATTTTA	TTTCTTGTC	TTATTCCCTA	AACAATACAG	TATAACAAC	27180

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ACAGCATTTA	CACTGTAGCG	TATAGATCTT	ATAATCTAGA	AATGATTTCA	AGTACACCAT	27240
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TTCCCCCATG	GATACAGAGG	GACAACTATA	TTTACTCAGT	GCTTACTAAA	TACCAGTTGG	27360
CCAATGTGTT	TTTCTTTTTC	TGTTTTCCCTG	TCTTTAGTTT	GCCCCCTGCC	AATTAATTCA	27420
ATAGTGCTGC	CAATGCCAGG	TGTACCTTCA	GAATATTCTA	TTCTAATTTT	GTCATCTCCA	27480
AGCTTAAAAA	TATTTAATGG	GCCAGGCGCA	GTGGCTCACA	CTTGTAATCC	CAGCATTTTG	27540
GGAGGCCAAG	GGGGGGTGTA	TCACTTGAGG	TCAGGAGTTC	CAGACCAGCC	TGGCCAACAT	27600
GGCGAAACCC	TGTCTCTACA	AAAAAGTATA	AAAGTTAACC	AGGTGCTGGA	GCATTTGCCT	27660
GTGGTCCCAG	CTACTCAGGA	GGCTGAGGCA	GGAAAATCAC	TTTAATCTGG	GAGGTGGAGT	27720
TTGCAGTGAG	CCAAGATCTC	TCCACTGCAC	TCCAGCCTGG	GTGACACAGC	AAGACTCTAT	27780
CTCAAAACAA	CAATAACAAC	AACAACGAAA	AACATTTAAT	GGCTGCACCT	TGCTGTGAA	27840
AAATGCATTT	CTTGCCAGA	TGTGGTGGCT	CAAACCTGTA	ATCCCAACAC	TTTGGGAAGC	27900
TAAGGCCAGG	AGTTCGAGAC	GAGCTGGGAT	ATATAGGAAG	ACACAATCTC	TACAAAAAAA	27960
AATCCACAAA	ATTAGTCAGG	CTTATTGTTC	ATGCCTGTAG	TCCCAGGTAC	TCAGGAGGCT	28020
GAGGCAGGAT	TCCTCAAGCC	CAGGAGTTCA	AGGCTTCCGT	GAGCTATGAT	GGCACAACCTG	28080
CACTCCATCT	TGGGTGACAG	AGCAAGGTCC	TATCTCTGGA	GAAAAAAAAA	AAAAGAAGGC	28140
ATTTCTTAGG	AGAGTTCTTC	TCTGTAGAGT	CCTAAGGGTT	CCATGGAACCT	CCTTAAAAGC	28200
ATCAGAGTAT	GTGAGTGCAA	TGGGAGGAAG	CATTTAGCCA	GAGCAGTTGT	GCTCCCATTG	28260
CATATTAATT	TTTAAAAAAC	AAAGCTATAA	AAAAAAGTTG	AAAACACTA	CGTTAGCATC	28320
AGCCTGACAT	TTAATGGCCT	CGTAAATCAA	ACCTTAATTG	ACTTTTTCAGC	CAGTTATGCT	28380
ACTAGCCAAC	TACAGACAAC	ACACTTTTTTA	ACCAAATTAG	ACTAATAGTT	GTCATCAGTG	28440
GAAATCAAGT	TTGCCATTCT	TCCATGCCTT	TGCTCACACC	ATTACCTTTT	CTGGAATGTC	28500
CTGTACTCAT	CTTCCTGTGT	TGAACTCTAT	ACCCAACTTT	AAAAACCTAG	CTCAAAGTTC	28560

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AACACTTCCA	TTCCATTTCA	AAAAGAGCTT	TCCTCTTCCT	TAAAGTTTAA	GAACTCATTT	28620
TCATGAATCT	TTTTGGCATT	TATTGCACAC	ATGCTTGCTT	TGTGTTATTT	GTGTTCAGCC	28680
TCATATGCCC	CCAAGGTGTT	TTAGACTCCT	TAACGGCAAA	AATGATGCTC	TAAACACCTT	28740
TCTATCTTTC	ATAGTGTCTT	AGTCTGTTTG	TGTTGCTATA	AAGGAATACC	TGAGGCTGGG	28800
GAATTTATTT	AAAAAAGAGG	TTTATTTGGC	TCACAGTTCT	GCAGCTATAT	AAGAAGCATA	28860
GTGTCAGCAT	CTGCTTCAGG	TGAGGGCTTC	AGGAAGTTTC	CACCCATGGT	AGAAGGCAAA	28920
GGGGAGCAGG	CATCACATAT	CAAGAGAGGA	GGAAAAAAG	GAAGGAAGAA	AGGAGGGTGC	28980
CATTCTCTTT	CAACAATCAG	TTCTTGTTGG	AACTAATGGG	ACAAGAGGCT	GGGCACGGTG	29040
GCTCATGCCT	GTAATCCCAG	CCCTTTGGGA	GACCAAGGTG	GGTGGATCAC	CTGAAGTCAG	29100
AAGCCTGAGA	CCAGCCTGGC	CAATGTGGTG	AAACTCCGTC	TCTACTAAAA	ATACAAAAAT	29160
TAGCTGGGCC	TGGTGGCGTG	TACCTGTAGT	CCCAGATACT	CAGGAGGCTG	AGGTAGGATA	29220
ATCACTTGAA	CCCGGAAGAC	AGAGGTTGCA	GTGAGCTTGT	GCCACTGCAC	TCCAGCCGGG	29280
GCAACAGAGT	GAGACGGTCT	CAAAAAATTT	TAAAACTTT	AAAAATAATA	GAGCAAGAAA	29340
GCACCAAGTT	ATTCAGGAGG	GATCCACCCC	CAATGACTCA	AATACCTCCC	ACCAGGCCTC	29400
ACTTCCAACA	CTGGGGATCA	ATTTCCGTAT	GAGATTTGGA	GGAGACAAAT	ATCCAAACTA	29460
TATCACATAG	TAATGAACAT	AGTACCTTAT	CTATAGAAAAG	CAATGGCTAG	ACAACCTGTTG	29520
AATGGCTAAC	CAAATCTGCT	TTCTTATGGT	CTCGCTCTAG	AGGGGGTCAG	TATGAGTTTC	29580
TGTCAAAAGG	AGAAAAAATA	ATGTATAGTC	AGTTTTGTGT	GTGTGTGTGT	TCATGTAAAA	29640
GAGATCAAGA	GAAAAGAACA	AGAGAAATCA	TGAAAAGGAG	GGGGAATATA	AGAATAATAC	29700
ATAGAAAAAA	GCAAATTATC	TTGTTTATCA	GTAATACCCA	AGGGGGTAGA	AATGGTAAGT	29760
AATAATCCTT	CTTCACTTTG	TCTGTAGTTC	ACTTTTTTGC	ACCTTTATTT	TGATGAATTC	29820
ACATCGAAGA	CATTAACTCA	TTAAGGCTTC	CAATATTTTT	GGAGATAAGA	AGGGCTGCTA	29880
TGCTCTTTAT	AGATGGAAAA	CTTGGGTCAT	TAATAACTCA	AACAAGGACA	TAACAAAGAA	29940

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ATGGAGCATA	AACTGCCAGG	TCCTGACTGT	AGATTTGGAT	TCCCAGTTGG	TGTC'TTGTCA	30000
CCCTTTGTTA	CTCTTCCTAA	AGTTATGATC	TTTTCTTGTG	CATAGGAAAT	TCATAGTGAT	30060
TTCCCATCAC	CCTTGGGATT	ATCATAGCTC	CTTTAAGGTC	CCCTCTATGC	ACTCAATAAC	30120
ATCAACAGTA	AGTGTTCCTC	GAGCACTTAC	TGAGTGTATA	TCATTGTGTT	CTCACGCAGC	30180
ACCCACAGAT	CTCACCAAGA	ACCTAGCTGA	AGCCTGTAGA	ATGAATAGGT	AAGTACTGCC	30240
ATGCCAATCT	GGAGTACTCA	AGCGATGCAA	ATGATTCCTT	TAATTGTACT	TTTGCAGGCT	30300
TGTCAGTTTT	GCTCATGGAG	AAGTGGCTAC	TGCATCCATG	TTATATCTAT	GTAATGTTGG	30360
ACTGCGAAGC	ATCACTTGAC	TTTTTCCAAG	CAGAAATTAC	AGCTGATGAC	AAGCTGCTGC	30420
TGAGAAAATG	GATATTTTTC	TGAATTCAGT	TCTACGTGGA	AACAGCTGAC	TAGTTTCCAT	30480
TGCTGTAAGA	ATGGCTCTTT	TGCTCTTGGT	TGATTTTGAG	TAATGGCTTT	ACTTCTGTAG	30540
AAAGGAGATT	TCATTTGAAG	TCCACTCAGG	GATTTGGTTC	AACAAACTGG	AGTACAGGTT	30600
TCAGAAAATA	TCTCTTTAAT	CCTCCAATAA	TAAATTTTCT	CATCTATAAT	TCCTGGAACA	30660
CTTCATCCTT	TGCAGCCGAG	CATATAGATA	GATTTGTTGC	TCACTGTGTT	CTGATTGCCA	30720
CTTTGACCTG	CTTTTCAAC	TTAGGTTACA	AATAGAACAG	AATCTCTCTG	ATTTTCTCTA	30780
TTAATTGTTT	GAATCCAC	TTTTCCTCAT	TAGCAAGAAG	TCCAGTATCT	TCCTGAGAAC	30840
TTCC'TTTTCT	CAATCTAGGA	ACTTACTTGG	TCCATAAGGT	AACAGTCTTA	TTTCTGACTA	30900
TCAAGGAGAG	AAATAACAGG	AGCCATTATC	ATCTTCATGG	TGTCACTTTT	GAAAACTGGT	30960
CCTCTGTAGA	TCTTCAGATT	CTTGCGTTAG	TCCATTCAGC	TGCTATAACA	AAATTGCATA	31020
GACAGCATGG	CTTATAAATA	ACAGAAATGT	ATTTCTGACA	GTTCTGAAGG	CTAGAAAGTC	31080
AAAGATTAAG	ACACTGGCTG	ATTTGGTGTC	TGGCGAAGGC	CCATTGCTC	ATAGATGGAC	31140
GATGACCTTT	CACTCTGTCT	GCACATGGCA	GAAGGGCAAG	AGAGCTCTCT	GGGTCTTTTT	31200
TATAAGGGCA	CTAATCTCAT	TTTTGAGGAC	CCTGCCCCCA	TGACTTAATC	ACCTCCCAAA	31260
GGCACTGTCT	CCCAATACCA	TCACCTTGAG	GGTTAGGATT	TCAACATATG	ATTTTGGGGG	31320

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GACAGAAACA CGCAGTCCAT CTCGCTTGTC CACTCCATGG TGGTATTCTT GCTGGATCAG 31380
TTTCCTCCTT GGGGTGCATT TGTGTTCCAT GTCTAACTTG CAAGTTATAG CAGGCCCGAT 31440
AGCAAAGTAT TCCAATGTTG GTATGCAGAG GCATTGAATA ATCAGAATGA ACCCACGCCA 31500
TAAACAACTG GTAGAGCTGC AGAGAGTACC AGCTGATTAT GAGCCCTGGG TAACAGTGGT 31560
TTTTAGTTC TATGTCCGTC AGCCCTTTTC TCCCATAGTA GCCCCACTGT GTTGAAGTGG 31620
CTGAATCGAC AGAAGCTTCC AGCTTGGGCC ACATGCTCAT GGAACCAATT CTCCTTATGA 31680
GCCGTACAAG AGCTGGGTTG CCATTCTGGA TACCCTCTTT TTTCAAGAGA TTTTATTTCA 31740
AGGATATTTT TTCTTTTATC AACTACAGGG ATTATTTAGA ATCTTAGGGC AGTGGTGCCC 31800
AACCTTTTGT GCCCCAGGGA CAGGTTTTGT GGGAGACAGT TTTTCCATGG ACCAGTGTC 31860
GGGGGCTGGG AGGCATGGTT TTGGGATGAG TCAAGTACAT TACGTTTGTT GTATACTTTA 31920
TTTCTATTAT TATTATATTG TAATATATAA TGAAATAATT ACACAACTCA CCATAATGTA 31980
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CCCCGGCATG TGCAGTTCAC AATAGGATTT GCTCACCTAT GAGAATCTAA TGCCACTGCT 32160
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AGGTCACAGA CTGGTACTGG TCCATGGCCA GGGAGTTGGG GACCCTGTCT TAGGGAGTAG 32340
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GAGTATCACA AACCAGGTGG CTA AAAACAG ACATGAATTC TCTCTTATTT TTGATGGCTT 32460
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TGCAGCACTT CAACATCTGC CTTTACTGTC TCATAGTGTT CTCCCCTCAT GTCTCCAGGT 32640
CTCTCTGTCT CTCTTCTTTG TATAAGGAAA CTAGTCATAT TGGATTAAGG GCCAACCCTA 32700

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CTCTAGTATG	ACCTCATCTT	AAGGTCACAT	GCAATGACTA	TTCCAGATAA	GGTCACATTC	32760
TGAAGAACTG	GGAGTTAGGA	CTTCATATCT	TTTGAAGGAA	CACAGTTCAA	CCAATAACAG	32820
CCCCTGTACT	GTTTTACAAA	TAGGTATTCC	TCTCCTTCCC	AAAGTTCTTC	ATAGCAGAGA	32880
CAACTGTGAC	CAAAAGGCAA	AATACCTTAT	TATGTAACCT	TAACCTAGGA	TCATAGATCC	32940
CTACTGTCTG	GTGCTTTATA	AGCACAGAAC	CACCGGGAAA	TCATTATTAA	GACAAGGAAA	33000
GGCCAAGTGC	AGTGGCTCAT	GCCTGTAATC	CCAGCACTTT	GGGAAATTGA	GGCGAGTGGA	33060
TCAACCTGAA	GTCAAGAGTT	TGAGACCAAA	CTGACCAGCA	TGACAGAACC	CCATCTCTAC	33120
TAAAAATACA	AAAATTAGTT	GGGCATGGTG	GCATGTGCCT	GTAATCCCAG	CTACTCAAAA	33180
GACTGAGGCA	GGAAAATCAC	TTGAACCGAG	GATGCCAAGA	TAGCAGTGAG	CCAATATCGT	33240
GCCACTGCAC	TCCAGTCTGG	ATGATAGAGC	AAGATCCTGT	CTCAAAAAAT	TAATAAATAA	33300
ATAAAAAGAC	AAGGAAAGCC	TTTTCOAAGG	AGACCCTTCT	GCTTTGCTAG	TTCAGAGAAC	33360
TTCTCTTTTG	GAGAAAACAA	ACACCCAGTC	CATTAGCAGC	AACGTCAGGG	ATTGAATTCT	33420
TAGGGCAGCA	GGCTGGGCAC	AGTGGCTCAT	GCCTGTAATC	CCAGTACTTT	GGGAGGCTGA	33480
GATGGGTGGA	TCACTTGACA	TCAGGTGTTT	GAGACCAGCC	TGGCCAACAT	GGTGAAAAC	33540
CATCTCTACA	AAAAATATGA	AAAAAAAAAA	AAAAAAAAAA	GCTGGGTGTG	TTGGCTTATG	33600
CCTGTAGTCT	CAGCTACCTG	GGAGGCTGAA	GCAGGAGAAT	CACTTGAACC	CGGGAGTTGG	33660
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CATCTCAAAA	AAATAAGAA	TTCTTCGGGC	AGCAGTCTTT	CCTCCACCTC	ATAGACCATG	33780
GAGGTGAGCC	AGCTCTGACA	AACCATGAGA	ACAATGGCAG	AGACATACCT	GTAACGTAAC	33840
TGACTGGGGC	AAAGACAAAG	GTGAGGAAAA	TGACAAGTTT	GAGGAACTAT	GAGACCAGGC	33900
AGTGGGGAAC	ACCACTAGCA	GAAATGATGG	AAGTTCTCAA	GAATAACAAC	AGAGAAATAG	33960
ACCATGGCCA	GAGTCTAGAA	CCCTCCAGGG	AAAGGAGATG	GGCTCCAGAG	GCAGAAGAGG	34020
ACGTTGAAGG	GAATGGGGAG	TGGGTGAAAT	ATATAGACGA	TGGGGACCAC	CCAAGAGCAG	34080

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TCGCTATTGC AAAACTGAGG AGAAGGAGAG TCTGGAGGGG GTGGTGGGAA GCTGGGTCTC	34140
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GGGGTTTGAG CAGAGAGTGG TGATTTTTCT AATGCAGAGT TGTGGGAGGT GGAGTGCAGG	34380
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GCTTGTAAGT ACTATGCTTT TCCCCAAAAA AGGGGGCTGG CACAAAAAGA GCTGAGGGGG	34680
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GTTTACTGGC TTTGGATAAA TTAAGTATAGC TTAAGTGAACC AACTTTGGAT TTTTATAGAG	35160
ATACTGTAAT GAAAGGAATA AGGTATCAGT CTTAGCAGAG CATCCAGAGT GTTCCTATTA	35220
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AAGTTAAAA CTCATCTTTC CAGTGGCCTG CAAGAGCCTA TGCTATCCGG TGTCTGACCT	35340
CATCTGTTGT TCCTTTCTCC CTCCCTTTCT TGGCTCCAGA CGCACTCTGG TCTCCTTGCT	35400
GTTCTTGAA TACACCAGGC AACTCTCTT CGCCTGAAAC ACTTTACCCC AGATATCTTA	35460

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GCTTACTCTC	TGCCTCCCTC	AATTCATTGA	TGAAATGTCT	CAGTGAAGTC	TTCTCTCTCT	35520
CCTCTGTAAA	AGTATACTCT	CTGTTCCCCT	TCTTTACTGT	TCTAGCTACT	ATTGCTGTGT	35580
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TATGCAGTGA	GAGTCAGATG	CTGGCTAAAA	CTGAAACAAA	GCAGGGTTCT	AGTAGCTGAG	35760
GGCTGGCTGG	GTCTCTCAGA	TATAGTTCAG	ATCTCCTCCA	GGGGGTCTCT	CCACGTGGGC	35820
TAGTCTGAAC	TTCTTCACAG	CATGGTGGCC	TCAGGGCAGT	GGACTCTGCA	TAGTGGCTGA	35880
AGGCTTCGCA	GCTGAGTATT	CCAGCAAGCA	AAGTGGGAGC	TGTATTGCCT	CATATGACCC	35940
AACCTTGGA	TCCACACAGC	ATCACTTCCG	TGTATTCTAC	GGGTGAAAA	GTCACAAAAA	36000
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TCACATTGTA	ATCAGAGCCT	ATGGGATACG	AAGTATTGCG	GTCAGGTATG	AAAAATTTGA	36120
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ACTTACGTCA	TTTCTGCGTT	TCCTGTCTTC	CACACTAAAA	TGTCAGCCTG	TTTTGTTCAC	36240
TGCTGTATCC	CCAGAGCCTA	GCACGGAGCC	CAGCATGTAG	TGGTATCCAA	TAAATACTTG	36300
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TAATCATCTT	ACAGACGAGG	GAAATGAGGC	TCAAGAAGAT	TTGGTAACTT	ATGCGGGATC	36420
ACTCAGCCAC	ATAATGGAAG	AGACAGCATT	GAAGTACACA	TGCTTGCTCT	GTCTGCTCTT	36480
CCAAGCTGCT	CATCACACAG	CTGCACCTCT	GAGGACTTCC	CTCCCCAGTC	CACCTCCACC	36540
CTTACCCAGA	GACACACATG	GCCACAATCC	ACTAGCAGAC	CAAAATTCAA	TTTTTCCCCA	36600
GTTGGTTGCA	CTCAAGCTGA	GAGCAAAGCA	ATTGCACTTT	AAATCCCCTT	ACAGCAGATA	36660
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TTACAAAAAC	ACAATTAAAT	GAAAGGTTAG	GTAGCTTTTG	AATGGCCAGC	TCAAAGTTTT	36780
GGCTTATTTT	TGCCTTGCTG	TCTTTATAGG	CATTTTACCA	ATATTTATCA	CTATTTCCCT	36840

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TAGGGAACCC	TTAGATCTGT	GATATTTGAA	ATAATAAAGC	CTCTCCATTG	GCCCTTTAAA	36900
AGGTTTGTGG	TAAAACCACA	CCATTAACAT	TCACAGTTCC	TTATTTATGA	GGCCTGATTG	36960
CACTTATTTT	CATATTTCTC	ACTGTTTCTC	CGATGAGGAT	TTCACATAAT	AGTGTTTGAA	37020
GGCTAAAGAC	TTCAAAGCAG	ATTCTTTACT	ATTTTTATCT	TGAAAAATAT	TCAATATTTG	37080
TGTAATTAAA	GTGAAGTCTT	CCTAGAGAAA	ATGACAACCT	AAATAATCTT	AAATGTACCT	37140
CCAAGAAAAA	AGCTGTCAAA	GTGACATTTA	GTAATAGAGT	CACATTCTCT	AAGGCCTTTG	37200
CTTCTCCTTC	TGATTCTTAT	CATCTTTGAA	GGTTATGTCA	TGGGCTGACT	TCAAATCAAC	37260
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CTTTTGCTCC	AGATTTTTTT	TACCGCGTCA	TTACCAAGCA	TCTTAAAACA	AAACCTAAAA	37380
ACAAAAATCT	TCCTTGACCT	GGTTTTTCCC	ACTAGCTAAC	ATCCTATTTT	TATCTTTCCC	37440
CTTTGCACTA	AAGGTTTTTA	AACGGATCTT	TATACCCTCT	GTCTCCATTT	TCTCATCTGC	37500
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GCTACACAGT	TGGTACTATA	ATTTATACAT	CCTTGACAC	AGGGCTTGCT	GGGATATTGA	37740
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ATTTGACATG	GATTTGATTG	GAAAAGCATG	ATACCATTTT	TTGCAATTAA	ACACAGGAAT	38220

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ACATAAATAA AATGCATCAG TATTTTTTAC AAATAGCTAC TAAGAGCTAC TAGAAAACCT	38280
GGGAATTCTT AAAACCTTAC CATGCTACTT GCTCTAAAT ATTTTATTTT ATGTTATTTT	38340
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TAACAACTTA TAGACACATT TAAAAAGTTT AAGATCTCAA GAGCTATGTC TGAATAGATA	38640
GGAGTAAAAA CTCTATTAAG TAATTAGGAA AATAACAAGA ACAGTGAATT TCTTAATGAA	38700
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GTGGCGTGAT CTCAGCTCAC TGCAACCTCC ACCTCCCAGG TTCAAGCGAT TCTGCTGCCT	38880
CAGCCTCCTG AGTAGCTGGG ATTACAGAGG CCTGCCACTG CACCCGGCTA ATTTCTGTAT	38940
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TCGAATGTCT TTATTATTTG AAGAGACAAC ATGGGCCTTA AATCTGTCTT CTATTGACA	39120
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CTCTCTCAGC TGTCTTCTG CATATGTAAG GTGGAATAAT GATGGCTTTC AAGGAGGAAT	39240
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GCCTGGCCAA CATGGTGAAA CCCTGTCTCT ACTAAAAACG CAAAAATTAG CCAGGTGTGG	39540
TGGCATGCAC CTGTAGTCCC AACTACTCAG GAGGTTGAGG GAGGAGAATT GCTTGAACCT	39600

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AGGAGGTGGA	GGTTGCAGTA	ACCCGAGATG	TCACTGCACT	CCAGCCTGGC	AACAGAGCAA	39660
GACTCCATAA	AGACAACAAA	AGCTTTGAAA	TTGTGTAAAT	GAGTTGTACC	TATCTTCATT	39720
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CACTGACTTT	ACACAAAATC	AGATCTGATT	GGCAACAGTT	GCAGATGTTT	TCAAAAGATT	39960
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CTGTTTTTCT	GGCTTCTGGG	AGAGGAGGAG	ACATGAATTC	AGTTAGCACC	TTGGTATTTT	40080
CTTTATCCTT	CATTTCAATA	CAGAAGATGC	TTCATATGCA	CAGTGGTGTC	AGGTCACATC	40140
AAAAGAAAGA	GAAACAGTTT	CTTGGTTTTT	AATTTTCAAC	CGGAAAGGAA	AGGCACCCAT	40200
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GAAGAAAATG	GCTCAGGAAG	ATGAACAATC	TCACAGAGCC	CTAACTAACT	GAAGCCAGGT	40380
GTTATAAAGC	ACAAGTCAAG	AGGGTGAGAA	ACTAACGTTC	TTGAAATCTC	CCACTTCTTT	40440
CTACGTCAGA	AGAGCCAAGC	TGATTATTTT	AGTTGGAATT	TAGAAATTTT	TAAAAATTAT	40500
TCTAAAGTCA	TGAACAAGCC	TAATTATAAA	GATAGTTGCT	GTGAAGGTGC	TGAAATAACT	40560
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CTACCAACGA	ACTCTTGTTT	TTCTAATGAG	GAAACAGAGG	CCCACAGTAT	TAACTATCT	40680
TAACCAATAC	AAAATGACTA	GTGCTCTGGT	CCTTTTATTA	AGCACTAAAA	TTTTGATCCA	40740
ATAATAAATC	TGTCCATTAG	AAGGAGTTTC	CCTAATGTAC	TGGTTCTAAC	TTGTTCCCTT	40800
CAAGGGGCCA	GTGTCCCGTA	CACATAGCTA	AATGGGACTT	CTCTTCAACT	ACCATTACCC	40860
AGAGGGCAGA	ACCTAAAATG	CTGTGAATGA	CATTCTGCTG	TTCACATCTC	AGCAGCA	40917

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(2) INFORMATION FOR SEQ ID NO:3b:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39678 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3b:

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GTGTTGCATT TGAGCTTCTG CAGGGCCACC CAGGACCTAT ATCTGCTCAG ATGTTTAACT      60
CATCTAATTC AGTGAACACT TCATTCTAGT TAACTGAACA TCTACTTTGT ACAAGGCACT      120
ACAGCGGTTC AGAGATGAAT AAAATCATGA GATTCCACTG TCTCCTATAA ACCATCACTT      180
TGGGAAATTT TAGAAATGTG GGTAAGCTCC AGGGCTTCCT GCAGCGTAGA AGTCACAAAC      240
TCAAATGCCT GCAGAGGCCC AGCTGACAAC ATAAGTAAAT GATTCTGGCT GGGCGGAAAA      300
CAATTACGGG TGGGTGGGTT TCCAGCTGGG GAGTGCACGC CTGTGTTAAA GGACAGCTGC      360
TACTCATTTT CAGCCAACTG TGTTCCCATG TAGAACTGCG GCCCAGTGTA GCCAGTACCG      420
AAGATTTCTC AGAAAAAGCC GGAGATCTCA ATGTTAGTGT AAAATCTCTC AAATTTCCAA      480
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CCCTCAGCCT CGTCCGACCC CAGCCTGGGT TCAATGAACA TTCGGTAAAG GAACACGGAA      720
TGTCAGCGC ATTAGAGACA ACCTTGAGAC ACATTCTCTT TGCGGTAAGC ACTTCACTGT      780
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TCAATTTTAG TGAACACTTC AAGGCTGAGA TACGCTAGGA GAGTCGTGTG GTGTTGCACA      900
GCAAAGAATT CCACTTTGAA GCGAGTGGGA AAAAAAGCAT CAAATGCCAC ATGTAACTCA      960

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GTTCAGAACA ACCCATTTTA CAGATAGGGA AATTGGGTCA GAAAGTTTCA GTAAC TTATC	2280
CAAGGTCAAC ACAATTGGCA AGTGCCAGAG CTGAGCCAGG AACTGAGGTC CTTCTAACAC	2340

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ATGATCAGAC	TACTAAAAAG	ACATCAGGAA	AGGGCCTGTG	ACATCTGAGG	GAAGTGGTTG	13200
CCCTCTCTGG	GATGTTGGTT	CGGGAAGAGG	GGCATGGAGG	AGTGCCTGCT	TTAGATGGTC	13260
ATTCAGGAAC	CCAGGCTGAT	AGTGAGAGGT	GAAGCCAGTT	GGGCTTCTGG	GCTAGGGGGG	13320
ACTTGAGAA	CTTTTGTC	TAGCTAAAGG	ATTGTAAATG	CACCAATCAG	CACTCTGTAA	13380

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AATGGACCAA TCAGCAGGAT GTGGGCAGGG CCAAATAAGG GAATAAAAGC TGGCCACCAG 13440

AGCCAGCAGT GGCAAACCTGC TCAGGTCCCC TTCCACGCTG TGGAAGCTTT GTTCTTTTGC 13500

TCTTCACAAT AAATCTTGCT GCTGCTCACT CTTTGGGTCT GCACTATCTT TATGAGCTGT 13560

AACACTCACC GTGAGGGTCT GTGGCTTCAT TCCTGAAGTC AGTGAGACCA CAAACCCACT 13620

GGGAGGAACA AACAACTCTG GACACGCCAA CTTTAAGAGC TGTAACATTC ACTGCGAAGG 13680

TCTGCGGCTT CACCTCTGAA GTCAGCGAGA CTATGAACCC ACTGGAAGGA AGAAACTCCA 13740

GACACATCTG AACATCTGAA GGAAGAACT CCAGACACAC CATCTTTAAG AGCTGTAACA 13800

CTCACTGCAA GGGTCTGCGG CTTCACTCTT GAAGTCAGCA AGACCAAGAA CCCACTGGAA 13860

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TTGGGCACCT GTCAGCCAGT TAAAAGCGAC TAGCATGGCT GCCAGACTTA AGAACTAAA 14040

GACACGGGTG TCAGACTTTC TGGGAAAGGG CTCTCTAATA ACCCCCACT CTTTGGAGTT 14100

GGGAGCGTTG GTTTGCCTGG AACCAGCTTC CACATTTTCCT GTACTTCTGG GCTGAGACGA 14160

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GTGGCCATGA TCACAACTCT CGAAGTCATG TTGCCCAAGC GAGACTCACC CATCTATCCT 14280

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GTTTCTCCTA TAAGAATGAT TTCTAGTATA AACTCCAGGA CTCTATTCTC TTCTTTAGGC 14460

ACCCGGGCTC ACCAATCAGA AAGCCATAAT TTTTGCCCAA AGCCCCATCT TAGGGGGGAC 14520

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CACTCTTCCA ATTCTGGAGA TCCCTTCCCT CCCTCAGGGT ATGGCCCTCC ACTTCACTTT 14700

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GGCCACTAAA	TCTGACATTC	CTTGGTCCTC	CTTGTGGTCT	AGGAGGAAAA	CTAGTGTTTC	14940
TGCTGCTGCA	TCAGTGAGCG	CAACTATTCC	AATCAACAGG	GTCCAGGGAC	CATTGTGGGT	15000
TCTTGGGCAA	GAGGTGTTTC	TGCTGCTGCA	TTGGTGGGCT	CAACTATTCC	AATCAGCAGG	15060
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TGTATCCTAA	GCCATTGGGA	CTAATTTGAC	CCGCAAACCC	TGAAAAAGAG	TGGCTCATTT	15240
TATTCTGCAC	TATGGCCTGG	TCCCAATATT	CTCTCTCTGA	TGGGGAAAAA	TGGCCACCTG	15300
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GCAAACTTA	CAATTCACAT	CCCACAAGAA	GAAGTCTCAC	TTACCCCCAT	ATCCTAGCTT	15480
CCCTATAGCT	CCCCTTCCTA	TTAATGATAA	GCCTCCTCTA	TCTCCCCACC	CAGAAGGAAA	15540
CAAGCAAAGA	AATCTCCAAA	GGACCACAAA	AACCCCTGGG	CTATCGGTTA	TGTCCCCTTC	15600
AAGCTGTAGC	GGGGGAGGGG	AATTTGGCCC	AACCCAGGTA	CATGTCCCCT	TCTCCCTCTC	15660
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TGGAGATACC	TGGTATCTTA	GTCAAGTAAA	TGATAGAATG	ACAGCTGGGG	AAAGGGACAA	15900
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TAGGAAAGAG	CCTATGAATT	ATTCAATGAT	GTCCACCATA	ACTCAGGAAA	AGGAAGAAAG	16080
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TTCAGTAAGT	GATAAGGAAA	CTCTTATAGA	AGCAGAGTTA	GGAAAATTGC	GAAATAAGTG	17640
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AGAATCAGGA	AGGAGCCATC	TATACCAATT	CTAAGTTAAT	ATGGACTGAA	CGAGGTTTTA	17760
TTAATAGCAA	AGAAAATTAA	AATCTCAAAC	TTACGAGGTT	TTCAAGTAAA	GTAAAGTTTG	17820
GTAAAAGTTA	ACAGCGTAAC	ATGTATTATC	CTAGTACCAC	ACATTCTCTC	AAAGGATTTG	17880
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CTAACAACTT	CTGCTGAGGA	CCCCTGGACC	GACCCGCTGG	CCCTTTCAAT	GGCCTAAAGA	18360
GCTCCCCTCT	GGAGGACACT	ACCACTGCAG	GGCCCCCTTCT	TCACCCCTAT	CCAGCAGGAA	18420
GTAGCTACAG	CGGTCATCGC	CAAATCCCAA	CAGCAGCTGG	GGTGTCTGT	TTGGAGGGGG	18480
GATTGAGAGG	TGAAGCCAGC	TGGGCTTCTG	GGTCAGGTGG	GGAATTGGAG	AACTTTTGTG	18540
TCTAGCTAAA	GGATTGTAAA	TGCACCAATC	AGCACTCTGT	GTCTAGCTAA	AGGATTGTAA	18600
ATGCACCAAT	CAGCACTCTG	TAAAATGGAC	CAATCAGCAG	GATGTGGGCG	GGGTCAAATA	18660
AGGGAGTAAA	AACTGGCCAC	CCGAGCCAGC	AGTGGCAACC	CACTCGGGTC	CCCTTCCACA	18720
CTGTGGAAGC	TTTGTTCTTT	TGCTCTTCAC	AATAAATCTT	GCTGCTGCTC	ATTCTTTGTG	18780
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GTCAACAGAC	CACGAACCCA	CTGGAAGGAA	CAAAGAACTC	CCGATGTGCT	GCCTTTAAGA	18900

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ACCATCTTTC	AGAGCTGTAA	CACTCACCCG	AAGGGTCTGT	GGCTTCATTC	TTGAAGTCAG	19080
CAAGACCAAG	AACCCACCGG	AAGGAACAAA	TTCCAGACAC	AGTAGGAAAT	CTGTATTTTT	19140
GATCTGTGGC	TTCCAGGGTT	ACTCCAGTCA	TTGAAGTCTC	CATTGCAGCC	TTAAGGAAAC	19200
AGAGAATGGT	TTGGAGGAGC	ACATGTGGGA	ATTGTTATGG	ACCAGGCTTG	AGATGCACAT	19260
AGGGCATTTC	TGATCAAACC	TAGCTGGAAG	CAGGGCCAGG	AAATATAATC	TAAGGAAGAC	19320
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AAGGGGTGTG	GATCACGAGG	TCAGGCGTTC	GAGACCAGCC	TGGCCAACAT	GGTGAAACCC	19500
CGTCTCTACT	AAAAATACAA	AAATTAGCCT	GGTGTGGTGG	CACGCATCTG	TAATCCCAGT	19560
ACTCAGGAGG	CTGAGGCAGG	GGAATCTCTT	GAACTTGGGA	GGCAGAGGTT	GCAGTGAGCC	19620
AAGATCACAC	CACAGCACTC	CATCCTGGGT	GACAGAGCGA	GACTCTGTCT	CAAAAAAAAA	19680
AAAAAAAAAA	GGAAAGGAAA	ATATAATCAA	GAATATTGAC	AGGTAACATT	TATTCAACAC	19740
TTACTATGCA	CCAGGCAATA	CACTAAGTGT	TTTACATGGA	TTAACTCATT	TAATCTTAAC	19800
AATAGCCCTA	TGAAGTCAGT	GCTGTTATTA	TCTCCACTTT	ATAGATAAGG	AAACTGAAGT	19860
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AGTCTGAGTT	GGGCAGTTGG	GGATGGAAGG	ATGGATGAAG	AACAGCTTGA	CAGAGAAGCT	20040
GACACTTGGC	AACTCTGTGG	GACCTTGAAG	GGTTAGAGGG	ACTTCACCAA	AGAACTGGT	20100
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AACCTCATGC	AAATATAAAA	TGAACACGTG	TCAAAGATCT	TATTTAATTT	ATTAATTAAT	20280

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GAGGGAACCT GTAAGATGTT ACAGCCAGTT CAAAGGATAA TTCAAATAAA TCCATGCACA	20340
TATGTAGGCA ATAAGGAATG CTGAAATGAA TTTAAAAGTA GATGTAACT GATTTATCCA	20400
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TTTTTCTCAT TTCAAAGTCT TTCACAAGTT TTCCTGATAA GGGAGTGTCATAAATACTGT	20640
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CTGAGGACTG AGCCTCCTCA TCCTAAATTC AGACACAATG CTGTACCTAT GCATTTGCCT	21240
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CCAGGAATAT GTGGTATTTT AAAAGAAGG CAAAGGGAAG AATAGTGGGG ATGGGGCAAA	21600
AACTTTAAAT AGATTCCCCC AATCATATAT GGCAATTGAA GATAATTAAA TTATCATTTT	21660

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TTGTGCAAAT GTGATACATT AAACCTAAGC TATTTTAATA AAACATCCAT TTTCGGAAGC	21780
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ATACTGTCTT TTGTCTGGTT AGTTTAGAGG TTAGATAAAC TGCAGTATGT TGTAGTGGAC	23040

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AGATCATAGA	ACTAGGAGTC	AGGATGTCTG	GATTCCTAGG	AAGCAATGAA	TAGGTTGCAC	23100
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CATTGATTTT	ATCCATATGG	TGACAATACT	ATTCATATAT	AAATGGTGTG	CTTCTCTTCA	24120
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GCATTTGTAC	CATGAGGCTT	GGCCAAGGCT	ACAAATCCAG	ACTTTTGTTT	TTCCCTCCTG	24240
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AACACAAACG TATCTACATG CCTTTCTTG TGAATAGATC TAATAATAAC GCTCTTCTAA	26400
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CCTGAATCCA AGCCCCAGA TCTATTTAAA GAATTTGAAG AATGTCAGAA AAGCACGTGG	26520
CTTCAAGGTT AATGTGTAAG ACTCACAGAA ACTTGAAAA TCACTATGAC TAAAAAGAAA	26580
GTATGAGCTC CTGCGATGCC TGTAATTTGG AATGACAGCC AAAACCAGTT AATTATAAAA	26640
ACAGCTAATT TAACAGGTTT TCAAATTTGT TTCTTTCTCC AAGTAGCATA TAGTCAATAA	26700
TCCTTAAAGA GAAAGCAAAG AAGGGGAAGC ACTGAACCAA ATTTGCTTTT TTGTACCTGC	26760
TCAGCTCAA TGCAGAGTTC TCTACCTGGA AATTGACTGC TTCCATAGTT TGATAGCCAC	26820
AGAGAGATGG GAACAGAAGG AGAGGTATAA TCCCAGACTT GATTGAGCTA TAGAGAATGA	26880
CAATAGTGTC AGAGGCCTTC CAACCAGAGC GACTCCATCT TGAATACGGG CTGGGTAAAA	26940
CAGGGCTGAG ACCTACTGGG CTGCATTCCC AGGAGGCTAA GCATTCTAAG TCACAGGATG	27000
AGACAGGAGG TCAGACAAG ACCTTGCTGA TAAACAGGT TGTAATAAAG AAGCCAGCCA	27060
AAACCCACCA AAACCAAGAT GGCCATGAGA GTTATCTGTG GTTGGTCTCA CTGCTCATTG	27120
TATGCTAATT ATAATGTATT AGCATGTAA AAGACACTCC CACCAGTGCT ATGACAGTTT	27180

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ACAGGTACAT TGGCAACTTC CGGAAGTTAC CCTCTATGGT CTAAAAAGGG GAGGAACCCCT	27240
CACCTCCCAG AATTGCCCAC CCCTTTCCTG GAAAACCTGT GAATAATTCA CCCTTGTTCA	27300
GCATATAATC AAGAAGTAAC TGTAAGTATC CTTAGGCCAG AAGCTCAGGC CACTGCTCTG	27360
AATGTGGAAT AGCCATTCTT TTATCCTTTA CTTCTTAAT AAACCTGCTT TCACTTTACT	27420
GTATGGACCC CTGTGAATTC TTTCTTGCAA GAGATCCAAA AACTCTCTCT TGGGGTCTGG	27480
ATCAGGACCT CTTCCCAGTA ACAATAGTAG TAAGGGGTCG GGGAACTGG ACAAAGGAGT	27540
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TGGGGAAGGA TAGCTGACTT AAGAAATTAT CTAGTTAGAC ATTTTTTGGA TGGGGTAATT	28560

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GATATTCTAT TTATATTCTG TAAGATTTTT TTTTAAAGG AAAAAATTCTT CCATGGTTGA	31320

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TGCCTTTTCC TCAGGCCAG GCCTCAATTT ACTGAGCAGT CACACCTCAC AGAGGGAGGT	32700

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TGCCAAGTTA AGTGCCCAAG CTTGCTCTTA AAAGCATACT GGATTTTGTT TTAGACTTTT 39600

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AGTGAAGTGA AGGGAATAAA CAAATCCCTC TGGGAGAACT TCTCCTCCAT CCTTGGTGAA 39660
 GTCATTCTGC CAGAATTC 39678

(2) INFORMATION FOR SEQ ID NO:4a:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41008 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4a:

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 TCCATACCAC CACAATAATA CAAATATGCA AGAAGTGGAT ATCACAATAA AGTGAGTCAC 780
 ACAAGTCTTT TGGCTTCCCA GTGCATATAA AAGTTTGGCT TATACTACAC TGTAGTCTGT 840

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TCAGTGTGCA ATAGTGTTAT GTCTAAAAAA ACACATACCT TAATTTTAAA ATGCTTTTATT	900
ACTAAAAAAT GCTAACAATC ATTTGAGCAT TCAGTGAGTT GTAATCTTTT TGCTGGTGGA	960
AGGTCTTTTC TTATTGATGA CTGATCGGGG GTCAGGTGCT GAAGCTTAGG GTGGCTGTGG	1020
CAGTTTCTTA AAACAACAGT GAAGATTGCA ATATCAGTTG ACTCTTCCTT TCATGAAAGA	1080
TTTCTCTCTA GTGTGTGATG CTTTTTGATA GCATTTTATG CACAGTAGAA CTTCTTTGAA	1140
AATTGGAGTC AATCCTCTCA AACCCCTGCTC TGCTTTAACA ACCTAAGTTA ATATAATATT	1200
CTGAATCCAT TGTGTGCATT TCAACAATTT TCACAGTGTC TTCACCAGGA GTAGATTCCA	1260
TCTCATTTCC TGAGATGGAA TCTTTGCTCA TCCATAAGAA GAAATTCCTC ATCTGTTCAA	1320
GTTTTATCAT GAGATTGCAG CAATACAGTC ATGTCTTCAG GCCTCACTTC ACTTTTAATT	1380
CCAGTTCTCT TGCTGTTTCT ACCACATCTG TGGTTCCTTC CTCCATGAA GTCTTGAACC	1440
TCTCCAAGTC ATCCATGAGG GCTGGAATCG ACTTCTTCCA AATTCCTGTT AATATTTATA	1500
TTTTGACCTC CCATGAATCA TGAATGTTCT TAATGGCACC TGGAAATGGTG AATCCTTTCC	1560
AAAAGGTTTT CAATTTACTT AGTCCAGATC CATCCATCCA GAGGATCCAC TTTCAATGCC	1620
AGTTATAGCC TTATGGAATG TATTTCTTCA ATAATAAGGC TTGAAAGTTG AAATTACTCC	1680
TTGATCCATT TTCTGCAAAA TAGATGTTGT GTTAGCAGGC ATGAAAGCAA CATTAATCTT	1740
TTTGTACATG TCCATCAGAG CTCTTGGGTG ACCAGGTATA TTGCCAGTGA GCAGTAATAC	1800
TTTGAAAGGA ATTATTTTTT TTAGCAGTAG GTCTCAACAA TGGGCTTAAA ATATTTGGTC	1860
CACCATTCTG TAAACTGATG TGCTGTCATC TAAACTTTGT AGTTTCATTT ATAGAGCACA	1920
GGCAGAGTAG ATGTAGCATA ATTCTTAAGG GACTTAGGAT TTTCAGAATG GTAAATGAAC	1980
ATTGGCATCA ATTTAAATCA CTAGCTGTAT TAGCCCCCAA CAAGAGAGTC AGCCTATTTT	2040
TTGAAGCTTT GAAGCCAAGC GTCGACTTCT CCTCCCTGGT TACAAAAGTC CTAAATGGCA	2100
TCTTCTTCCA ATATAAGGCT GTTTTATCTA CATTGAAAAT CTGTTGTTTA GTGTAGCCAC	2160
CTTCATCAAT GATACTATCT AAATCTCTTG GATAACTTGT GCAGCTTCTA CATCAGCATT	2220

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TGCTACTTCA CCTTGACTC TTATGTAATG GAGTGGCATC TTCCTCGTA CCTCATGAAC	2280
CAACCTCTGC TAGCTTCCAA CTTTCTTCT GTAGTTTCCT CGCCTCTCTC AGCCTTCATA	2340
GACTTGAGGA TAGTTAGAGA CTTGCTTTGG ATTAGATTTT GGCTTCAGGA AATGTTGTGG	2400
CTGGTTTGAT CTTCTATCCA GACCACTAAA ACTTTATCCA TATCAGCAAT AAGGCTGTTT	2460
TGCTTTCTTA TTATTTGTGT GTTCACTGGA GTAGCACTTT TAATTTGCTT CAAGATATAT	2520
TTCTTTGCAT TCACAACCTG GCTGACTGGT GCAAGAGGCC TAGCTTTCAG ACTATCTTGG	2580
CTTTTGACAT GCCTTCCTCA CTAAGCTTAA TCATTTCTAG CTTTGTATTT AAAATGAGAG	2640
ATGTAGGCCA GGCACAGTGG CAGGCACAGT GGCATATGCC TGTAATTCCA ACACATTAAG	2700
AGGCCAAGGT GGGAGGATTG CTTGAACCCA GGAGGTGGAG GTTGTAGAGA TCACACCACT	2760
GCATTCCGTC CTGGATGACA GAGCAAGACC CTTTCTCAA ATAAAATGAG AGGTGTGCTT	2820
CTTCTTTTGT TTTGAGCCCA TAGAAGCCAT AGTATGATTT TTAATTGGCC TAATTTCAAT	2880
ACTGTTGTGT CTCAGAGAAT AGGGAGGTCT GAAGAGAGGG AGAGAGGTGG GGGAAATGGCT	2940
GGTCAGTGGA GCAGTCAGAA CACACATAAC ACTAATAAAT TGTTTGCTGT CTTATATGGA	3000
TGTGGTTTGT GATGCCCCCA AACAAATTACA ATAGTTACAG CAAATATCAC TGATCACAGA	3060
TCACCATAAC AGATATAAGA ATCATGGAAA AGTTTGAAAT ATTTTGAGAA TTAGCAAAGT	3120
GTGACACAGA GAAACAAAGT GAGCACATGC TGTTGGAAAA AATTGGTGT TATAGACTTG	3180
CTCCATGTAA GTTTGCCATA CGCCTTCAAT TTATAAAAA CACAATATCT AGGAAGTTCA	3240
ATAAAGTGAA GTGCAATAAG ATGAAGTATG CCTGTAAATA TTTCAGGCTT TCCAGACCAT	3300
AGGGTTTCTG TTGCAACTGC TCACCTCTGC CATTATAGCA TGAAAGCAGC TATAGAAAAT	3360
ATACATAAAT GAGGCCTGTA ATCCCAACAC TTTGGGAGCC CAAGGTGGAT GGATCACTTG	3420
AGGTCAGGAA TTCGAGACCA GCTTGCCCAA CATGGCAAAA CCCCCTCTCT ACTAAAAATA	3480
CAAAAATGAG CCAGGACTAC GCATGCCTGT AGTCCCAGCT ACTTGGGAGG CTGAGGCAGG	3540
AGAATCTCTT GAACCCGGGA AGGGGAGGTT ACAGTGAGCC AAGATTGTGC CACTGCACTC	3600

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CAGCCTGGGC AACAGAGTGA GACTGTCTCA CAAAAAAAAA AAAAGGAAAA GAAAATACAC	3660
ATAAATGAAT GTATGTGGCT GTGTACCAGT ATATCCTCAT GCTCTAGCTT GCCAACCCCTT	3720
GCTTTACACT GTCAGTTACC TTCTAAAGAG ATTAAAAATC ATAACAATAT CTATTACGTT	3780
TATTCACATC CTAGTGTCTT TTCTTCCTTA TGTAGAATCA AATTTTCATTC TGGTATCATA	3840
TTTCTTCTTT CTAAATAAATT TCCTTTAATA TTTTTTATAG CACAGGTCTA ATAGCAATGC	3900
ATTATGCAAT TCATTGCTAT TAGACCTGTG CTATAAAATA GCAATGAATT ATGTCAGTTT	3960
TTATTTGTCT GAAAAAGTTT TTTGTTTTTG AAATATACTT TTGCTGGGTA TATAAATCCA	4020
TGTTGCATAA CTTCTCTTTT CTTCAGCACT TTAATGAAGT CACTCAGTTA TCTTCTGGCT	4080
TGTATAGTTT CTCTGGCTGC CTTCAAGATT TTTTCATGTG CTTTAATTTT TAGCAGTTTG	4140
ATGTGTCTAG GAGTGATTTT CTTTGTATTT ATCCTTTTGG GGGCCTCTTA ATTTCTTTGA	4200
TCCTTTTTTT CTTTTTTTTT TTTTTTAAAC CATTTTGGGT CTTTCCCCC ATTTGGGGTG	4260
AAAAAAAAA AAAAATAAAA TCATAGTTTA AAAAATAAT TTTGGAAAAT TTTCAGCTAT	4320
CATTTCTTCA AATATTTATC CTACTCTATG CTCCCCCTCT CCCCTTTCCT TCTGTGACTC	4380
AAATTACAGG TATATTTAAC CATTTTATTT GTTCACGGCA CTTGGATGCT CTGCTTTCTT	4440
ATTTTTTGTC TTTCATTTTG GATAATTTCT ACTGACCTAT CTTCAAGTTC ACTGATTCTT	4500
TTCTCAGTCA TGTCTAGTGT GCTCAACGCC TGTTGAAGAA ATCCTTTGTC TTTAATATCA	4560
TGTTTTTTAT TTCTAGCATT TTCATGTAAC TCTTTGTTCT GGTTCATC TCTCTACTCA	4620
CTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTAGA CAGAGTCTCG CTCTGTCACC	4680
CAGGCTGGAG TGTAGTGGCG CGATCTCGGC TCACTGCAAC TTCCGTCCCC TGGGTTCAG	4740
TGATTCTCCT GCCTCATCCT CCCGAATAGT TGGAATTACA GGTGCCCACC ACCGTGGCTG	4800
GCTAATTTTT GTATTTTTTT AGTGGAACA GGGTTTCACC ATGTTGGCCA GGCTGGTCTT	4860
GAATTCCTGA CCTCAGGTGA TCCACCTGCC TCAGCCTCCC CAATTGCTGA AATTACTGGC	4920
ATGAGGCACT GCACCCAGCT CTGCTGACAT TTTTATCTT TTGCTGCATT TTGTCTACCT	4980

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TTTCCATGAA ATCCTTTAAC ATAGTAGTCA TAATTACTTT CAATTCCTTG TCTGACAGTT	5040
CTGACATTCA AGTCTAGGTC TGTTAATACT TTGTGAATCT GTTAACAGCT TTTTTCATT	5100
CTTGCTGTG TGTTTGTAT TTCTTGATTG TATGCCAAAT ATTGCCTGTA AAATAAACTT	5160
AGATAAGTCA TACTTCTATC CAGAAATAGC ACATTTTTTG TGTCCAGTCA TTATGTGGAG	5220
GAGTTGGGGC AGTCTATCAG TGGCTGAACT AGTTTGGATT TGTTGATGCT ATACTTAGAA	5280
TGCACCAGAC TTCCATTAC TGCAAGAGTG GGCTGCTGCG CTTTGTGATT CATGTGAGGC	5340
CTGAATTGTG GAAGGGTTTT TCCTTAGTGT GTCCCTCCAT GCTCAGATTT CAGCAAGTCT	5400
TCATATCTGT GCCACAGAAG GAATCTGACC CATGCTCTTT TTGACCTCCC CAAGTGATCA	5460
ACTGTTGCTT GTTATAGCTT GTCATGGAGT AAGAGGGTGT TTTTTTAGTT TTCATCCTCC	5520
AGCCTTGGTC TTGGGCCCTG AGCTCCTAGA CTCCAGGAGT GGATGGAATC CAGTGATTTC	5580
TCAGTAATTC AGCCCCTCT CCAGTAGTGG CAGATCTCTG CTTTGTATCA GTGCAAGATC	5640
CTGGGCTGAG CTCATTTTCT GCCCTTCCTC GAGTGGCAGA CAGCTCTTGC TTTCACCCTT	5700
CTACCAAAGG CAGTGCATCT TTTCTTGGGC CTCTCCCCAT TGAACCTATG ACTTTCACAT	5760
AAGAGAAGGG CTCATGTATC AGAGAATTCT GTGACTTTGT GCCACATACA GAGTCTCTCA	5820
GTTCTCTTGC CCTGCCCCAG TCTTTTTTGT GAGCACCTAG TAGAGACCCT TGGAGAAGAG	5880
CAAGGAAGCG AGTATGGACT TCTTTTGTGT CTGTCGATTG CTTTGTCTCT CAACTGCTAC	5940
TCTTGGAATT TAAGAATTCA TTAAAATTTC AGCTGTTTTT TTTTTTCTT TCGTTTTTCT	6000
TTTTTTTTTT TTTTTTTTTT AGATGGAGTC TTGCTCTGTT GCCCAGGCTG GAGTGCAGTG	6060
GTGTGATCTT GGCTTGCTGC AACCTCCGCC TCCCGGGTTC AAGCGATTCT CCTGCCTCAG	6120
CCTCCCAAGT AGTTGGGATT ACAGGTGCCC ACCACCACAC CTGGCTAATT TTTGTATTTT	6180
TAGTAGACAC AGGGTTTCAC CATTTTGGTC AGGCTTGCTC CAAACTCCTG ACCTCATGAT	6240
CTGCCCCCCT CAGCCTCCCA AAGTGCTGGG ATTACAGGCA TGAGCCACCG CGCCAGGCCT	6300
CAGCTGTTCT CTTTTTACCT GCTGGGATGG CTAGTTTTCT GTGTCAACTT GACTGGGCCA	6360

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TGGGATGTCC AGATATGTAA TTAAACAGTA TTTCTGGGTG TTTCTGTGAG GGTGTCTTCA	6420
GAAGAGATTT GCATTTGAAT TGGTGAAC TA AGTAAAGCAG AGGGCCCTGT CTAGTAGGGG	6480
TAGGCATCAT CCAGTCTGTT GAGGACTTGA ATAGAACAAA AGGCAGGGGA AGGTTTGAAT	6540
TGCCCCCTCT CTGCTTGAGC TGAGACATCT ATCCTGCCCT TGGCACTCCT GGTTCCTCAGG	6600
GGTTCAGACC TGGATTCTCTG GTCTCCACCT TGCCCATGGC AGACTGTGGG ACTTCTCAGC	6660
CTCCTATCTA ATTAATAAAT TTTTTTTTAC ACACACACAC ACACACACAC ACACACACAC	6720
ACACACACAC ACACACCCTA TGTATCCTTC TGTTTTTCTG CAGAACCATA TTTAATACAC	6780
CTGCTTTTAT GACGATTACC TATCGATTCT GTATTCTGCC AAAACTGAAA ACAGTTCATT	6840
TTTCCATCTC TTCTCAGAGA GGCTTGTCAG CCATTAGTTC TCTGATGGGC TCAAGAAGTT	6900
ATGCAGTTTT TTTTTTCTCA CTGTTAGGAT GGAATTGATA TTCTGTTGAA ACTTTCTATA	6960
CCTAAGTGGA AACTTGTTTT GAGGTATTT TCTCTACTTA CTTTGTGCTGG AAATGGAACA	7020
CTCTGTATCT AGTTAAGACA CATAAACTGA CTTGTGATAC CATAATGTTG TGTGAATTT	7080
TATATTCTTA GAAAATCATC TGTCAAGGTG TTAAC TAATG GCAAAGCATT TAATAAATCA	7140
GCATTCATGT ATTCAGGTGC TCTGAATTAT CTGACTTTTA AATTCTTACT TTATAAATGA	7200
GAAAATTGGG GCATGGAAAA GTTAACTCTC CTAACCCCGA ATTATTACAT TATTAAGGAC	7260
AGGACTTAGA GGCCAGATAT CTTAAGTCAT TAATATTCTT TGGCTCACAG AATTGGCAGT	7320
ATAACCTAAA GGTAATAACT AGGTGATTTT CTTTTATATC AATTAAATAT GTCAGTTTTT	7380
AAATATTCAT AAGTACCTAC TGTGCAGGGA AAGAACATGC CATACAAAG ATGTAGTCCA	7440
GGCCTTTAAG AAAC TTTCAT TTAATGGGAA CTCAAGAAGT GTACATATAA GGAGGGAAGT	7500
AGCAGTATGG TACAAGATAA TACATACATA TCAGTGAATG ATATTGCCAA AAAGTGCTAT	7560
TGATAGAGCA ATAATTCATT TCTGCAAACA GCTGCTGATC TCCTACTGAA AACAGAGGAG	7620
GGAGAACAGG ACGCCTCGTG GTCAGGATAG AAGAGAAAGA CCTTGAGTTG AGCCTTGAAC	7680
AGTATTTAAT ATTCAAAAGG TTAAGAGAGG AGAGCAATTG AGGAGGGGAG AATAGTTCCA	7740

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GCACAAATGA	TGGTGTACAA	GATGAACACA	GTCAGTAAAG	AGCAGACTGG	TCTGGATGGA	7800
GAGGAGGATT	TGCATCATTT	GGGATTACGT	CATTTAGACC	CTTGAAAGCC	AGGATTGAGT	7860
AAAGCCACAG	TGAAGCGACT	GGCTCGTATG	GAAGCTTTAT	TTTAAGAAGA	TTAATCTGGT	7920
AGTGACATGT	GCCAAAAACT	GAATAGGTAG	AAATGAGATG	CAGAGAGCCC	AGTTAGAACT	7980
AAGTCTGGTG	CAGTAATGCA	GGATTGAGGC	AATAAACACC	AAACTACAGT	ATCACCAGAT	8040
AATGGATGTT	TGAACGGACG	GTTTAAAGGA	AAATTGATGG	TATTTGGTAA	TTTATTAGAT	8100
AATCCAGGGC	CATGGAATGA	GAGGGGAAAA	TGACTAACCA	TAGTCATCAA	ATGGTTTTTC	8160
TTAATGAATC	TGAATTTTGG	TGTAAGAGCA	ACATTTTCTT	AGGCCTTGCC	TAGTTGGTAC	8220
AGCTGACTAT	GATAATGACT	GCTACCATGC	TTGTTCTCTT	TTTAGCAGCT	GTGAGTCCCC	8280
CACCAGCCAA	ACAATGAGCC	TCTTGAAAAG	GACGATGCCT	TTTCACTTCT	CTCCAAGTGC	8340
TTGGCAAATA	GGAGGCCTTT	TGAAGTTACT	TTATAGTTAG	GGGTTCCCAG	TGAGTATTTG	8400
AAATATTAAG	TCATGCCCCG	GGTTGACAGC	ATGGCCCTAC	TGCTCATCAT	CAGCTATTAA	8460
CCTTAGGCAA	GTTAATGAAC	TTTTCTAAGC	CCCAGTCTAC	TCATTTATAA	AGTGGGATTA	8520
TTAATAATGT	CTACTTCATA	AAATTATGAA	GCCTGAGTTA	GGTCATTCAG	ATAGTGTTTA	8580
GTCTGATTCT	TCGAACCTAG	TAAACAGTCA	GTAAACAGAA	GCAAATGCCA	CATGCCTGAT	8640
TTATATCCAA	GGGGAGAAAG	GTAAAAGTGA	AATTTTCATG	ATTTATGGAT	TCAAATTATA	8700
CATTTCAAAG	ATGCTTTATA	AGCTATTGTT	TTGGTAAGAA	GAATTGAGCT	GAAACAGAAT	8760
TTTCTGACAG	CAGTGATTAT	TAAATGGTGA	AATAGGCTAT	TGATGTCTTT	AGAGGATATA	8820
GATGTTCAAC	TTTTGCATAT	AAGTGACAAA	AAATTCACCTA	AGTAGATATG	TCTGTCTACA	8880
CAGAGAGAGA	GAGCGTGAGA	GCATTAAAGT	TAGTAAACAT	CCCCCTCGCT	TTTTTTTTTT	8940
TGAGACAGGG	TCTTACTCTG	TTGCCTAGGC	TGGAGTGCAG	TGGTGCAATC	GTGGCTCACT	9000
GCAGTCTCAA	CATCCTGGGC	TCAAGCGATC	CTCTCGCTCA	GCCTCCTGAG	TAGCTGAGGT	9060
GTGCACCACC	ACACCCGGCT	AATTTTTTAA	TTTTTTTATT	GTAAAGGTGA	GGTTTCACCA	9120

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TGTTGCCCAG GTCTCAAACCT CCTGAGCTCA AGCAATCTGC TCACTTCAGC CTCCAAAAAT	9180
GCTGGGATTA CAGGCGTGAG CCACCACGCC TGGCCAGTAA ACCCCATTCA TTTACATCAT	9240
CTTACTTGTC CCTCCAAAAAT CCTGCAAAGT AGGTAGGTTC TGTCTTTATT TGTTATTTAG	9300
GTGAAGAACT TGAAGTGGTG TTGAGGAATA GGTGTTTTGC CAAGAGTCAC GCAGCTGGAG	9360
TGGCAGAGCT GTATACTCTT CTGATTCCAC CAACGCTGTT TACATCACAT CTGGAGAAAA	9420
GTGCTCTGAG GCACAGATGT TTAGTGGGAG GGATGAGACA CAGGCTGCAA TGCCTAAAGA	9480
TAATCGGGAA TAAAAGCAGA AAACAAGACG TTTGTTTCTG TTAAAATGAG ACAGAAAATA	9540
AGGCGTTTGT TGTTTGGGAT TGAGCACTTG GAGAAGTGGG GAGCGATTG ATTTGGGTGA	9600
GACTGCTCCT GGAATGCTGC ATCTGGTTCT GGACTACTCA TTACTAGGCT TATAGAACT	9660
AGCTGGAGGA GGTTCAAAGA AAAGCTCCAA AATGATTAGC GGGCTGACGG GATTGATTTA	9720
TAAGAAATAT TAAAAGAATT AAATGTGTAT AGCTCAGCTA AGCAAAGATG AAAGAGACCA	9780
GCTAAATGTA TACAAATATC TGAAACGTGC AAACTTTAAA AAGAGAGATT AATTATTTAA	9840
CATGATACAC GGGGGCACAA TATGCAGTCA CAGGATGAAA ATTCAGCTG AGTATCTAGA	9900
AGAATTCCCC GATAGTGAAT CTGTTAAGGC TGTCTGTAGT GTGGCCTTTC CCTGGAGAGG	9960
CAATAGAAAT TTCAAGTCTT ACGATTTTAA AAGTTTCTTG GGAAGTAGGT ATTAGATGAT	10020
GTTAGAGAAT TATTATTAAT TTGGTCAGGT ATGATAATGG TATTGTAGTT CTATAAGAAA	10080
AATTGTATTT TTTAGAGTTA CATACCCTGA AATATAAGCA TAGAATATGA TGTAGGAGAT	10140
TTGCTTTAAA ATACCACAGT AAGGAAAGAA AGGAAGGAGG AAGAAAAGAA AGGAAGGGGA	10200
AGAAAGGGAA AAAGAGGCAA AGAAGGAAGA GAAGGTAAGA GAAAGAAAAA GAATGAAGGA	10260
AGAAGGCTGG GCACTGTGGC TCATGCCTAT AATCCCAGCA TTTAGGAGGC CAAGTTGGGA	10320
GGATCACTTA ATTAAGCCCA GGAGTTCAAG GCTGCAGTGA GCTGTGATTG CGCCACTGCA	10380
CTCCAGCCTG GGTGGCAGAG TGAAGCCCTG TCTCTAAAAA AAAAAAATAA GTTAAAAAGA	10440
AAGAAAAGGA TAGATGAAGT ATGGCAAGAT GTTGGTAATG TTGAACCTGA AGGAAGTTAA	10500

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TATGTGAGTT CACTTTCCTC TTCAGTCTTC TTTATGTATG TTTGCCAACT TTCATAATAA	10560
ACAATTTAAA TTATATTTTC CTGATCAAAA CTTAGTAGCA GTATTAATCC CTGGGCTTCC	10620
TGACTAGAAC AGCCTCATTA CCACATGGGC AGAGTTCCTGG CCGACCAGGG ACCACGTAGT	10680
GGTTCACCAT CTTGCTCTGG TAATGTGGTC TGGGCTGAAG GGCCCTTCTT AAGGTTGTAG	10740
ATAGAAATCC AGGAAACTTG TTAGAACTGC AGACCTATCA GGGTACCTGC AGGAGGTGAG	10800
TCTACTAAGG TGAAAAAGCA GAGGGCAGAG GTCGTGATTA GCAGCTGACC GCCCCCTGCT	10860
TTTCTGTCCC TCATTCTGG AAAATTGAGT GGAGCTCAAT TTTGAGTGGA GCTCTAAGTA	10920
GCTCCACTTG TAGACATTGA GTGGAGCTCT AAGTGTCTTC AGAATAGCAA AACACTAGTT	10980
TTCTTTTCT TTTCTTTTTT TTTTTTTGGG AGACAGAGTC TTGGTCTGTC CCCCAGGCTG	11040
GAGTGCAATG GCACGATCTC CGCTCACTGA ACTCTGCCTC CCGGGTTCAA GCGACTCTCC	11100
TGCCTCAGCC TCCCAGTAG CTGGGATTAC AGGTGCCCAC CACCACGCC AGCTAATTTT	11160
CCTATTTTFA GTAGAGATGA GGTTCACCG TGTGGCCAG GCTGGTCTCA AACTCCTGGC	11220
CTCAAGTGAT CCGCCTGCCT TGGCCTCCCA AAGTCCTGGG ATTACAGGTG TGAGCCACCA	11280
CACCCAGCTG CAAAACCTA TTTTCTTGA ATGGAGAAAC ACTTTCCCCT TATTTATTGA	11340
GTTTGGAAG CAAGAAGAGG GGTAATTCAT TAAGTGAAA TTTCCAAAAT CCAGAAAACA	11400
TCGATAAAGC AGCAGCTTAA TTTTTTTAAG GAAGAATTTT TTAAACTATC TTCTTTTGAG	11460
CCTCTTTAGG AAGACCTCAC GTCCTTGCCT TGAATGTTGA GAGTGGGAAA TCCAGGGAGG	11520
TTTTGGAATG CATGCCTTAT GTCTGCTTTT TTGTTTGTTA GAGAAATATA AATATTTTAT	11580
CTAGGTTTTG CTGATGGCAG TCAAGCATGA ACACAACCCA CTGTTTGAGA AGCTGTAATT	11640
TCTGAATTC TGCAGAGTGC ACATCTAGGC CAGCAAATGG CAGTAAGAGT GAGGTGGATT	11700
TAGCTCAGTG TAAGGATGAA CTCCAGAACC ATCGGCTCTG ACTGAAAGTG AAGCGGCAGC	11760
CGCGTTGTGG GAAAGCTGGC TGGAGTCTCT CTCATAAGCA GGCATTCTTT TTCTCCAGCC	11820
CGTCACTGTG TTGGTTTGGG CCCACGGTAA GCCTCCTGGC CTCTAGGCTG TAACCCCCAC	11880

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CATCCTCCTC	TGCCTCGCCT	CCAGAGTGAT	TGTTCTGAAG	CACAACTGGA	TGTCATTCCC	11940
CTTCTGAAC	TCCTAGCACC	TACAGGGACT	CCATCCCTTG	TGCCCCACAT	ACCTCACACG	12000
TAGACATTCC	TAATGAAGAT	TTGATTGAAT	TATTGTAAAC	TCAGTGCCTC	CCACTCTTCT	12060
AGTTGCCTCT	CTGCCTGCCT	TTGTACATTT	ATTTATTTAT	TTATTTATTT	ATTTATTTAT	12120
GAGACAGAGT	CTTACTGTAT	CACCCAGGCT	GGAGTTTAGT	GGCACCATCT	CAGCTCACTG	12180
CAACCTCTAC	CTCCCAGACT	CAAGCAATCC	TCCCACCTCA	GCCTCCCGAG	GAGCTGGGAC	12240
CATAGGCACG	TGCCACTATG	CCCGGTTAAT	TTATTGTAAT	TTTTGTAGAG	ATGGGGTTTC	12300
ATCGTGTTC	CCAGGCTAGT	CTTGAATCC	TGGACTCAGG	CGATTGCCCC	GTCTCAGTCT	12360
CCCAAAGTGC	TGGGATTATA	GGCGTGAGCC	ACCATGCCCA	GCCGCTAGCA	CTCATCTTAA	12420
TCGTATATTT	ACTTATCTGG	CTTTCCCACC	AGACTGCGGG	CTCTTCAAGA	GTAAATGCCA	12480
TGTTTTTACC	TTTATTTCCC	CAGTTTGTGG	CACATTCTAG	GCACTCGCCA	TCATGAAATA	12540
AACCTCTGGA	GCTGTGATAT	TACAAACGTG	AAAAGATGAC	GAGCACTCAG	CAACTTTCAG	12600
TGAGTAAACA	AAGGCTTTCA	TTCAGCATGT	ATTTATTGAC	TGCCCTGATC	TGGGCTGCTT	12660
CCTGTCTGTG	GTTCAAGGAG	AGCATAGTCT	ACAGAACCAG	AGACCTGGCT	ACTCTGGAAG	12720
TTAGACTTAA	CCCCACCCCG	GTCTTGAAT	GGGGAAATAT	TTCCCTTCAT	TCCTGTGTTT	12780
TAGGGACAGA	AAGATGAGTA	ATGCAGTGAT	ACATGCTGGA	AATGTTTATT	CCACTACCCG	12840
AAGCTGCCCT	TCAACTTAAC	AATCCATGAA	AGAAACAAGA	TGGTATATAA	CTTTTCTTAA	12900
TTTGTGATGC	CTTGTTTAT	TTGTTTCCGG	TTAAAAGAGG	AGGTGGCATT	GAATTGTTTG	12960
TTTGGTTTGG	TTTCTTCTTC	AATAAGAAGC	ATCTTAATAT	AACTAGACTG	GACATCTGTC	13020
CCATTTTCAA	AAATTACAAG	TTTCGATCAT	TGCTAAATTG	TACAGATCCC	AATCTGTCTG	13080
CTCTGCATAC	ATTTGCATTT	ATAAAAGCAG	AAGCAGACTA	GCAGTCTTTC	TAATGCAATC	13140
CCCCAAATGC	ATGAAGTATT	AGATTGCTTC	TCCCTATTGG	TTTATGCATT	GCTAAAGGCT	13200
TAAAAGGATC	ATTGATTTTA	ATTATTTAAT	GTGTACAGCA	GGCTGAGCTT	CCTTCTTTTT	13260

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TTAAGGGAAG AACCTTCAGG GGCATTGCTT TAGTTTTTTA ATGTTAAATC TCATTTTTCT	13320
TTGAAAATAA GAAGTTAAAG CTGTATTCAC ACAAGCTCTC AAAGTGCCAG ATTTTCATTG	13380
TGTTTTTAAA CCATCTAGGA AATGTTTGAT TCTAATGAAA CATTACTGCT GAAAATTGGG	13440
CTGAAATTGC TGGGCTGAAA ATATTGTTAT AACTTCACAT GATTCCAGTG TTGTATTATT	13500
ATTTTTTCTT TTCCTTTTTT TGACCCGATA TAGATGAAGC GAAGAGACAA GGGAGCAATC	13560
CCATGTGTAA TAAAAAAGG CAGCCTGAAT TGTGTGTGCT GTTTTTGAAA TTTAAGCTGG	13620
TTTTCAATTA AATTCAGTAA ATGGTCCAGG ACTATAAATG TTGAACATTT TTTACCGTGT	13680
GATTTAAAT TTAGTTTAA TGTTTTTTTT TTGGGTTTTT TTTTTTTTGA TGGTTTACAT	13740
TTCCCCATG GAAAGCAGCT ATGTCATGTC GGCATGATTC ATCATGGTAA CATCTCGGGT	13800
TATTTTGGTT TGTGTTATGT TCAGAAAGCG GAATGCCAAA AATAAAGAGT GGTGTGTGAT	13860
GTCTAGTGTG TCTTCCTTTA ACAAATCAA GGCTTTTATT TAATCCACTT AATGGGACAC	13920
TGCAGAAATT TAAAAATGG AAGTCCCATC CACAGAAGGC AGGTACTATG ATGTAAAAAG	13980
TTTAGGTGGG GGATTAATAG AGTGATCATA TAATTTATGA GCTAAACCGG AGGCACTTTT	14040
TTTTTTGAGA TCGAGTCTCA CTGTTGCCTA GGCTGGAGTG CAGTGACGTG ATCACAGCTC	14100
ACTGCAACCT CCGCTCCCG GGTTCAGCG ATTCTCATGC CTCAGCCTCC TGAGTAGCTG	14160
GGACTATAGG CGCCCACCAC CATGCCCAGC TAATTTTTGT GTTTTTTGTA GAGATGGGGT	14220
TTCACCATGT TGGCCAGGCT TGTCTCAAAC TCCTGACCTC AGGTGATCCG CCCACCTCGA	14280
CCTCCTAAAC TGCTGGGATT ACAGGCGTAA GCCACCATGC CTGGCCCAGA GACACTTTTG	14340
AGAGTGAAGA GGAAGCTGAG AATAATTCAC TGATCTACAA CTGGGACCAT CCAGGGCAAG	14400
CCAGATGCCA TTACCACTAG CTAGAAAGCT TGCCAAGGTC TCATTTACCT TGGTATATAG	14460
CAAATCTTC TTTGAATCTT GGAAATTCTG GTAAGTCATT GAGGTAGCTC TGTGCCAAGG	14520
AGCAATATGG TAGAATTCTA ATATTTTCAAG CAGTACAACA CTTTCCTGCA TTTGTAGCAG	14580
GTAAAGGGAG GTCAGGGCAG AAGACAAAAC CACTGGGACT CGACAAAGGG CATAAACGTC	14640

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TAATGCACCT GATGTAGCTG ATGGTAAATT GTTATCAGCT AAAGATCTTT CATAATAAAT	14700
AAACTTATCA TTTGTAGGAG GGCACAGAAA TCGTGGAAAG CTGGGATTCA GGTTCCTGT	14760
GGCTTTAATT CTGGAATCAG AAATATTAGT CAAGGATATC AGTCTATGAA GTAAGTTTTC	14820
AATGTTATAT GCCACAAGAT GCAGCTGTCC TATTTTCACT TCCAGTAATT CCTTCTGAAT	14880
TAATACACCT TAAAAATAGC TGCAGCTTCT CAAATCTGTG AGAATCGTAT GTGCTGCTTG	14940
CTACACTTTC CTTTTTCCTG AAGGCCTCTT TGAGGTCTTT CAAGAACTCA ATTCAATTCA	15000
GCAACAATTA GGGGGTCTAA GGTATACAGA CGCTGTGCAA GATGCTCCTG AGACACAAAG	15060
AGGAGGTCAA GCCCCTGCCT TCAGGCACCT CTCTATAATA TAGGAGGAGA AAGAGAAGAA	15120
ACACTAATAC ACATAGGTAG GTGCCATTAA AAGGGTGCAT ACATTAAAGC CAGGTGGTAG	15180
GTGCAAGAAG ATTTGTAACG TGAGAATTTT CTGCATGTTT GAAATATCTT ATAATTTTTA	15240
AAAATTAAAA TGGGAGATAC ATATATATGT ATTTATGTAT GTATATATGT ATGTACATAT	15300
ACACACATAT ATACATAAAT ATATACATAA ATATGTATAT ATGTGTATAT AGACATAAAT	15360
ATGTATATAT GTGTATATAT ACATAAATAT GTATATATGT GTATATAGAC ATAAATATGT	15420
ATATATGTGT ATATAGACAT AAATATGTAT ATATGTGTAT ATAGACATAA ATATGTATAT	15480
GTGTATATAG ACATAAATAT GTATATATGT GTATATAGAC ATAAATATGT ATATATGTGT	15540
ATATAGACAT AAATATGTAT ATATGTGTAT ATAGACATAA ATATGTATAT ATGTGTATAT	15600
AGACATAAAT ATGTATATAT GTGTATATAG ACATAAATAT GTATATATGT GTATATAGAC	15660
ATAAATATGT ATATATGTGT ATATAGACAT AAATATGTAT ATATGTGTAT ATAGACATAA	15720
ATATGTATAT GTGTGTATAT AGACATAAAT ATGTATATAT GTGTGTATAT AGACATAAAT	15780
ATGTATATAT GTGTGTATAT AATAATGTGT GTACATATAC ACACATATAT ACATACATAA	15840
ACATTCTGCA TTATACCATT CACTTTGTAA CCCATCTTCC CTAAAACTG TCTCATAAAG	15900
AGTCTTCTTT TCCCTGTACC TATGCAATGG TAAGTAGCAA AACACACATT CTTTGGGTC	15960
CCCATAACAT TCCCTGTAGT TTGCCCTTAA CAGTCTTTGA TGTGAAATTT ACTGTTTCTG	16020

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TCTTAACCTT	GCCTGTCTCG	CGTACATGGA	GTTTTGGCTC	CTGGCTCCTA	GTCTGCATCT	16080
TCACCCCATC	CCTTGCCCCA	AGAATCTGGT	TATGTGACCA	CTGCTCATCT	TTTCTGCTGT	16140
CACAACTCCA	GTCCAAGCCA	CAAACCTCTC	TCTCCTGGAC	TCCTGCGGGG	AGTTCCTTTC	16200
TCTCCCTGCA	TGAGTCTATT	CTCCGCACAA	CTGGCAGAGG	TAAGTGAGAC	TGCGGAAGAG	16260
GCAAGTTTGC	AAGTCCAGAG	GAAATGAAGA	CTCTGCTTGT	GCACATGCTG	GGTTTGACGG	16320
GTGCTGGATA	TCCGATGGAT	GGCCCTTAAG	GTGAGCTCAA	GGCTTAAGGG	AGAGATAGGG	16380
GCTGATGATC	TGAGATTTCAT	CAGTGTGTGG	CTGATGTTTA	AACCCAGGGG	ACAGGATAAG	16440
AAGGTTATTC	CAGGGAGAGC	GTAGATAAAG	AAGCTAAATG	GCTTCTGGGT	CCTTAGTCAT	16500
TCAAAATCGG	ACCTCTGAGG	CAGGAGGAAA	GCCCAGAAAG	AGTAGATTCC	TGGGACTCAC	16560
GGGATAAAGA	CTTTCAAAAA	GTGGGGGCTG	GCCAGTGCTG	CTGAAGGAAG	TAGCAGGACC	16620
GGAACAGAAG	GGTAATCGTT	GGACCTGGAG	AACCTGAATT	TGAATTTTAA	GGTTGGTAAC	16680
CTTAAAAAAG	AGCAATTTTA	GATACCTTTT	GAAATTATTT	GCAAGATTTG	TTTGGTATAT	16740
GTGTTATTCC	AGGCAAAGGG	ACCAGAAAAG	TAAAAAATAC	TTACTGAACA	GTTACTGCAT	16800
GCCTGGCACT	GTAACACCCT	GTTTAATTCT	CACGGCAACC	CTATAGAGTA	GGTGTCTATCA	16860
TCCCCATCTT	ACAGATGAGG	ATATGAGGTG	CAGCTAGATT	AAGCAGTTTG	CCTCAGGTTA	16920
CACCAACTGG	TTAACGTAGA	GCTAGGATTT	GAACCCGGAT	GGGCTGATCC	CAGAGCTCAT	16980
GCTTTAAATC	GCTAGACTGG	TGCTCACAGA	AGACTGGGAC	CGAAAAAAT	TAATAAAAAA	17040
AATAAGGAGC	CCCCTGGGCT	AGCAAATTAG	GAGTTGTTCA	GACAGATGTG	AAAAGGAAAG	17100
CAAGGCAGAG	GGAAAGTCAC	TGTACAGAAG	AGAGAGACCC	ATGACAGCAG	AGACAGTGAG	17160
CTGGTAAAGT	GGCTGGCGAT	CTAGCCCCTG	AAAATACCTC	CAGAGAGGCA	GGCTCACGCC	17220
TGTAATCCCA	GCACTTTGGG	AGGCCGAGGT	GGGCAGATCA	CCTGAGGTCA	GGAGTTTGAG	17280
ACCAGCCTGG	CCAATGGCGA	AATCCCGTCT	CTACTAAAAA	TACAAAAATT	AGCCGAGCAT	17340
GGTGACAGGC	ACCTGTAATC	CCAGCTGTTC	AGTTGGCTGA	GTCAGGAGAA	TAGCCTGGAT	17400

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CCGGGAAGTG GAGGTTGTAG TAAGCCAAGA TTGCGCCACT GCATGCCAGC CTGGGCGACA	17460
GAGCAAGACT TTTCTTAAAA CAAACAAACA AAAAAGAAAA AAGAAAAGGA AAGAAGAAAG	17520
AGACAAAGAA AGAAAGAGAG AAGGAAAGAA AGGAAGGAAG GAAGAGAAGG AAGGAAGGAA	17580
AGAAAGAAAA GGAAAGAAAG AAAAAGAAAG AAGAAAGAAA GGAAAGAAAA GAAAGAAAAA	17640
GAAAGAAAGA AAATACCTCC AGAGAGCCAG GTCTCTTAGG CCTTCTGAGA AACTCACATC	17700
CCTTTTGATG AACACAAATG CTTCACTCTC TCAATGTTAT TGGTAATCCA AGTTATCAAT	17760
ATACCTAAAT CACTTAGTAC TGAATCTGGC ATATAGTAAT CACCTAATGA AGAGATAAGA	17820
GTCATGGAGT ATTCTGAAGC AATTAGAATC AATAGACTCA ATATACACAT GGCAACAAAG	17880
TTGGATCTTA AAAACCGACC TGAGTGAAAA AGGAAAGGGA AAGATACATA ACACGGTACC	17940
ATTATGTAAA TTGATAATAT ATGCTTACAC AATTGTGAAG AACACATACA AATAGATACA	18000
TGTATATTAA ACATACTCGA ACGGTTACCC TATGGGGTGG TGGCTGGAGT GGGGGTAAGT	18060
CCGTAAGCTG TAATGGAACC TAAACAAATA CATGAAACGA GTAGGAATCA GAAGGAGTAA	18120
CAATAAAAAT GTGCCATGAA CTGAGGAGTG TAAATTAATC AACTCACTGC ATCTGAGGTT	18180
AAAAATAGAA AGATGATAAT TGTATTCTT ATTACTCCTA GGTCTTCCAC TTGCACTCAG	18240
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GCTTTTTCCT CCAGCTTCTT AGGTGATTTA ATATATCAGG GAATAAGTAT AAAAAAAGGC	18360
ACGGTGCTCC CTGGGTAGCC TTTCTGGACT TCAGAGCTAA ATTGCAAAGT CAGTTTTACA	18420
CATGTGATTT CATCTATGAA ATTAGGGCAA GGTATAAAAC TGGCACAGAA AAAATGTGAT	18480
TTATTATGGT GTTACTATCC CTTACAAGCG GAGTGTCAGC TGCCTCTTTT TGTCCACTGA	18540
TTTAAGGCAA GATGAACTGA AAGTGGCTAT GATCACGTCT TCAAAAGCAC ACTCTGGCCC	18600
CTCGGCTGCA GCGGCCCTGC ACATTCCCCA GCTGCGTGTC CGGTGGTGAC ACAGTGCATA	18660
ATTGTGGCGC CTTCTGGTG CAACTGTCT CACTTAGCTC CGTCTTGCTG GCACAGCAGA	18720
AAGGAAGAAA TCGAAAATGT TTGGATTTC AAGGTAACAA GAAGCTGGAA AACAACTACT	18780

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GGCCGAGTCT	GAGAGTTTCA	GCGGAGACTG	GTGCAGCCTT	GTGTTTTTCC	ACTGACAGCT	18840
GAAATGAGC	CCAGCTTCAG	TGAAGCTTGT	TTCTTCCCT	CCTCAAGGTT	ACCCACAATT	18900
CTCAGTTCTC	TCAGGAAAGC	CAAAAAATGA	ATTTGAGGGT	TTAGGATTGT	GGTTCTTTTA	18960
TCTATTACAG	GATTGATAAT	ATGTTCCCTC	ACCAGATGTT	CTGCTTGTA	CAATACTCAC	19020
TTCTTGACAC	TACTGCATAT	GCAGGAGTGT	CACTACCAAG	GTAAACACAG	AATTGGCTGC	19080
CCAATTCCAA	ATCCCTGAAC	TGAGTGAGAG	AAATCAGAAT	TATAATAGGG	GATTCAACAG	19140
AGCTGGCTAC	GGATGTGCCA	GTGGTCAGAT	ACTTTGCTCA	TCATACGCAG	GTGCTGCTGC	19200
TCTAGCAACT	GCTCACTGCT	TCATTCCCTG	CCTTGGTCTT	TAAATACTGC	TTTTCTCAGC	19260
TCAATTGGCT	TTCTTCCCTC	TGGCAGTCAC	GTTTCTTTGG	GTCAAACAGC	AAATGATTCT	19320
TTAGAATCAC	CTGGTACTCA	AAGGAGCTAC	AAGACATTGG	GCATCCACTT	CCACTCTCTT	19380
GGAAAAACAA	TTTTATGGAA	GCCAAGGTTG	CCATAGTGCC	TCTTGAGGTT	GTTTGCTCAG	19440
CCAAGGCCCA	AGCTTTGTGC	TTCAAACATG	AAATTAGAGA	GCTTCAGAAC	AAGATCCACA	19500
TTTTCAATGG	CCTCACCCAA	CTGGATAAAA	GAACAATTGC	CATATCTCAA	TGACCACCTT	19560
TTCTCAGGTG	GGATGGTAGA	TGCTGGAATG	GGTCACAGCA	TTGCCCAACC	AAACTTTGCA	19620
AAAAAGGCTG	GAAGCTCTGA	CTGGGGACCC	TAAATATGCA	AAAGTTAATA	GGCTCTTCAT	19680
GCAGAATATG	AACCCCGTGT	ATGGATATAG	CTAAAGGGTT	GGCCTTTATG	TTTCTATTCC	19740
TTCACAAACC	TGGTAGAATA	GATATGCTTG	TTTCCCTTTA	AAAAATGTCA	ACAATTGCAT	19800
TTATGATGCT	GTGTATAGTA	ACTCACAGAT	CATGCTCCAT	GAAAATGCTT	CAGAACCCAA	19860
TATAAGGAGA	TTTTTTAGCC	ATGTGTGACA	AAAGAGAGGC	CATTTCAAGT	TTGAAATTGT	19920
TCAGAGAAGT	ATTTGATTAT	GTTTTCTCAG	ATCTTTTTAT	TTTTATTTTT	TTTGAAACAG	19980
AGTCTCACTT	TGTCACCCAG	GCTGGAGTAC	AGTGGCTGTG	GTCTCGGCTC	ACTGCAACCT	20040
CTGCCTCCCA	GGTTCAAGCG	ATTCTCCTGT	CAGCTTCCCG	AATAGCTGGG	ATTACAGGCG	20100
CATGCACCAC	CATGCCTAAT	TTTTGTATTT	TTAGTAGAGA	CAGAGTTTCG	CCATGTTGAC	20160

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CAGGCTTGCC TTGAACTCCT GACTTCAGGT GATCCACCCA CCTCAGCCTC CCAAAGCACT	20220
GGGATTACAG GCATGAGCCA CCGTGCCCAG CCTGTTTCTCT CAGATCCTGT ATTTTGTTTC	20280
TGAAGCCTTC ATTTCTATCT TCTTATTCAT TTTGGAAGTA GTACACCTAA GTAAGGTTTT	20340
TAACAATCAA ATATCTTTGG AAAATTCCTT GGTTCCTTTC TTATTCCTAC AAAAATATGT	20400
TCAGTATAGC TGATGTTATG TTTCTTTCAA ATTATTCATT TCTCTATCTC AGAATTTATC	20460
TCATGCCTAA TTGTATTGA ATAGTCTTCA CTTCTTGTC TCCAGTTTCT GGTCTCTTAT	20520
TTCACTCTAA GTCTAATTGG CTATTAGAAT AAAGAGCTTG TAACAGATTC TTTCTCCAAT	20580
ATGTCTTATC TTTTGACTGC ATGCCAGTGA CAAACTGTTA ACTGTTTTGA TTCTTCATAA	20640
CATTCCACAG AACATGCTGA CTCCTCTCTT CCTGAAAGCA ATGCCCAAGC ACAGCATTGT	20700
TAGATAGTAT GTACGCAACA GGGACATGGG TGCATAGCAA AAAC TAGAAG GAAGGAGGAC	20760
CTTCCTTAGC AATGGGTGAT ATGGTCCCTG GACTTAGACT CCAAAGGGTC GTGAGGTGAA	20820
ACACACATCG TCCATACCCA GGAAGCACAC AGGTGGGATG GAAGAGCTGT GCCTAATGAA	20880
ACTTCATCCA CGTGGAGGTG GAGGAGGCTG CAGCTGCAAG AACTCAGAGC TGCCTTACCC	20940
AGACCAGGGA CCAGGGAGGG CTTTCTGGAG GAAACAGCCT CTGAACTGCC AGCTGATAGA	21000
GGAGCTCTAC CTCAACTCTT CTGGTTCCCC AGGGCTGCTT TTCCACGTCC ATTTATTGGC	21060
ACTGAAGTTT GAATACCTTC AGGGGCCCGA AAGCCTGCCA GGTCTCTTTC TCTGCAGAGC	21120
AATCACACCA ACCTGCAAAG GGCTAGGAAA GGGCTGTCTAT CATCTCCTAC TCAGAACTG	21180
GTTCACTGGA AGGACTCAGG GGCCACTGAA TACATCCTGG CAGCTTTCAC AAGAAGGGCT	21240
TCTGACTCAA GGATGTTTCC ATCTTTGCCA GGTCGCCTTT TCTCCTTCTC TTAGAGTTTG	21300
GAGGACGCAA ATGTGCTGAG AAGTCAACCT TTCCTGCAAG GTGAGACACA AGGGCCTTTC	21360
CCAGCAGAAA GAAGAGAGCA AATGGAAGGT CCTTCTTCCT CCAGTAGAGG ATGGACTCTG	21420
TCTGGCAGCC ACCCAACAGG AAAAGCACAA TGCATGCCTG CCTGCTTCCC TCCCTCCCTC	21480
CGTTTCTCCC TCCCTCCCTC CTTCTCCCT TCCATTCTCT TCCCTTCCCC TCCCTTCCCT	21540

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TCCCCTCCCT	TCCCTTCCCC	TCCCCTCCCC	TTCCCTTCTC	CCTCTCCTTC	CCTTCCTCTT	21600
CCCTTCCTTC	CTCTTCCCTT	CCTTTCCCCCT	CCCCTTCCTT	TCCCTTCCTC	CCTCCCTTCC	21660
TCCCTTCTTT	CCTTCCCTTC	TTTCCTTCCT	CATTTCCTCC	CTTCCTTCCT	TCCTTCCTTC	21720
CTTTCTTCCT	ACTTTCCTAC	CTTTAGGGCT	CTGTGTCTTT	GGAGTCCATT	CTGATTATGC	21780
TGTAATGTCT	GCCCCCTCCT	CTTCTCTGTC	AAAAAATGAA	AGACATGGAA	GCCACTTGCC	21840
TTTTACTGAA	TTAAAAATTA	GTAAAAGAGC	TAAAAATTAA	TGGTTAAAAA	TGTACGCATA	21900
AATTATGCAG	TATACTAACC	AATGAAAAGA	TACACTTCTC	TTAATTAAAA	GCTGACAGGG	21960
AGGGAAACAA	GAAAAGAGAA	ACACAAAACA	ATAATCTAAA	TGACCTATTA	GTTGGAAGAA	22020
CAACATCAGA	GAAAATAGAT	ACTGTGTATA	GTCATGTGTA	TGTCTATGGA	ATAACATTTG	22080
TAGAGAAATC	TGGACTGATC	CTTCTGAGT	AAAGAGAGCT	GTGGGTACAA	TTAAGGGGAG	22140
ATTGAAAGGA	ATCCAAAAGC	ATAGCAGATG	CTGTGCCTCA	CTGGAATGGT	TGCCGATCTC	22200
CTCCAAACTA	TGAAGTGTTT	GAGGCTCAAC	TTTAATATAA	TTAAGATACA	AAGACAGAAT	22260
GAGAGAAAGA	GAGAAGGGAG	CTCACTGGAA	GAACACTCAA	GATTCCTTAC	TACTCATTTCT	22320
CTAAAATTAC	AATTGTTCTA	GATGGAAAAG	AAAAAAGCT	TCTCTGTTAA	AAAAGGAGCT	22380
TGTGCTATAG	GAGGTTTAAA	ATATACTTCT	GACCCATCTC	CAACATTCTA	AATCCTTCCC	22440
AGAAAAGTAT	GCCAATCCCA	AGAAATATTC	AATCAAATTG	CTGGAAAGAA	AAATACAAAA	22500
TATTAAAATG	TATTAGGAAG	CGACAGTAAT	TAAATCAGAA	CTGGAGCAGG	AATAGACCAG	22560
CAGATCAATG	AGACAGACAT	CAAGTCCCGG	AATGTGGACT	TGCAAATGCA	TTAAGTAATA	22620
TGATATGCAA	TAAAGGTGGC	ACAGTGAACC	AATGGGAAAA	AAATTAATCT	TATAATAATT	22680
GATATTGCAA	TAATTGTCTA	GTAATTGGGG	GAAGAAATAA	GCTTATTCCT	TATCTCATTT	22740
CTTTTTTTCT	TTTTGAGACA	GAGTCTCACT	CTGGTAGCCC	AGGCTGGAGT	GCAGCGATGC	22800
GATCTCTGCC	CACTGCAACC	TTGCTCTCCC	GGGCTCAGGC	GATTCTCCCA	CCTCAGCCTC	22860
CCGAGCAGCT	GAAC TACAGG	CGTGTGCCAC	CAC TCCCGGC	AATTTTTTTT	TCCATTTTTA	22920

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GTAGAAATGG	GGTTTCACCA	TGTTGCCTGG	GCTGGTCTTG	AACTCCTGGG	CTCAGGCAAT	22980
CCACCCGCCT	TGGCCTCCCA	AAGTGCTAGC	ATTACAGGCA	TGAGCCACCG	CGCCTGGCAG	23040
CTCATTTTTT	AGACTAAATA	AATTGGAGAT	GGCTAAAAGA	TTTTTATGTA	GGCCAACAT	23100
GTTTTTAAAA	AGTTTTTTTT	TTTAAGGATA	TCTGCTGGAA	CCAATCATGC	CACCAACCAA	23160
AGATGCAAGA	CTATAAAACA	TACCCAGTTT	TTCAAAGCAT	TTAAAAATTA	TTCTAAAAAT	23220
ATTTTTTCTC	CAGAAATTTT	GCATTGATTC	CCTGAAGAAG	CATTAATATG	GGACCTGACT	23280
TATAAAATGA	TGAACTCAAT	CTCCCCACTC	AAGGTAGGAG	TCTCTCAGAT	TTAAAAAATA	23340
AGCATCCTAG	TCCTCTTGTC	CCTGTAAAAG	TTAACCCTTA	CACCTGAAAC	ACCAGGAGAC	23400
TGGCGGTTGT	TTGCATAGGG	GTTACAATTA	AAGTTGAGCT	ACCTCTGACA	TCTATTAACA	23460
CCAAAATTAG	TAAACTATGC	ATGTATGGAG	ACTTTTATGA	TTGAACTTGT	TTATTGAGTC	23520
AAGAGATATA	GTTTACAATG	AAAATTGGG	GCATATCAAA	ATGACCTTGG	CTTAGCTTAG	23580
CATTTGCTGA	TGTTAACTAT	TTTCTTCATT	GGGCTGATTT	TAGTTGCTTA	GGAAAAATAC	23640
AAACACACAC	ACTTTAAAAT	TATATTAAAA	TCCCGTCCTA	AACCTCAGAG	TCCAGAACCG	23700
CATCCTAACA	CTGGTCATGC	ATAATATGTT	TAAATTTTGT	TGCTTTAAAA	ACTACAAATA	23760
AGGAATGTAT	TAATAGTTCC	ACAATCAATG	GTCAGTTAGC	CGAGGGAAGA	TTAGCATAGT	23820
TAAAGACTTA	AAATGGCTTA	ACAACATATA	TCAAAAGGAC	AAAATAAGGG	GAACAGAGTC	23880
TAGAAATGAG	GAAACTGGGA	CACAGGCAAA	AAAAAAAAAT	GAGAACTGGG	ACATGAATAA	23940
CGCAAGGGAT	AAGACTAATA	CACAAAACAC	CCCAAATAAA	TAGCCAGCAT	TTGCTGAGCT	24000
CTTACTGTGA	GCCTGTTCTA	AGCACTTTAC	ATATATTAAC	TCATTTTCATC	CTCAAGGAAC	24060
CATCTGAGGC	AGGCACTGTT	ATCATCTCCA	TTTTACAGAT	AAGGAATAGA	CCCAGAGAGG	24120
CTGAGCAACT	GGGCCTATTC	CACAGCTACT	ATGGTGAGGA	TGAGATTTAA	ATCTAATCAT	24180
TGGCTCCAGA	GCCCATGCAC	CCAATGGCTG	CACTAAGTGA	ATGCATGCGC	TATCAACGTT	24240
GCCAAAAGTG	GGCCACAGCT	CGGATCTGCG	TTTTCCAGTA	GCCAAAGCAG	AGAGTGTGAT	24300

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CAGACCTCAC	TTTAATAAGC	AAGTCTCAAG	CCAGAGAGAG	GTGGTATCAG	GCAGCAAACA	24360
GGCTGCTAGT	CGAAATCCCA	CTTCTTCTCT	GAGTGGTCCA	TACAGTTTTA	CTCTACTTGC	24420
TTACAGAATG	AAAATAGCTG	GAGTTCAGGT	GCGCTTTCAA	TGCCCTGTTG	TCAGGATTGG	24480
GCTTTTCAAG	TTTATTTTTT	GTTGTTGTTT	TTAATAGACT	GTACTTTTTA	GAAAATTTTT	24540
AGATTTACAG	AAAGATTGAG	AGGATAGTAC	AGAGAGTTCC	CGTATACCTC	ACACCCAGTT	24600
TCTGCAATTA	TTAACCTCTT	ACATTCATGC	GGTACATTTG	TTACAATTAA	TGAGCCAGGG	24660
CCGGCCGGGC	ACAGTGGTTC	AGGCCCTTAA	TCCCAGCACT	TTGGGAGGCA	GAGGCAAGCG	24720
AATCACTTGA	GGTCAGGAGT	TCGAGACTAG	CCTGACCAAC	ATGGTAAACC	CTTCTGTAC	24780
TAAAAATACA	AAAAATTAGC	CAGGCATGGT	GCTGGTTGCC	TGTATTCCCA	GATACTCAGG	24840
AGGCTGAGGC	ACAAGAATTG	CTTGAACCAG	GGAGGCGGAG	GTTGCAGTAA	GCCGAGATCG	24900
TGCCACTGCA	CTCCAGCCTG	GGCAACAGAG	CGAGACTCCA	TCTCAAAAAA	AAAAAAAAAA	24960
AAAAGAAGGA	AGGAAGGAAG	GAAAATTAAT	GAGCCAATAT	TGAGACATTA	TTATTACTAA	25020
AGTCCATGCT	TTATGCAGAT	TTTCTTAGTT	TTTACCTGCT	GTCATTTTTT	AGTTCCAGGA	25080
ATGCATTGAG	GATGCCATAC	CACATTTAGT	TCTCATATCT	GCTTAGGCTC	CTCTTGGCTA	25140
GACTGAGTTT	TAATCTACTT	TCTGCAGAGC	CTGAGAACTT	TAGCATAATT	TCCTTGAAAT	25200
TACAGCTCAA	TATTTTCAAG	CACTTATACA	AACAGCCTAA	TGTTACGTTG	GCCCATAACA	25260
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CTCCTGCCAG	ATGATGAACT	GGGTACACAC	GAGCATTTTT	CCAGGTAAAG	CATATTTTCGT	25380
GCGACTTCTT	AAGCTGCAGC	CTTATATGCA	ATAATTGTCC	ATTTACAAGA	CTTATGTTTCG	25440
AATTCAGGC	ACTCTGTTTT	CACTAACCAT	ATCTTCAACT	TTGATAAGTA	CTGCTTTAAT	25500
CACTCAGAAA	ATTTAACTTG	ACTAATTTTT	TTTACCATC	AGTTTTTTTT	CTGTTGACTC	25560
TTTCTCCTTT	TTCTGTTTGC	CCAGAAACAT	GCTCAGGATT	CTCTCAGGCT	TTAAAAAATG	25620
AAAAATGTT	TCCTGCAATC	TAGTTACTCC	TTGATTCTCT	TGTTCTGTTT	ATCGCTGGAA	25680

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TTCTTGAAAG	CTTGGTGTAT	TAGTCTTTTT	TCATGCTGCT	GATAAAGATA	TACCTGAGAC	25740
TGGATAATTT	ATAAAGAAAA	AGAGGTTTAA	TGGACTCACA	GTTCCACGTG	GCTGAGGAAG	25800
CCTCACAAATC	ATGGTGGAAG	GCAAAAGGCA	TGTCTTACAT	GGCAGCAGAC	AAGAGAGAAT	25860
GAGAACCAAG	GGATTTCCCC	TTATAAAACC	ATCAGATCTT	GTGAGACTTA	TTCCTACCA	25920
CAAGAACAAT	ATGGGGTAAA	CCGCCCCCAT	GATTCAATTA	TCTCCCACCG	GGGCCCTCCC	25980
ACAACACGTG	GGAATTATGG	GAGCTACAAT	TCAAGATGAC	ATTTGGGTGG	GGACATGGCC	26040
AAACCATATC	ACCTGGCCTA	TAGCATTATT	TCCATTTCTT	CCCCATCCTT	TTATTCCTCA	26100
AACCGGTACA	ACCAGACCTC	TTTTTTTTTT	TTTCTACCTG	AACTGCTCT	TTTGAGGGTA	26160
GCTGATAAGT	CCAAAATACT	GTCACCTTTT	CTCAATTCCG	TTCTTCTTA	TGCCTTTGA	26220
GCAATTGACT	GTGTTGGTTG	CCCCCTCCTT	TAAAGTGTCT	CTCACTTGGT	TTTTATGACT	26280
AATGATCATG	ATTTTCTTTT	TCCTCTCTAA	ACATTCCGCT	ATCTTTTCTAG	CTTCCCTTCC	26340
CCCTCCCATC	CCCTAAATGT	CCTTGTTTCC	CAGAATCTGC	CTCACCTCTT	TGACTTCTCT	26400
ATGCCCTGTC	ATTCACTCAT	GGGTCTTTAT	TACATTATTG	CATCTGTGTC	AATAACTCTG	26460
GTCTTTCTCT	TAAGTTCCAG	TCTCCCATTT	TCAAATGTCC	CCAGACATTT	CCAATTGAGT	26520
ATCTCTCCAA	TGTATTTAAC	CTGCTAAATA	TCTAACACAT	AATCTTTCCC	ATCAAATCGT	26580
TTCTCTTAA	GCTTTTCTTA	TTTCCTATTA	GTACTCCTGC	ACTTCTCCCA	GGAGCCCAGA	26640
CTTAAACCT	TGAATTTCTC	ACCATAACCT	CTCTTTTGTC	TCCCATAATC	AATTAGTAGC	26700
AAGTGTATC	AATGATTACT	TGACAATATC	TTTTTCTATT	TCCCTCCCTG	CTATGATCAT	26760
TCATCTAGCA	AGAAGAGTTG	GCCCTTTGTA	TCTGTGGTTT	CTGCATCCCT	GGATTCAACC	26820
AACTGTAGAT	GGAAAATATT	TGAAGAAAAA	AGCGTCTATA	CTGAGTATGA	AAAAATTTTA	26880
TTTCTTGTC	TTATTCCTTA	AACAATACAG	TATAACAAC	ACAGCATTTA	CACTGTAGCG	26940
TATAGATCTT	ATAATCTAGA	AATGATTTCA	AGTACACCAT	TATATATAAG	GGACTTGAGC	27000
ATCTGTGAAG	TTTGGTATTT	GTGGGGCATA	CTGGGACCAA	TTCCCCCATG	GATACAGAGG	27060

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GACAACTATA	TTTACTCAGT	GCTTACTAAA	TACCAGTTGG	CCAATGTGTT	TTTCTTTTTC	27120
TGTTTTCTCG	TCTTTAGTTT	CCCCCTTGCC	AATTAATTCA	ATAGTGCTGC	CAATGCCAGG	27180
TGTACCTTCA	GAATATTCTA	TTCTAATTTT	GTCATCTCCA	AGCTTAAAAA	TATTTAATGG	27240
GCCAGGCGCA	GTGGCTCACA	CTTGTAATCC	CAGCATTTTG	GGAGGCCAAG	GGGGGGTGTA	27300
TCACTTGAGG	TCAGGAGTTC	CAGACCAGCC	TGGCCAACAT	GGCGAAACCC	TGTCTCTACA	27360
AAAAAGTATA	AAAGTTAACC	AGGTGCTGGA	GCATTGCGCT	GTGGTCCCAG	CTACTCACGA	27420
GGCTGAGGCA	AGAGAATCGC	TTTAATCTGG	GAGGTGGAGT	TTGCAGTGAG	CCAAGATCTC	27480
TCCACTGCAC	TCCAGCCTGG	GTGACACAGC	AAGACTCTAT	CTCAAAACAA	CAATAACAAC	27540
AACAACGAAA	AACATTTAAT	GGCTGCACCT	TGCCTGTGAA	AAATGCATTT	CTTGCCAGA	27600
TGTGGTGGCT	CAAACCTGTA	ATCCCAACAC	TTTGGGAAGC	TAAGGCCAGG	AGTTCGAGAC	27660
GAGCTGGGAT	ATATAGGAAG	ACACAATCTC	TACAAAAAAA	AATCCACAAA	ATTAGTCAGG	27720
CTTAGTGTTT	ATGCCTGTAG	TCCCAGGTAC	TCAGGAGGCT	GAGGCAGGAT	TCCTCAAGCC	27780
CAGGAGTTCA	AGGCTTCCGT	GAGCTATGAT	GGCACAACTG	CACTCCATCT	TGGGTGACAG	27840
AGCAAGGTCC	TATCTCTGGA	GAAAAAAAAA	AAAGAAGGCA	TTTCTTAGGA	GAGTTCTTCT	27900
CTGTAGAGTC	CTAAGGGTTC	CATGGAATCT	CTTAAAAGCA	TCAGAGTATG	TGAGTGCAAT	27960
GGGAGGAAGC	ATTTAGCCAG	AGCAGTTGTG	CTCCCATTGC	ATATTAATTT	TTAAAAACA	28020
AAGCTATAAA	AAAAAGTTGA	AACTACTAC	GTTAGCATCA	GCCTGACATT	TAATGGCCTC	28080
GTAAATCAAA	CCTTAATTGA	CTTTTGTAGC	AGTTATGCTA	CTAGCCAAC	ACAGACAACA	28140
CACTTTTAA	CCAAATTAGA	CTAATAGTTG	TCATCAGTGG	AAATCAAGTT	TGCCATTCTT	28200
CCATGCCTTT	GCTCACACCA	TTACCTTTTC	TGGAATGTCC	TGTACTCATC	TTCCTGTGTT	28260
GAAGCTCTATA	CCCAACTTTA	AAAACCTAGC	TCAAAGTTCA	ACACTTCCAT	TCCATTTCAT	28320
AAAGAGCTTT	CCTCTTCCTT	AAAGTTAAG	AACTCATTTT	CATGAATCTT	TTTGGCATTT	28380
ATTGCACACA	TGCTTGCTTT	GTGTTATTTG	TGTTTCATGCC	TCATATGCCC	CCAAGGTGTT	28440

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TTAGACTCCT TAACGGCAAA AATGATGCTC TAAACACCTT TCTATCTTTC ATAGTGCTCTT	28500
AGTCTGTTTG TGTGCTATA AAGGAATACC TGAGGCTGGG GAATTTATTT AAAAAAGAGG	28560
TTTATTTGGC TCACAGTTCT GCAGCTATAT AAGAAGCATA GTGTCAGCAT CTGCTTCAGG	28620
TGAGGGCTTC AGGAAGTTTC CACCCATGGT AGAAGGCAAA GGGGAGCAGG CATCACATAT	28680
CAAGAGAGGA GGAAAAAAG GAAGGAAGAA AGGAGGGTGC CATTCTCTTT CAACAATCAG	28740
TTCTTGTTGG AACTAATGGG ACAAGAGGCT GGGCACGGTG GCTCATGCCT GTAATCCCAG	28800
CCCTTTGGGA GACCAAGGTG GGTGGATCAC CAGAAGTCAG AAGCCTGAGA CCAGCCTGGC	28860
CAATGTGGTG AAATCCGTC TCTACTAAAG ATACATAAAT TAGATCTAGC TGGGCCTGGT	28920
GGCGTGTTACC TGTAGTCCCA GATACTCAGG AGGCTGAGGT AGGATAATCA CTTGAACCCG	28980
GAAGACAGAG GTTGCAGTGA GCTTGTGCCA CTGCACTCCA GCCGGGGCAA CAGAGTGAGA	29040
CGGTCTCAAA AAATTTTAAA AACTTTAAAA ATAATAGAGC AAGAAAGCAC CAAGTTATTC	29100
AGGAGGGATC CACCCCCAAT GACTCAAATA CCTCCCACCA GGCCTCACTT CCAACACTGG	29160
GGATCAATTT CCGTATGAGA TTTGGAGGAG ACAAATATCC AAATATATC ACATAGTAAT	29220
GAACATAGTA CCTTATCTAT AGAAAGCAAT GGCTAGACAA CTGTTGAATG GCTAACCAAA	29280
TCTGCTTTCC TATGGTCTCG CTCTAGAGGG GGTCACTATG AGTTTCTGTC AAAAGGAGAA	29340
AAAAAATGT ATAGTCAGTT TTGTGTGTGT GTGTGTTTTCAT GTAAAAGAGA TCAAGAGAAA	29400
AGAACAAGAG AAATCATGAA AAGGAGGGGG AATATAAGAA TAATACATAG AAAAAAGCAA	29460
ATTATCTTGT TTATCAGTAA TACCCAAGGG GGTAGAAATG GTAAGTAATA ATCCTTCTTC	29520
ACTTTGTCTG TAGTTCACTT TTTTGCACCT TTATTTTGAT GAATTCACAT CGAAGACATT	29580
AACTCATTA AAGCTTCCAAT ATTTTGGAG ATAAGAAGGG CTGCTATGCT CTTTATAGAT	29640
GGAAACTTG GGTCAATTAAT AACTCAAACA AGGACATAAC AAAGAAATGG AGCATAACT	29700
GCCAGGTCCT GACTGTAGAT TTGGATTCCC AGTTGGTGTC TTGTCACCCT TTGTTACTCT	29760
TCCTAAAGTT ATGATCTTTT CTGTGCATA GGAAATTCAT AGTGATTTCC CATCACCTT	29820

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GGGATTATCA TAGCTCCTTT AAGGTCCCCT CTATGCACTC AATAACATCA ACAGTAAGTG	29880
TTCTTCGAGC ACTTACTGAG TGTATATCAT TGTGTTCTCA CGCAGCACCC ACAGATCTCA	29940
CCAAGAACCT AGCTGAAGCC TGTAGAATGA ATAGGTAAGT ACTGCCATGC CAATCTGGAG	30000
TACTCAAGCG ATGCAAATGA TTCCTTTAAT TGTACTTTTG CAGGCTTGTC AGTTTGTGCTC	30060
ATGGAGAAGT GGCTACTGCA TCCATGTTAT ATCTATGTAA TGTTGGACTG CGAAGCATCA	30120
CTTGACTTTT TCCAAGCAGA AATTACAGCT GATGACAAGC TGCTGCTGAG AAAATGGATA	30180
TTTTTCTGAA TTCAGTTCTA CGTGGAACA GCTGACTAGT TTCCATTGCT GTAAGATGGC	30240
TCTTTTGCTC TTGGTTGATT TTGAGTAATG GCTTTACTTC TGTAGAAAGG AGATTTCATT	30300
TGAAGTCCAC TCAGGGATTT GGTTCACAA ACTGGAGTAC AGGTTTCAGA AAATATCTCT	30360
TTAATCCTCC AATAATAAAT TTTCTCATCT ATAATTCCTG GAACACTTCA TCCTTTGCAG	30420
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TCAACTTAGG TTACAAATAG AACAGAATCT CTCTGATTTT TCTCATTAAT TGTTTGAATT	30540
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ACAGGAGCCA TTATCATCTT CATGGTGTC CTTTTGAAAA CTGGTCCTCT GTAGATCTTC	30720
AGATTCTTGC GTTAGTCCAT TCAGCTGCTA TAACAAAATT GCATAGACAG CATGGCTTAT	30780
AAATAACAGA AATGTATTTT TGACAGTTCT GAAGGCTAGA AAGTCAAAGA TTAAGACACT	30840
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TGTCTGCACA TGGCAGAAGG GCAAGAGAGC TCTCTGGGTC TTTTTTATAA GGGCACTAAT	30960
CTCATTTTTG AGGACCCTGC CCCCATGACT TAATCACCTC CCAAAGGCAC TGTCTCCCAA	31020
TACCATCACC TTGAGGGTTA GGATTTCAAC ATATGATTTT GGGGGGACAG AAACACGCAG	31080
TCCATCTCGC TTGTCCACTC CATGGTGGTA TTCTTGCTGG ATCAGTTTCC TCCTTGGGGT	31140
GCATTTGTGT TCCATGTCTA ACTTGCAAGT TATAGCAGGC CCGATAGCAA AGTATTCCAA	31200

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TGTTGGTATG CAGAGGCATT GAATAATCAG AATGAACCCA CGCCATAAAC AACTGGTAGA	31260
GCTGCAGAGA GTACCAGCTG ATTATGAGCC CTGGGTAACA GTGGTTTTTA GTTCCATATGT	31320
CCGTCAGCCC TTTTCTCCCA TAGTAGCCCC ACTGTGTTGA AGTGGCTGAA TCGACAGAAG	31380
CTTCCAGCTT GGGCCACATG CTCATGGAAC CAATTCTCCT TATGAGCCGT ACAAGAGCTG	31440
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TTATCAACTA CAGGGATTAT TTAGAATCTT AGGGCAGTGG TGCCCAACCT TTTTGGCCCC	31560
AGGGACAGGT TTTGTGGGAG ACAATTTTTC CATGGACCAG TGTCAGGGGG CTGGGAGGCA	31620
TGGTTTTGGG ATGAGTCAAG TACATTACGT TTGTGTATA CTTTATTCT ATTATTATTA	31680
TATTGTAATA TATAATGAAA TAATTACACA ACTCACCATA ATGTAGGAAT CAGTGGGGAG	31740
CCCTAAGTTT GTTTTCCTGC AACTAGACAG TCCCATCTGG GGGCAATGGG AGATAGTGAC	31800
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GGAGCTCGGG CAGTAATGCG AGGGTTGGGG AGCAGCTGTC AATATAGATG AAGCTTTGCT	31980
CGCTCGCCTG CCACTCACCT CCTGCTGTGT GGTCCACTTC CTAACAGGTC ACAGACTGGT	32040
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GGTGCTGCCA GGGCCATGCT CCCTCTGAAA TGTGTAGGGG AGAATCCTTC CTTCTCTTT	32280
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CTGCCTTTAC TGTCTCATAG TGTCTCCCC TCATGTCTCC AGGTCTCTCT GTCTCTCTTC	32400
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TCTTAAGGTC ACATGCAATG ACTATTCCAG ATAAGGTCAC ATTCTGAAGA ACTGGGAGTT	32520
AGGACTTCAT ATCTTTTGAA GGAACACAGT TCAACCAATA ACAGCCCCTG TACTGTTTTA	32580

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CAAATAGGTA TTCTCTCCT TCCCAAAGTT CTTCATAGCA GAGACAACTT GTACCAAAAG	32640
GCAAAATACC TTATTATGTA ACCTTAACCT AGGATCATAG ATCCCTACTT GTCTGGTGCT	32700
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TGGTTCATGC CTGTAATCCC AGCACTTTGG GAAATTGAGG CGAGTGGATC ACCTGAAGTC	32820
AAGAGTTTGA GACCAAACTG ACCAGCATGA CAGAACCCCA TCTTTACTAA AAATACAAAA	32880
ATTAGTTGGG CATGGTGGCA TGTGCCTGTA ATCCCAGCTA CTCAAAAGAC TGAGGCAGGA	32940
AAATCACTTG AACCGAGGAT GCCAAGATAG CAGTGAGCCA ATATCGTGCC ACTGCACTCC	33000
AGTCTGGATG ATAGAGCAAG ATCCTGTCTC AAAAAATTAA TAAATAAATA AAAAGACAAG	33060
GAAAGCCTTT TCCAAGGAGA CCCTTCTGCT TTGCTAGTTC AGAGAACTTC TCTTTGGAGA	33120
AAACAAACAC CCAGTCCATT AGCAGCAACG TCAGGGATTG AATTCTTAGG GCAGCAGGCT	33180
GGGCACAGTG GTCATGCCT GTAATCCCAG TACTTTGGGA GGCTGAGATG GGTGGATCAC	33240
TTGACATCAG GTGTTGAGA CCAGCCTGGC CAACATGGTG AAAACTCATC TCTACAAAAA	33300
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GAGGCTGAAG CAGGAGAATC ACTTGAACCC GGGAGTTGGA GGTGTCAGTG AGCTGAGATT	33420
GCCCTACTGT ACTCCAACCT GGGTGACAGA GAGAGACTCC ATCTCAAAAA AATAAAGAAT	33480
TCTTCGGGCA GCAGTCTTTC CTCCACCTCA TAGACCATGG AGGTGAGCCA GCTCTGACAA	33540
ACCATGAGAA CAATGGCAGA GACATACCTG TAACGTAACCT GACTGGGGCA AAGACAAAGG	33600
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CCTCCAGGGA AAGGAGATGG GCTCCAGAGG CAGAAGAGGA CGTTGAAGGG AATGGGGAGT	33780
GGGTGAAATA TATAGACGAT GGGGACCACC CAAGAGCAGT CGCTATTGCA AACTGAGGA	33840
GAAGGAGAGT CTGGAGGGGG TGGTGGGAAG CTGGGTCTCC TAAGGAGGTT TTGACAAAAG	33900
CAGTCATGGA GCGGGCTTAG AAATCACAGT TGGGGACAGG GTAAAGTTCC TCGGGATATA	33960

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GAGGATGAGA	TTAGAAGAGG	TTCCAAC TAG	GGTAGTGTGG	AGAAAAGCAC	TATTGACCCA	34020
AAAAGGAAGG	AGAATGTGGG	TGGAAGTGGC	AGAGAAAGAG	GGGTTTGAGC	AGAGAGTGGT	34080
GATTTTCTA	ATGCAGAGTT	GTGGGAGGTG	GAGTGCAGGG	AGCCAGGCTG	GGTGGCTGTG	34140
CTGATGTGAT	TAAGCACTTA	CTGACTGCCA	GGCAATGGGC	TAAGTACCTG	AGATGCTTTG	34200
TCTGTTATCC	CTCCCGAAAC	CCCTCTGAGC	AGGTGCAGTT	ATTATTCTCA	CTTCACAGAT	34260
AAGGAAATTG	AGGCACAGAG	AATTGAGTAA	CTTACCCAAG	GTGACATAGC	TCATATATGG	34320
TAAAGCAGGC	TTTGAAC TCA	GTCTAGCTCC	CGAACCTAAG	CTTGTAAC TA	CTATGCTTTT	34380
CCCCAAAAA	GGGGGCTGGC	ACAAAAAGAG	CTGAGGGGGG	CTGGGCATGG	TGGCTCATGC	34440
CTGTAATCCC	AGCACTTCGG	GAGACTGAGG	CAGGTGGTTC	ACCAGAGGTC	AGGAGTTCGA	34500
GACCAGCCTG	GTCAACATGG	TGAAGCCCTG	TCTCTACTAA	AAATACAAAA	ATTAGCTGGG	34560
TGTGGTGGTG	TGCACCTGTA	GTCCCAGCTA	CTTTGGGAGG	CTGAGGCAGG	AGAATCGCTT	34620
GAACCC CAGA	GGCGGATGTT	G TAGTGAGCC	AAGATCATGC	CACTGGACTC	CAGCCTGGGT	34680
GACAGAGTGA	GACTCCATCC	AAAAAAAAGA	AGAGCTGAGG	TGATGGCCAC	CATCAGCATC	34740
AGCCTGGAAG	TTATAGCAGG	ATGCTAAGTT	TCTCTAAAGC	TGTCTTTCTT	AGGACTTGAA	34800
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AGGTATCAGT	CTTAGCAGAG	CATCCAGAGT	GTTCTATTA	AAACCTAAAT	CATATCCTGT	34980
CATTGCTCTG	CCCCAAACCA	TTCAATGGCT	TCCCAACTCA	AAGTTAAAAA	CTCATCTTTC	35040
CAGTGGCCTG	CAAGAGCCTA	TGCTATCCGG	TGTCTGACCT	CATCTGTTGT	TCCTTTCTCC	35100
CTCCCTTTCT	TGGCTCCAGA	CGCACTCTGG	TCTCCTTGCT	GTTCTTGAA	TACACCAGGC	35160
ACACTCTTTT	CACCTGAAAC	ACTTTACCCC	AGATATCTTA	GCTTACTCTC	TGCCCTCCCTC	35220
AATTCATTGA	TGAAATGTCT	CAGTGAAGTC	TTCTCTCTCT	CCTCTGTAAA	AGTATACTCT	35280
CTGTTCCCCT	TCTTTACTGT	TCTAGCTACT	ATTGCTGTGT	AACAAATCAC	TCCCCAAATT	35340

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TAATGAGTGA	AAACATCAGC	CATCATCTTA	TTTCTCACGG	TTTCTGAGGG	TCAGGAATTC	35400
TGGAAGGGCT	CAGCTGGGAG	GTTCTGGCTC	TATAATCTCT	TATGCAGTGA	GAGTCAGATG	35460
CTGGCTAAAA	CTGAAACAAA	GCAGGGTTCT	AGTAGCTGAG	GGCTGGCTGG	GTCTCTCAGA	35520
TATAGTTCAG	ATCTCCTCCA	GGGGGTCTCT	CCACGTGGGC	TAGTCTGAAC	TTCCTCACAG	35580
CATGGTGGCC	TCAGGGCAGT	GGACTCTGCA	TAGTGGCTGA	AGGCTTCGCA	GCTGAGTATT	35640
CCAGCAAGCA	AAGTGGGAGC	TGTATTGCCT	CATATGACCC	AACCTTGGAA	TCCACACAGC	35700
ATCACTTCCG	TGTATTCTAC	GGGTTGAAAA	GTCACAAAAA	CCAACCAGTT	TCAAGGAGAA	35760
GGAACAGAGA	TCACATTTCT	CAATTGGAGA	AGGGTCAAAG	TCACATTGTA	ATCAGAGCCT	35820
ATGGGATACG	AAGTATTGCG	GTCAGGTATG	AAAAATTTGA	TTTGCTGCAT	CTGCTTTACT	35880
TTCTCCACAG	CGTTCATGAT	CTGCTTCTCA	CATGATATTG	ACTTACGTCA	TTTCTGCATT	35940
TCCTGTCTTC	CACACTAAAA	TGTCAGCCTG	TTTTGTTCAC	TGCTGTATCC	CCAGAGCCTA	36000
GCACGGAGCC	CAGCATGTAG	TGGTATCCAA	TAAATACTTG	TTGCATGAAT	GAATTCGTGC	36060
TTTTAATCCT	AGCTATAGGT	TTCTAAGTTA	AATATTACTA	TAATCATCTT	ACAGACGAGG	36120
GAAATGAGGC	TCAAGAAGAT	TTGGTAACTT	ATGCGGGATC	ACTCAGCCAC	ATAATGGAAG	36180
AGACAGCATT	GAAGTACACA	TGCTTGCTCT	GTCTGCTCTT	CCAAGCTGCT	CATCACACAG	36240
CTGCACCTCT	GAGGACTTCC	CTCCCCAGTC	CACCTCCACC	CTTACCCAGA	GACACACATG	36300
GCCACAATCC	ACTAGCAGAC	CAAAATTCAA	TTTTTCCCCA	GTTGGTTGCA	CTCAAGCTGA	36360
GAGCAAAGCA	ATTGCACTTT	AAATCCCCTT	ACAGCAGATA	TTTCAGAGCA	TGTTCGGAAG	36420
AACCCATCAC	ACTTGCTTTT	TAGATCTTAT	TTCTGGTTTG	TTACAAAAAC	ACAATTAAAT	36480
GAAAGGTTAG	GTAGCTTTTG	AATGGCCAGC	TCAAAGTTTT	GGCTTATTTT	TGCCTTGCTG	36540
TCTTTATAGG	CATTTTACCA	ATATTTATCA	CTATTTCCCT	TAGGGAACCC	TTAGATCTGT	36600
GATATTTGAA	ATAATAAAGC	CTCTCCATTG	GCCCTTTAAA	AGGTTTGTGG	TAAAACCACA	36660
CCATTAACAT	TCACAGTTCC	TTATTTATGA	GGCCTGATTG	CACTTATTTT	CATATTTCTC	36720

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ACTGTTTCTC	CGATGAGGAT	TTCACATAAT	AGTGTTTGAA	GGCTAAAGAC	TTCAAAGCAG	36780
ATTCTTTACT	ATTTTATCT	TGAAAAATAT	TCAATATTTG	TGTAATTAAA	GTGAAGTCTT	36840
CCTAGAGAAA	ATGACAACTC	AAATAATCTT	AAATGTACCT	CCAAGAAAAA	AGCTGTCAAA	36900
GTGACATTTA	G TAGTAGAGT	CACATTCTCT	AAGGCCTTTG	CTTCTCCTTC	TGAGTTCTTA	36960
TCATCTTTGA	AGGTTATGTC	ATGGCTGACT	TCAAATCACT	TTTAAAATTA	TTATGGCCTT	37020
CTTTAAATGT	GAGTCTGAA	GGTGAGGGGC	TTTATCTTTC	TTTTGCTCCA	GATTTTTTCT	37080
ACCGCGTCAT	TACCAAGCAT	CTTAAAACAA	AACCTAAAAA	CAAAAATCTT	CCTTGACCTG	37140
GTTTTTCCCA	CTAGCTAACA	TCCTATTTTT	ATCTTTCCCT	TTGCACTAAA	GGTTTTTAAA	37200
CGGATCTTTA	TACCCTCTGT	CTCCATTTTC	TCATCTGCTA	ACTTATATGG	CAAAGATTAC	37260
CACTGCCTTT	CAACATAATT	GGCCAATCTA	CAGAAAGTTT	TCAAGTTCTC	TTTTTAATTG	37320
ACCACCTCCT	GCCTACCTCC	CCACCTTTGA	CATCTTGCTT	CTCACTTGGC	ACCTTACCCA	37380
GTGTTCAAGA	TTCCCTCCTT	TAGGATGTCT	TCAGAGCAGC	TACACAGTTG	GTACTATAAT	37440
TTATACATCC	TTGTACACAG	GGCTTGCTGG	GATATTGATG	GAGAGAAGGA	GGAAACTGGA	37500
AGTAGTTCAG	GCCAGAGCTA	GGGAAATGTA	CCCATCTCCA	GGTCTCAGGT	CTGCAAGGGG	37560
AGCTCACAGC	TTAACACATG	GAGTCTAGAA	ACTTGCTGCTG	GACCTTGACC	AACACCAGCC	37620
CATGGAGTCC	AATACAGTGC	TCAATAGGGA	TTTCCAGGAA	ATTGCTATAT	TTATTCAAAG	37680
AGAACTTACC	AAGTGTGAGC	TACGTGTTGG	GCATTGTGTT	AGGCACAGGG	ACCACAAAGA	37740
TAAGACATTG	TAGCTTTCCT	TAAGTTGCTC	ACTGAGTAAA	TAGAGAGACA	GAAAGGTAAA	37800
CAGGTAAGTG	CAAAAATACA	TACAATTCTG	CAATAGTGTT	CATAGTGGCT	ATGGAGAGAA	37860
CGCTCACTAA	CTTTGTTTAA	ACAGTTGTTC	TTTCAAGGAT	TTGACATGGA	TTTGATTGGA	37920
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TTTTTTACAA	ATAGCTACTA	AGAGCTACTA	GAAAACCTGG	GAATTCTTAA	AACCTTACCA	38040
TGCTACTTGC	TCTAAAATAT	TTTATTTTAT	GTTATTTTGT	ACATTTCTTT	ACCTACACAA	38100

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ACACCACTGT	TTTCTTCATT	TCTTAGTCTA	TTTAAACCTC	ACACCCTTTC	AGCATCTCTT	38160
AATTATTTAC	TACCATCTGT	TAGTTCTCCT	GTCTGAATG	AAACAAAAT	GGCAGAATGT	38220
AAAACGAGGG	CGAACAGATT	TTTGACAGGA	AGTATTCAGA	GGTAGAAGGA	AATAGTCAAG	38280
ACACATATGA	TAAACGAAAA	CAATAATAAC	TTTATACATA	ACAACCTATA	GACACATTTA	38340
AAAAGTTTAA	GATCTCAAGA	GCTATGTCTG	AATAGATAGA	AGTAAAACT	CTATTAAGTA	38400
ATTAGGAAAA	TAACAAGAAC	AGTGAATTTT	TTAATGAATG	GCATGTAATC	AAAACGTGAC	38460
TTATCGTCTA	ATTCATAATC	TTGAATGTTT	TTATTTTATT	TATTTATTTT	TTTATTTTTT	38520
GAGACAGAGT	CTTGCTCTGT	CACCCAGGCT	AGAGTACAGT	GGCGTGATCT	CAGCTCACTG	38580
CAACCTCCAC	CTCCAGGTT	CAAGCGATTC	TGCTGCCTCA	GCCTCCTGAG	TAGCTGGGAT	38640
TACAGAGGCC	TGCCACTGCA	CCCGGCTAAT	TTCTGTATTT	TTAGTAGAGA	TGGGGTTTCA	38700
CCATCTTGGC	CAGGCTGGTC	TTGAACTCCT	GACCTCATGA	TCCACCAGCC	TTGGCCTCCC	38760
AAAGTGCTGG	GATTACAGGC	GTGAGCCACC	ACGCCTGGTC	GAATGTTTTT	ATTATTTGAA	38820
GAGACAACAT	GGGCCTTAAA	TCTGTCTTCT	ATTTGACAGA	CTTTGATGGA	GTCAAATCCC	38880
AATGCTGCCA	CTTACTGAAC	GGCCTTAAAT	GACTTAGTCT	CTCTCAGCTG	TCTTTCTGCA	38940
TATGTAAGGT	GGAATAATGA	TGGCTTCAAG	GAGGAATAAA	CCTATGAAAA	GTGTTGAGGA	39000
TAGTGTCTGA	TATGAAATAA	GGATTCAACA	AGTAGTAGCT	GCTATTGAAG	ATTTAAGAGT	39060
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GTGGGCGGAT	CACCTGAGGT	CAGGAGTTTA	AGACCAGCCT	GGCCAACATG	GTGAAACCCT	39240
GTCTCTACTA	AAAACGCAAA	AATTAGCCAG	GTGTGGTGGC	ATGCACCTGT	AGTCCCAACT	39300
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GAGATGTCAC	TGCACTCCAG	CCTGGCAACA	GAGCAAGACT	CCATAAAGAC	AACAAAAGCT	39420
TTGAAATTGT	GTAAATGAGT	TGTACCTATC	TTCATTTAAG	AAATTCATCT	TTGTTTATCT	39480

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CACTGGCTAT	GTGATAAACA	AATTATTGTC	TAAAATAATA	TTCTTGCTTC	TTTTTTAAGG	39600
AATTGTCTCC	CTAGAAACGG	TTTGTACCAA	ACAATACACT	GACTTTACAC	AAAATCAGAT	39660
CTGATTGGCA	ACAGTTGCAG	ATGTTTTCAA	AGGATTTTCA	TTTGAGAAGG	GGCCCATTG	39720
GGTATTTAG	ATTCTAAGAA	CTGAACTGC	TTTGTCTCTGT	TTTTCTGGCT	TCTGGGAGAG	39780
GAGGAGACAT	GAATTCAGTT	AGCACCTTGG	TATTTTCTTT	ATCCTTCATT	TCAATACAGA	39840
AGATGCTTCA	TATGCACAGT	GGTGTCTAGT	CACATCAAAA	GAAAGAGAAA	CAGTTTCTTG	39900
GTTTTAAATT	TTCAACCGGA	AAGGAAAGGC	ACCCATTTTG	TTCCGCTCTA	ATTAGCCAGT	39960
GCATGACTTA	GAGAGCAGGC	AGATGCTTTG	AAGGCGTGGT	AACACAGGTC	TTCATTAATC	40020
TCCACGCAGG	ACTTGCACTT	CTACTATGCC	TAGGCTGAAG	AAAATGGCTC	AGGAAGATGA	40080
ACAATCTCAC	AGAGCCCTAA	CTAACTGAAG	CCAGGTGTTA	TAAAGCACAA	GTCAAGAGGG	40140
TGAGAAACTA	ACGTTCCTGA	AATCTCCAC	TTCTTTCTAC	GTCAGAAGAG	CCAAGCTGAT	40200
TATTTTAGTT	GGAATTTAGA	AATTTTAA	AATTATTCTA	AAGTCATGAA	CAAGCCTAAT	40260
TATAAAGATA	GTTGCTGTGA	AGGTGCTGAA	ATAACTCGAT	TTACCAACC	CCCTCTTCTG	40320
GAGGAAGCCA	GAATGGAATC	CTGTAGAATG	TTCACTCTAC	CAACGAACTC	TTGTTTTTCT	40380
AATGAGGAAA	CAGAGGCCCA	CAGTAGTAAA	CTATCTTAAC	CAAGACAAA	TGACTAGTGC	40440
TCTGGTCCTT	TTATTAAGCA	CTAAAATTTT	GATCCAATAA	TAAATCTGTC	CAGTAGAAGG	40500
AGTTCCCTA	ATGTACTGGT	TCTAACTTGT	TCCCTTCAAG	GGGCCAGTGT	CCCGTACACA	40560
TAGCTAAATG	GGACTTCTCT	TCAACTACCA	TTACCCAGAG	GGCAGAACCT	AAAATGCTGT	40620
GAATGACATT	CTGCTGTTCA	CATCTCAGCA	GCAGTGTTGC	ATTTGAGCTT	CTGCAGGGCC	40680
ACCCAGGACC	TATATCTGCT	CAGATGTTTA	ACTCATCTAA	TTCAGTGAAC	ACTTCATTCT	40740
AGTTAACTGA	ACATCTACTT	TGTACAAGGC	ACTACAGCGG	TTCAGAGATG	AATAAAATCA	40800
TGAGATTCCA	CTGTCTCCTA	TAAACCATCA	CTTTGGGAAA	TTTGTAGAAAT	GTGGGTAAGC	40860

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TCCAGGGCTT CCTGCAGCGT AGAAGTCACA AACTCAAATG CCTGCAGAGG CCCAGCTGAC 40920
AACATAAGTA AATGATTCTG GCTGGGCGGA AAACAATTAC GGGTGGGTGG GTTTCAGCT 40980
GGGGAGTGCA CGCCTGTGTT AAAGGACA 41008

(2) INFORMATION FOR SEQ ID NO:4b:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39238 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4b:

GCTGCTACTC ATTTCCAGCC AACTGTGTTC CCATGTAGAA CTGCGGCCCA GTGTAGCCAG 60
TACCGAAGAT TTCTCAGAAA AAGCCGGAGA TCTCAATGTT AGTGTAATAAT CTCTCAAATT 120
TCCAAGAGGA TTATATGGGG CAAAGGTTCT CAGATCAGTT TGCAGTCTCT TACTTAGCCC 180
ATGTGCAGAG CAGTCGTAGA GGGTAGCATG CAGTGTCCCTA CATAATAATT CTTTTTTATT 240
TTATTTTATG CCTTCCTCCT TCCTGTCTCT CTTTAACCTT TCTTCTTCCC TCAGGCTGGC 300
TTCTTCCCTC AGCCTCGTCC GACCCAGCC TGGGTTCAAT GAACATTCGG TAAAGGAACA 360
CGGAATGTCA AGCGCATTAG AGACAACCTT GAGACACATT CCTCTTGCGG TAAGCACTTC 420
ACTGTAGATT TTTAATTTTA AACAAGACAA TGTTTACGAC TTGCTTCTTT CAGGGAAGAG 480
CGATATCAAT TTTAGTGAAC ACTTCAAGGC TGAGATACGC TAGGAGAGTC GTGTGGTGTT 540
GCACAGCAAA GAATTCCACT TTGAAGCGAG TGGGAAAAAA AGCATCAAAT GCCACATGTA 600
ACTCACC GCC TGAAGGGTTA CATTGGTATG AAACCTGGGT TTAAAAAGGG ACCGAATAGA 660
CTAGCCATTA AAAGACCTGC GTACAACCTC TCTCTCTCTC TTTGAGAGAT AATGTATCTG 720
GACAATAAAC ATGAACAGAG TGGAGTCTAT CCTGTTTAAA ACATTGCCTA CTGTACAGGC 780

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ACCAGGAGCT GAAGGGTCAG AATATTAGCA GTGGGAGCTT GATTAGAAGT TGATGAGAGA	840
TGGGTAGTAG GAGGAAAGAG TGAGATAGAG GAAGAGGACA TGGGGGTAC CCGTAAGTGG	900
AGAGTAGAAA AGTAGAATCA GCTGGCCATC AAAGGGCGTG GGAAGTGAAG ACAGTATGGC	960
ATGTATTAAA TATACTAAGC GCTGACATTG GAGGAGAACT AGGAAGGTAA ATGAAATCAA	1020
TAGGGGATGA TGGAGAATAG TTAGGTGTGC AGGGATTAGG GTTATGATAG AAATACATGT	1080
GAATACATGC AGTATTGTCC TGGAAAATGG TTAACAGTTG GTTCTCCTGG GGGGTGAGGG	1140
GAAGCCCTGA TTTGTAATAT TTGCCTATTT CTGTGGTGCA AATACTCCCA CCATGACCAG	1200
TTTCAAGCTA TGAATGTGAA TCACAAAAGC AGGTTGGGAG GAGATGCGCA CATTTGTTCC	1260
CCGGCAAGGT GGAAGGTAAG GAAGGTGAAA TCAACAAGGT CAAAGAAAAC TCAAGATTTT	1320
GAGGTGCCTC AGGTCTGAGG GGCAATGAAG TCTAGGAATG GCTGTGCTGA GGTAGCTGAA	1380
ATAGAAGTGA CTGCAGAGGT CATGAAGCTG AAGAGGTGAA AACAGAAATT AGAAAGGCAA	1440
ACCCCCACCG CCCAACCCCC ACCCCTGCAG CCAGTTTCTG AGGGTGACAA TAGAGGAAAG	1500
GGTGGAGATG GAGTTCAGGT CCAGAAGCCA TAGAAGCGAG TGTGACATTG TGCTCAAGGT	1560
CAGCACATGT CAGTGTGGGG TGTCACATGC TGTGTGAAC CATCATTTAT CACCAATTAT	1620
GGAAGACCTC CTATGGGCAT CTTGCCATAT GCATTATAAA GATGTGTAAG AAGACATTTT	1680
CCTCCACTTG GTGAGGAGAA TTAGGGCTGT ACACAGATAC TGTAAGTGC CATGTGCCTG	1740
GTACAGATAA GGTGTGTTAG AGGTTAAAAG ATGAGGCTCT TAATATTAAT GATAGATCCC	1800
ACTTACCTGA GTCTGACTTA CAATGTGCCT AGCATTAAGT GTTTTACCTG CATTCCCTTT	1860
GACCTTCAGA ACAACCCATT TTACAGATAG GGAAATTGGG TCAGAAAGTT TCAGTAACTT	1920
ATCCAAGGTC ACACAATTGG CAAGTGCCAG AGCTGAGCCA GGAAGTGAAG TCCTTCTAAC	1980
ACCAAACAGC TTGTCTCCCC AATCACTGTG CTATTTTCCC TCCCCAGAA GATAATACTC	2040
TGATGGAAAT GAAGGATAGT GTAATAGGAG ATTCGGTGTT CCTTTTTTTA AAAAAAATTC	2100
AGCTTGCATA TTCCTAAAGA GTCAATTCAT GTTTAAAAA AATTTCCTT GTGCTTGCAT	2160

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CTGTAAAATC TCTGCCATCT CAGGTCTTGG AACAAGCACA AAGAGATGTG TTCTCGATTT	2340
ATTATTCCTAT GTACATCCCC AGATGAATGA CTAGTTAAAG GTATTGTTAA AGCATTTTAA	2400
ATGACCCACT TCCAGCAGCG AACAAAATCA CTTGCTGTGC CAAGCCAAC T GGCATTTCTG	2460
AGATGATAAA ACCACAAAGT GAGGAAAACG TTAAACTGC TAAAGCAAAA ATGATACACA	2520
ATAATGGAGA AGGAGAAAAA TTGAGCTTTA TTGTCTGCCT AGGCAGATGG CTGACCACTA	2580
GGTGGGCTCG GCGTCACGTC CAGGGTAATT GGTGCTGGG GTGTTTCTGG CGAGGAAGAT	2640
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TTTGATAATT ATACCCTCTA AATGAGGGG AAGTGGCTAA TTATGCCAC ATGTGGCCGA	2940
TTGCACTCCC CATTAGCCAA TTATGTGCTC AATTATTTGT GCACATGAAT AATTGCACTC	3000
ATGGAAAATA GCGGCCCTCC TTTCAAATCC TCGTGCTTGG AGTGGCTGAT GGAGTAATTG	3060
TCACACTGGA AATGCACTTG GTGGGGAGGG AAAGAGTATC AGATACCAGG AAACGCATAA	3120
GTGACCAGAG CTCGCAGATG TTCACTGCCA CAAATGGCCT TAGGAGCCAG AGAGAGCGGG	3180
AAGGACCACA GGATGGAACG GGCCAGCCTG TGAGTTAGGA AGCCTGCTTC TGAAGTTGCC	3240
TGGGCAGCTC ATGTGCGGTG ACCTTGGGCA AGTCATTAAC TTTCTTCAG GTCTAACTGG	3300
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TCAGACTATT TAAAAGGATT TACAATCTGC TTGGGTAAAA GCTTTACATA AATATGAGGC	3420
ATTATCATGT CGCTTGGTAC ATCTCCAATT ATGAAGGAAG GGTAATGACC CTCCACAGCA	3480
ATGCAGGACT CCTGGTTTGG AGGGAGGGAA AGTTTGAGAA GGACAGGAAG CTTGTTGCCC	3540

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AAGACTCAGT	CCTGCCTTAG	GAGGTCACCTG	GCACATTGGC	CCGGGCCCCCT	GTTTTTGGGCC	3720
TTTTACTCTG	ACCTGTGCTG	ATTTGCAAAT	AGTGGGAAAT	TTTATCTCAA	GTCTAGGAAA	3780
TCTGGCATGC	ATTTTCACGG	TTTGATTGCC	AGGTACATTC	GATGGCAATG	AGTCTTATAA	3840
TGTTTGGTTA	CCTTCATTTA	CCTAAAACT	GTGGTTGTTG	CTGTGGTTGT	TGTTTTTGT	3900
GTTTTTGAGA	CGGAGTCTTG	CTCTGTCATC	CAGGCTGGAG	TGCAGTGGCA	TGATCTCCGG	3960
TCACTGCAAA	CTCCACCTCC	CAGGTTCAAG	CGATTCTCAT	GCCTCAGCCC	CCTCAGTAGC	4020
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TTAATGACAA	TGCTAAAAAG	TGGTATATGT	CACAGTGTCTG	GGTGGGGCTA	AGAGGCACAT	4260
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CAGAGAGGCA	CCTCACTTTG	ACCTTCTTCC	TCAAAGACAT	TCTCTGTGAC	CTGCCTGGCC	4380
CTTATTACCT	CTCTAGCTTT	GCCACTTCCC	TATGTCTCCA	TCTCCCCCTCT	CACACGTAGT	4440
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ATTAGTCTTC	AAAGATGAGG	TATTTGCTAA	ATGAATGAGA	CAAAGGGATT	GGGGCCACAT	4560
TACAGGAAAT	TGAGGTATGT	AATAGCCTGG	TGCAGGTTAA	GAGTGTGGAC	TCTGAAACCA	4620
GACTCAGCCT	GGAATTGAAT	CCTGGCTGTG	TGATGTTGGG	CCAGTGACTT	AACCTCTCTG	4680
TGCTTTTATT	CACTCTTCTA	TAAAATGGGG	ATTATAATAA	ACCTACCTTA	TAAGGTTATT	4740
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CTTGTTTGCC	ATTATTTTTA	TTACTTGACT	AAAAATATAC	CAAAAAGACC	ATCCAAGAAA	4860
AGCCTTTAAG	CTGCTAGTGC	AGAAAGATTC	CCCTTGTTGT	TGTGTGCTGG	GGGGTCAGTG	4920

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TGTCTAAAAT CATCACATGG ACAACTTATT AAGGAAAGCA AATGCCTGGG CTCCATCCTC	5040
AGAGAGTCTC ATTCACTGGG TCAGGATAGA GCCCAGGAAT CTTTACCTTA AAGAACCATC	5100
CCACCTCCCA CCTCATATGA TCCTTATGCA GGTGATCTGG GGGCCACAC TTTGAGAAAT	5160
AGACTCAGGT CAAAGTGGGC TCTAACTGCA TCTCATTTCT TACCTGGCAT ATCTAATAGT	5220
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TCCACAAAGA ATTGGTTCTG CCTGCTGTGC TTCAGTGCTT AAGGGAAGTG GTTCTCAAA	6060
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GGTGATGAGT GGATGAGTGG CCTGGTGTAT TTCATAACAT CTCCCAGGGT CCAAATGCTA	6240
AAGCAATTGC TGAAAAGATA CCATGTGTAC CGGAACCTTG CAGAGGTATT TTGTTGGCAT	6300

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AAAAAGAAAT	ATTGATCATC	TATAGTAAAA	ATGGTCTAC	TTTAATACTA	CTGAGAAAAG	6360
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ACTAACACCA	TAATGTGTGC	TGTCCTTTGT	AATGTAGTCC	ACAGATCTCA	TAAACTGTCA	6480
GAAATAGCAG	AGATTGTAAG	GTCATCCACT	TCCCCTGTAA	GGCCTGCGTC	CCTCACTTAC	6540
ATCCCTAATA	ACGTCCTCTA	ACCTCTGCTG	GAGGGCAGAT	TTAGCTGCCA	GCTGGGAAGA	6600
GCTCTGCCCT	AGTCAACATT	TTTATCTGTG	GCTTTCAGAT	GAGAACACTG	GATGCTTATC	6660
TGAAAAAAGC	TCCTCAGGCT	GGAGGGAGGG	ATTGGCTCTA	ACAAGATGCA	ATGTGATAAG	6720
AATAAAAGCG	AAGCCAAACT	CTAGGCCCAA	AGGCTCTAGC	AACACACTTT	TGAGAACCTT	6780
GGAGACGAGT	TTTGGCTGAT	GCGAGCTTCT	CCGCCTGCTA	AAGTAGCCCA	TTCCATTTGG	6840
ACGGCTCTAG	AGGCTGGCAT	GTTCTTCTCC	ACGTTGTGTT	AATGTACTCC	AGTTTCTTCC	6900
TGCCATGAAC	TGGCATGCCC	TGGCTCCTCC	TACCTTCCCC	ACTTTAAGTC	TTCCCTCCCT	6960
CCTTCTGACC	TTCCCATTC	AGCCACACTG	GCCTTTTGTC	TGGTCCTAAC	AAACCATGCC	7020
TTTCCTGCCT	CCAAGCCCTA	CACCTGCTAT	CCATCCCTCT	GTCTGAGAGA	CACTCCCACC	7080
CCTTCACAAA	GCCTGTTTCT	CATCCTTCCA	GTTCAGATGT	CTTCTCAGCT	TGCCTCAACT	7140
GACCTCTTTC	AGCTATTCTC	ACTCTTTGTA	CTCTGTTTAT	TTCCCTCCTG	GCAGTCACCA	7200
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TCTCTCTGTG	CCTTTCTTAT	TCACTGCAGG	CTTCTTATG	TAAGTAATTT	ATTTACTTAA	7320
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ACTTTGGGAG	GCCGAGGTGG	GTAGATCAGC	TGAGGTCAGG	AGTTCGAGAC	CAGCCTGGCC	7440
AACATGGTGA	AATCCCATCT	CTATTTAAAA	TACAAAAACT	AGCCGGGCGT	GGTGGTATGC	7500
ACCTGTAATC	CCAGCTACTC	GGGAGGTTGA	GGGAGGAGAA	TCACTTGAAC	CGGGGAGGTG	7560
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GTTTTCACTT GCAATTCTCT GATGATTAGT GATATTGAGC ATTGTTTTAT GTTGTGTTGGC	7860
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GATGCATAGT TTGTGAATAT TTTCTCCCAT CCTATAGTTC TGTTTACTCT GTTGATAGTT	8040
CCTGTTTTGT TATGTTTTGT TTTTTTGCTG TACAGAAGCT GTTTAATCTA ATTGGTCCCA	8100
CTTGTC AATT TTTGTTTTTG TTGCAATGGC TTTTGAATTT TAATAATAAA TTCTTTCCTA	8160
AGGCTGATGC CCAGAACAGC ATTTTCTAGG TTTTCTTCTA GGATTCTTAT AGTTCAAAGT	8220
CTTATATTTA AGCTTTTAAAT CCACCTCAAG TTAATTTTTA TATATAGTGA AATGCAGGGG	8280
TCCTGTTTCA TTCTTTTGCA TGTGGCCAGC CAGCAATCCC AGAACCATTT ATTGAATAAG	8340
GAATCTTTTC CTCATTGCTT ATTTTGTC AA CTTTGTCAAA GATCGGATGA CTGTAGGAGT	8400
GTGGCTTTTT CTGGGTATC TACTCTGTTA CATTGGTCTA TGTGTCTGTT TTGTATCAG	8460
TATCATGCTG TTTTGTAC TATGGTCTCA TAACATAGTT TAAAGTTGGA TAATGTTATG	8520
CCTCTGCTTT GCTGTTTTTG CTTAAGATTG CTTTGGCTAT TGAGGCTCTT TTTTCACTTC	8580
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TCCTATCCAT GAGCATGGAA TATTTTCCA TTTGTTTG TG TCATCTACTA TTTCCTTTAG	8760
CAATGTTTTT TAGTTTTCTT GTAGAGATC CTCCTAGGTA TTTCATTTTT TATGTGACTA	8820
TTTTAAATGG GATTGCATTC TTCATGTGGC TCTCAGCTTG AATGTTATTG GTGTATAGAA	8880
ATGCTACAGA GTTTTGTACA CTGATTCTGT ATCCTGAAAC CTTACTGAAG TCATTTATCA	8940
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TCTGATTGCT	CTTCCAGTAC	TACGTTGAAT	AGGAGTGCTG	AGAGTGAGCA	TCCTTGTCTT	9120
GTTCCACCTC	TCAAGGGA	TGGTCCAGC	TTTTGCCCAT	TCAATATGAT	GTTGGCCATG	9180
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GTGAATTGCA	TTTATTGAAT	TGTGCATGTT	GAGCCAACT	TCCATCCCAG	GGATTAAACC	9360
TACTTAATCA	TGGTGTTAAC	TTTTTGATGT	GCTGCTGGAT	TGGTTTGCT	AATTTTTTTT	9420
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GCTCACTGCA	AGCTCCACCT	CCCGATTTC	TGCCATTCTC	CTGCCTCAGC	CTCCCGATTA	9540
GCTGGGACTA	CAGGCACCCG	CTACCATACC	CAGCTAATTT	TTGTATTTTT	TAGTAAAAAC	9600
AGGATTCAC	CATGTTAGCC	AGGATGGTCT	TGATCTCCTG	ACCTCGTGAT	CTGCCTGCCT	9660
CAGCCTCCCA	AAGTGGCTAG	TATTTTTTTA	ATTACTATTT	TTTCTCACCC	TTGCTGCCAT	9720
CTTATGATTT	TCTAGTATTT	TGTTGAAGAT	TTTTGCATCT	ATTTTCATCA	GGGATATTGG	9780
CCTGTAATTT	TCTTTTTTCA	TTTCATCTTT	ACCACATTTT	TGTATCAGGT	TCATACTGGC	9840
TTCATAGAAT	GAGTTCAGGA	ATGGTCCCTC	CTCCTCGAAT	TTTCTCTGTA	GAATTAGTAC	9900
CAGCTCTTTG	TGTGTCTGGG	AGAAGTTGTA	TGCCAATAAT	TTAAATGCAG	TTAATATTTA	9960
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AGTGGCATGA	TCTCGGCTCA	CTGCAACATC	CGCCTCCTGG	GTTCAAGCAA	TTATACTGCC	10260
TCAGCCTCCC	CAGTAGCTGG	GACTACAGGC	TCACGCCACC	ACGCCTGGCT	AATTTTGTA	10320
TTTTTAGTAG	AGATGGGGTT	TCACCATATT	GGCCAGGCTG	GTGTTGAACT	CCTGGCCTCA	10380
TGATCCACCC	GCCTCGGCCT	CCCAATGTGC	TGGGCTTACA	GGCGTGAGCC	ACCGCACCCG	10440

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GGTGTATCAG GCACAAGGCC TGTTTCAGATT ATGTGGTCTC TGAAGATATG GCTCTCCAGG	10560
GTTGACAATG TGGATAAGGA TTCACCTGGT TTAGGATTTA CACATTCGCC TTGAATGTCT	10620
GTTGCATCAA GTAGACAGTC CATCCCAACT TGGCCATTTG GTCAGAGCTG TAAGGAGACA	10680
AGGAGGTGGG CAGCCGCTGC TGTGAACTGC TTGGACAAAG ACTGCCAAAT AGCTATCAGA	10740
CAGTGTTAAC AACAGCTGAT TTAGGTTTGA AGGGGGCAGT CTCTTGGGCC ACTTACTATG	10800
CTGCATCATC CTCTTTGGAA AATGCTCTTC AGGTAAGTGC CTAACAGACT GAGAAAATAA	10860
AATGCTCACA GAGAAAAAAG ACCCGGAAAG TCTGACTTCT CAGAGCTCAG TGTTTAGGTG	10920
CAGAACTGGA TTGTGAAAGG ATTTTAAAT TTTTATATT CATTGCAGGG AACATTCAAT	10980
TATTCCATCC TTCTCCACTC CCACCTGTCT GTCGTTGTCT TTGTCTCTGT CTCCCCACCT	11040
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TCTTTACTTC TTGGAGAGAA AAGCCTCAAT CTGAGGAAGC TGTGCTGACT AGCCTTGCTC	11220
TTAATCATGG AGACAATGCT TTATGCCTTT ATCTTTGCAC AGCTGAAAGC CATGGCAGAA	11280
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GACACGGGCC ATGGTGGCCA GCATTCTTGC TCTTGACAAT GGTGAAGGGA AGGGTTGTAG	11700
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GCCAAGGGCT GTGCTAAACA CTTTACCATA TGATGACATC TTTTCTCAC AGGTATCAAA	11820

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AAACAATAGG	ACATACCGGA	TAGCTACAAT	CTTTGGGCCC	CTGCAAACAC	AATAATGTGT	11880
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AAAATAAAAA	CATATAAAGT	ACTACTTTTG	TTTTTTGAGA	TGGAGTCTCG	CTCTGTCACC	12000
CAGACTGGAG	TGCAATAGCA	TGATCGTGGC	TCAGTGAAC	CCCCTGCTCC	TGGGCTCAAG	12060
TGATTCTCCT	GACTCAGCCT	CTCAAGTAGC	TGGGATTACA	GGCGCACGCC	CCCATGCCTG	12120
GCTAATTTTT	GTACTTTTAA	TAGAGACCAG	GTTTCACCAT	GTTGGCCAGG	CTGGTCTCAA	12180
ACTCCTGACC	TCAAGTGATC	CACCTGCCTC	GGCCTTCCAA	AGTGCTGGCA	TTACAGATGT	12240
GAGCCACTGC	ACCCGGCCCA	TATAAAGTAC	TACTAATGTA	ACAGGGTGCT	AGTCCAGACA	12300
GTGACCACAC	GTGGTGTTC	TTGAAGGCTG	GACTAACAAC	TCCAGCCTCT	CCGCCATCAC	12360
AGAGTGATGA	CTGCCTTCCC	TGAAGCAAAG	CTTCTGGTTC	AAGGAAAGGC	CAGTAAGTGA	12420
CTGCTCTTTG	TTGTATACAT	GTTAGATGAT	CAGGCCTCAA	GAAAAGTATA	AAGAGATCTT	12480
TGTGCTCTCT	GGGACTCAA	AAGCTGCACT	CTTTGGGGGA	AGGATAGCCA	GGTAAAAGTG	12540
GCCCAGGTAA	AGAGGGCCTG	GTACACCTGG	TTCTGCAAGA	TGGTAGACAC	AAAAATGAGA	12600
GCCACATTTG	GAGCTTATGT	GCCCCTAACT	CTGTACATAA	CCTGCAAGAT	CTAATTACTA	12660
ACAAC TGGA	TCTTGGAAC	ACCTGTAGTA	CATCCTTGGC	TAAGGTTAGC	CCCAACAGAG	12720
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ATGATCAGAC	TACTAAAAAG	ACATCAGGAA	AGGGCCTGTG	ACATCTGAGG	GAAGTG GTTG	12840
CCCTCTCTGG	GATGTTGGTT	CGGGAAGAGG	GGCATGGAGG	AGTGCCTGCT	TTAGATGGTC	12900
ATT CAGGAAC	CCAGGCTGAT	AGTGAGAGGT	GAAGCCAGCT	GGGCTTCTGG	GCTAGGGGGG	12960
ACTTGAGAA	CTTTTGTGTC	TAGCTAAAGG	ATTGTAAATG	CACCAATCAG	CACTCTGTAA	13020
AATGGACCAA	TCAGCACTCT	GTAAAATGGA	CCAATCAGCA	GGATGTGGGC	AGGGCCAAAT	13080
AAGGGAATAA	AAGCTGGCCA	CCAGAGCCAG	CAGTGGCAAA	CTGCTCAGGT	CCCCTTCCAC	13140
GCTGTGGAAG	CTTTGTTCCT	TTGCTCTTCA	CAATAAATCT	TGCTGCTGCT	CACTCTTTGG	13200

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GTCTGCACTA TCTTTATGAG CTGTAACACT CACCGTGAGG GTCTGTGGCT TCATTCCCTGA	13260
AGTCAGTGAG ACCACAAACC CACTGGGAGG AACAAACAAC TCTGGACACG CCAACTTTAA	13320
GAGCTGTAAC ATTCACGCG AAGGTCTGCG GCTTCACCTC TGAAGTCAGC GAGACTATGA	13380
ACCCACTGGA AGGAAGAAAC TCCAGACACA TCTGAACATC TGAAGGAAGA AACTCCAGAC	13440
ACACCATCTT TAAGAGCTGT AACACTCACT GCAAGGGTCT GCGGCTTCAT TCTTGAAGTC	13500
AGCAAGACCA AGAACCCACT GGAAGGAAAC AATTCCGGAC ACATTTTGGT GACCCAGATG	13560
GGACTATCAC CAAGTGGTGA GTACCATCAA CCCCTTTCAC TTGTTATTCT GTCCTATTTT	13620
TCCTTAGAAT TCGGGGGCTA AATATTGGGC ACCTGTCAGC CAGTTAAAAG CGACTAGCAT	13680
GGCTGCCAGA CTTAAGAGAC TAAAGACACG GGTGTCAGAC TTTCTGGGAA AGGGCTCTCT	13740
AATAACCCCC AACTCTTTGG AGTTGGGAGC GTTGGTTTGC CTGGAACCAG CTTCCACATT	13800
TCCTGTACTT CTGGGCTGAG ACGAGGGTCA ACAGAGAGGA AAGCCATTCA GCTCTGGGGT	13860
CCCGACAGCA AGTTGGTTGA CCCTGTGGCC ATGAACAGAA CTCTCGAAGT CATGTTGCCC	13920
AAGCGAGACT CACCCATCTA TCCTATCTAT CCTGACTCTT GCTTCCTGGG TCCTAATGCC	13980
TGGAAGACAA AACTTCCTCT TGTCTCTGTT CTCCAAGGCT AGTCCCACTT CTAAAAACCA	14040
CTCCCTGTCT CTGGTGCTTT TCTAGTTTCT CCTATAAGAA TGATTTCTAG TATAAACTCC	14100
AGGACTCTAT TCTCTTCTTT AGGCACCCGG GCTCACCAAT CAGAAAGCCA TAATTTTGC	14160
CCAAAGCCCC ATCTTAGGGG GGAATCTCTG GAATTTTAGG ATCCCTCCTC AGACAAGCAG	14220
GCCTAACAAA AGCTATTCCT GAAGCTAGGA TATGGGGAGC CTCAGAAATG ATATCCTTCC	14280
TATTCAAGTG AGGACAAAAG GCATCACTCT TCCAATTCTG GAAATCCCTT CCCTCCCTCA	14340
GGGTATGGCC CTCCACTTCA CTTTGGGGC ATAACGTCTT TATAGGACAC GGGTAAAGTC	14400
CCAATGCTAA CAGGAGAATG TTTAGGACTC TAACAGGTTT TCAAGAATGT GTCGGTAAGG	14460
GCCACTAAAT CCGATTTTTC TCAGTCCTCT TTGTGGTCTA GGAGGACAGG TAAGGGTGCA	14520
GGTTTTCAAA AATGTGTTGG TAAGGGCCAC TAAATCTGAC ATTCCTTGGT CCTCCTTGTG	14580

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GTCTAGGAGG AAAACTAGTG TTTCTGCTGC TGCATCAGTG AGCGCAACTA TTCCAATCAA	14640
CAGGGTCCAG GGACCATTGT GGGTTCTTGG GCAAGAGGTG TTTCTGCTGC TGCATTGGTG	14700
GGCTCAACTA TTCCAATCAG CAGGGTCCAG TGACCTTTGC GGGTTCTTGG GTCGGGGGGT	14760
GGGGGGAACA AACAGACCAA AACTGGGGGC AGTTTTGTCT TTCAGATGGG AAACACTCAG	14820
GCACCAACAG GCTCACCTT GAAATGTATC CTAAGCCATT GGGACTAATT TGACCCGCAA	14880
ACCCTGAAAA AGAGTGGCTC ATTTTATTCT GCACTATGGC CTGGTCCCAA TATCTCTCT	14940
CTGATGGGGA AAAATGGCCA CCTGAAGGAA GTATAAATTA CAATACTATC CTGCAGCTTG	15000
ACCTTTTCTG TAAGAAGGAA AGCAAATGGA GTGAAATACC TTATGTCCAA ACTTTCTTTT	15060
CATTAAAGGA AAATCCACAA CTATGCAAAA CTTACAATTC ACATCCCACA AGAGGACCTC	15120
TCAGCTTACC CCCATATCAT AGCTTCCCTA TAGCTCCCCT TCCTATTAAT GATAAGCCTC	15180
CTTAATCTCC CCCACCCAGA AGGAAACAAG CAAAGAAATC TCCAAAGGAC CACAAAAACC	15240
CCTGGGCTAT CGGTTATGTC CCCTTCAAGC TGTAGCGGGG GAGGGGAATT TGGCCCAACC	15300
CAGGTACATG TCCCCTTCTC CCTCTCTGAT TTAAAGCAGA TCAAGGCAGA CCAGGGGAAG	15360
CTTTCAGATG ATCCTGATAG GTATACAGAT GTCCTACAGG GTCTAGGGCA AACCTTCAAT	15420
CTCACTTGGA GAGATGTCAT GCTATTGTTA GATCAAACCC TGGCCTTTAA TTAAAGAAT	15480
GTGGCTTTAG CCACAGCCCG AGAGTTTGGA GATACCTGGT ATCTTAGTCA AGTAAATGAT	15540
AGAATGACAG CTGGGGAAAG GGACAAAGTC TCTCCCGGTC AGCAAGCCAT CCCTAGTGTG	15600
GATCCCCACT GGGACCTAGA CTCAGATCAT TGGGACTGGA GTCGCAAAACA TCTGTTGACC	15660
TGTGTTCTAG AAAGACTAAG GAGAATTAGG AAAGAGCCTA TGAATTATTC AATGATGTCC	15720
ACCATAACTC AGGAAAAGGA AGAAAGTCTT GCCTTCCCTT GAGTGGCTAC AGGGAGGCCT	15780
TAAGGAAAAT ATAACCTCCC TGTCACCCAA CTCACTTCAA GGGTTAATTG ATTCTAAAAG	15840
ATATGTTTAT TACTCAATCA GCTGCAGATA TCAGGAGAAA GCTCCAAAAG CAAGCCCTTG	15900
GCCCTGAACA AAATCTGGAG GCATTATTAA ACCTGGCAAC CTTGGTGTTT TATAATAGGG	15960

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GCCAAGAGGA GCAGGCCAAA ATGGAAAAGC GAGATAAGAG AAAGGCCACA GCCTTAGTCA	16020
TGGCCCTCAG ACAAACAAAC CTTGGTGGTT CAGAGAGGAC AGAAAATGGA GCAGGCCAAT	16080
CACCCAGTAG GGCTTGTTGT CAGTGTGGTT TGCAAGGACA GTTTAAAAAA GATTGTCCTA	16140
TGAGAAACAA GCTGCCCCCT CACCCATGTC CACTATGCTG AAGCAATCAC TGGAAGCCAC	16200
ACTGCCCCAA AGGACAAAGA TTATCTGGGC CAGAAGCCCC CAAGCAGATG ATCCAACCAC	16260
AGGACTGAGG GTGCTCAGG TTAGCGCCAG CTCATGTCAT CACCCTCACT GAGCCCTGGG	16320
TACATTTAAC CATTGAGGGC CAGGAAATTG ACTTCCTACT GGACACTGGT GCGGCTTTCT	16380
CAGTGTTAAC CTCCTGTCCT GGACAGCTGT CCTCAAGGTC TGTACCATC CGAGGAATCC	16440
TGGGACAGCC TATATCCAGG TATTTCTCCC ACCTCCTCAG TTGTAAGTGG GAGACTTTGC	16500
TACAGATAGT AAGTATGCTT ACCTAATCCT ACATGCCCAT GCTGCGATAT GGAAAGAAAG	16560
GGAATTCCTA ACTTCTGGGT GAACCCCAT TAAATATCAC AAGGAACTA TGGAGTTATT	16620
GCACACAGTG CAAAACCCA AGGAGGTGGC GGTCTTACAT TGCCGAAGCC ATCAAAGGG	16680
GAAGGAGAGG GGAGAACTGC AGCATAAGTG GCTGGCAGAG GCAGGGAAAG ACAAGCAGAA	16740
AGGAAAGAGA GAAAGAGCAG AAAGTGAGAG AGAAAGAGAG ATAGGAAGTG ATAGCAAAGA	16800
GGGAGTCCGA AAGAAAAGAG AGAGGAGAGA GAGAGGGGGA AAGACAGAGA GAGACAGAGG	16860
AAGAGACAGA GAGACAGAAA GAGAGAAGCA AAGAGAGGAA GAGACAAAGA AGGAGTCAAA	16920
GAGAGGGAAA GAGAAGTAGT AAAGAAAAAA CAGTGTACCC TATTCCTTTA AAAGCCAGGT	16980
TAAATTTAAA ACCTATAATT GATAATTGAA GGCCTTTTCT GTAACCCTAT AATACTCCAA	17040
TACCACCTTG TTGTCAGTGT AAACAAGGGT ATAGCCCAA AGCACTGAGG CCACTGACAA	17100
CCCGTAGCCT TCTTATCAA AATCCTTAAC ACAGCAGGTT TCCTAACAGG GAATCTAAAT	17160
CTTAAGGTCG GACCAGACAT AGGAGGAACT GCCTTCAGGA CAGGATGATA GATGGTTCCT	17220
CCCAGGTGAT TAAGGAAAAA GACACAATGG GTATTGAGTA AGTGATAAGG AAACCTTTAT	17280
AGAAGCAGAG TTAGGAAAAT TGCCTAATAA GTGGTCTGCT CAAACGTTGA AGCTGTTTGC	17340

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TGTTTGC	ACT CAGCTAAACC	TTAAAGTACT	TACAGAATCA	GGAAGGAGCC	ATCTATACCA	17400
ATTCTAAGTT	AATATGGACT	GAACGAGGTT	TTATTAATAG	CAAAGAAAAT	TAAAATCTCA	17460
AAC TTACAAG	GTTTTCAACT	AAAGTAAAGT	TTGCTAAAAG	TTAACAGCGT	AACATGTATT	17520
ATCCTACTAC	CTCACACTCT	CTCAAAGGAT	TTCTCAGACA	GTTTGCAAAA	AAGAACGAAA	17580
TCTGTCCTTA	CTCTACAATC	CCAAATAGAC	TCTTTGGCAG	CAGTGACTCT	CCAAAACCGC	17640
TGAGGCCTAG	ACTCTCTTAC	TGCTGAGAAA	GGAAGATTCT	GCACTTCTTA	GGGGTAGAGT	17700
GTTGTTTTTA	TACTAACCAG	TCAGGGATAA	TATGAGATAC	CACCCAGTGT	TTACAGGAAA	17760
AGGCTTCTGA	AATCAGACAA	TGCCTTTCAA	ACTCTTATAC	CAACCTCTGG	AGTTGGGCGA	17820
CATGGCTTCT	CCCCTTTCTA	GGTCCTGTGA	CAGCCATCTT	GCTAATAGTC	GCATTTGGGC	17880
CCTGTATTTT	TAACCTCTTG	GTCAAATTTG	TTTCTCTTAG	GATCGAGGCC	ATCAAGCTAC	17940
AGATGATCTT	ACAAATGTAA	CCCCAAATGA	GCTCAACTAA	CAACTTCTGC	TGAGGACCCC	18000
TGGACCGACC	CGCTGGCCCT	TTCAATGGCC	TAAAGAGCTC	CCCTCTGGAG	GACACTACCA	18060
CTGCAGGGCC	CCTTCTTCAC	CCCTATCCAG	CAGGAAGTAG	CTACAGCGGT	CATCGCCAAA	18120
TCCCAACAGC	AGCTGGGGTG	TCCTGTTTGG	AGGGGGGATT	GAGAGGTGAA	GCCAGCTGGG	18180
CTTCTGGGTC	AGGTGGGGAC	TTGGAGAACT	TTTGTGTCTA	GCTAAAGGAT	TGTAAATGCA	18240
CCAATCAGCA	CTCTGTGTCT	AGCTAAAGGA	TTGTAAATGC	ACCAATCAGC	ACTCTGTAAA	18300
ATGGACCAAT	CAGCAGGATG	TGGGCGGGGT	CAAATAAGGG	AGTAAAAACT	GGCCACCCGA	18360
GCCAGCAGTG	GCAACCCACT	CGGGTCCCCT	TCCACACTGT	GGAAGCTTTG	TTCTTTTGCT	18420
CTTCACAATA	AATCTTGCTG	CTGCTCATTC	TTTGTGTCCA	CACTACCTTT	ATGAGCTGTA	18480
AACTCACTG	CGAGGGTCTG	TGGCTTCATT	CCTGAAGTCA	ACAGACCACG	AACCCACTGG	18540
AAGGAACAAA	GAAC TCCCGA	TGTGCTGCCT	TTAAGAGCTG	TAACACTCAC	TGCGAAGCTC	18600
TGCAGCTTCA	CTCCTGAAGT	CAGTGAGACC	ACAAACCCAC	CAGAAGGAAG	AAACTCTGGA	18660
CACACCTGAA	TATCTGAAGG	AACAAACTCC	AGACACACCA	TCTTTCAGAG	CTGTAACACT	18720

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CACCGCAAGG	GTCTGTGGCT	TCATTCTTGA	AGTCAGCAAG	ACCAAGAACC	CACCGGAAGG	18780
AACAAATTCC	AGACACAGTA	GGAAATCTGT	ATTTTGTATC	TGTGGCTTCC	AGGGTTACTC	18840
CAGTCATTGA	AGTCTCCATT	GCAGCCTTAA	GGAAACAGAG	AATGGTTTGG	AGGAGCACAT	18900
GTGGGAATTG	TTATGGACCA	GGCTTGAGAT	GCACATAGGG	CATTTCGTAT	CAAACCTAGC	18960
TGGAAGCAGG	GCCAGGAAAT	ATAATCTAAG	GAAGACAGTT	TTTGTAGACA	GTAGTAGTCT	19020
TTGCATCTGA	GACATGTAGA	TTATCAAGCA	ATTAATTAGA	AAAAATATAG	CCAGGTGCGA	19080
TGGCTCATGC	CTGTAATCCC	AGCACTTTGG	GAGGCCAAGG	GGTGTGGATC	ACAAGGTCAG	19140
GCGTTCGAGA	CCAGCCTGGC	CAACATGGTG	AAACCCCGTC	TCTACTAAAA	ATACAAAAAT	19200
TAGCCTGGTG	TGGTGGCACG	CATCTGTAAT	CCCAGTACTC	AGGAGGCTGA	GGCAGGGGAA	19260
TCTCTTGAAC	TTGGGAGGCA	GAGGTTGCAG	TGAGCCAAGA	TCACACCACA	GCACTCCATC	19320
CTGGGTGACA	GAGCGAGACT	CTGTCTCAAA	AAAAAAAAAA	AAAAAAGGAA	AGGAAAATAT	19380
AATCAAGAAT	ATTGACAGGT	AACATTTATT	CAACACTTAC	TATGCACCAG	GCAATACACT	19440
AAGTGTTTTA	CATGGATTAA	CTCATTTAAT	CTTAACAATA	GCCCTATGAA	GTCAGTGCTG	19500
TTATTATCTC	CACTTTATAG	ATAAGGAAAC	TGAAGTACAG	AAAGGTCAAG	TAGAGAAATG	19560
GCCATGCTTG	CATTCTCAGT	TTTTGAAGCA	ACTGTTACAG	GAATCTGGTG	TGAGAAATGC	19620
TCTAACAAGA	TGTGAGTCAG	GGGTGGGAG	GTACTGAGTC	TGAGTTGGGC	AGTTGGGGAT	19680
GGAAGGATGG	ATGAAGAACA	GCTTGACAGA	GAAGCTGACA	CTTGCCAAC	CTGTGGGACC	19740
TTGAAGGGTT	AGAGGGACTT	CACCAAAGAA	ACTGGTGGTC	AGGGAACGG	GAGGGTCACG	19800
GCAAGGAGGG	AAAGGAACT	GTACCACAGC	AGAGAGTCTG	AAGCTACTAC	AGTGTAGTTC	19860
AGCGTATAAA	GAATAATTAT	TTTAAGGTAA	ACTTATAACC	TCATGCAAAT	ATAAAATGAA	19920
CACGTGTCAA	AGATCTTATT	TAATTTATTA	ATTAATGAGG	GAACCTGTAA	GATGTTACAG	19980
CCAGTTCAAA	GGATAATTCA	AATAAATCCA	TGCACATATG	TAGGCAATAA	GGAATGCTGA	20040
AATGAATTTA	AAAGTAGATG	TAACTGATT	TATCCACAGA	GAAATAATCA	GTTGCATTTT	20100

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ACATAACAAA	ATTCAGTTGC	TTTTCTACAG	AAGGAATTGT	TTGCATCATT	ACCAATTTTT	20160
CTACAACATA	CAGAATTATA	AAATAACTCA	AACACAATGA	AAGGCAGATA	TAACCCACAA	20220
TGGTATGATA	GATACAATAT	CCACATCCAG	GATGTTTTTT	TCTCATTTCA	AAGTCTTTCA	20280
CAAGTTTTCC	TGATAAGGGA	GTGTCAATAA	TACTGTATGG	CAGGCAATAA	GACTGGATGG	20340
ATGGTTGGGG	CCAGGTTTTA	AGGGGTAATA	AATGCCATGT	AAAGGTATGT	GCATACTGTG	20400
CAACATGTCG	GGGGAATCTC	AAATTATTGG	TAGAGTATGT	AGGAAACACT	TGTGGGAGCT	20460
TGTTAATAAA	TTCAAATTCC	CAGACCCAAC	TCCTCAAGGG	GTCTAATACA	GTAGGTTTGG	20520
AGTAAAGCCT	GAAAATCTGC	AATTGTGCAA	AAAAAAAACC	CAGGTGATTG	TGATACACTT	20580
TGAGAAGCAC	TGGTGGAAC	AATAGTCACT	GAACGTTTTT	GAGCAGGGGA	GAAACCTGAG	20640
GACGTCTATG	TTGCAGCAGT	GGAACTTGA	TTAGAAGTAG	GAGAAGATGC	ATGGTCTTAA	20700
AAGAATGCAA	AATGATGGCT	AATATTTGAG	TGCTTATGAT	GGGCCAGGGG	CTGTGCTAGG	20760
CGCGTGGCAC	ACATTCAATA	CGATGGAAGC	CTGTACCAGT	CAGTATTAGT	GGGGTATCTT	20820
TAAGAGTGAC	CAGAATTAAG	GGGGGTTTTT	ACCAAAGCCT	GAGGACTGAG	CCTCCTCATC	20880
CTAAATTCAG	ACACAATGCT	GTACCTATGC	ATTTGCCTCC	AGGCTGTTCC	TGGGCCTCCA	20940
GGGACTGGCC	CAGGCTCCTG	ATAAATAGGG	ACTCCCAACA	ACATAAAGCC	TGGATTTTGG	21000
AACTTCCTGA	ATGTTACTCA	GGCTTTCTAG	TAAGTGTGGA	GATCTGAATA	ATAACACAAT	21060
TCTAAGTTCC	CCTACTCATA	AAGCTGCTCA	TCATTTAGAT	GGGGTAAAGC	ACCTGAAATA	21120
CAATGAGCAT	CACTATTTTC	ATTCATCCAT	GAAATGAACA	TTCCGGGGAG	ATCAGTAAGT	21180
TGATGTATCA	CCCTTGAACA	GGGCAAAATG	AATACTCACC	AGGAATATGT	GGTATTTTAA	21240
AAAGAAGGCA	AAGGGAAGAA	TAGTGGGGAT	GGGGCAAAAA	CTTTAAATAG	ATTCCCCCAA	21300
TCATATATGG	CAATTGAAGA	TAATTAAATT	ATCATTTTAA	TTGAGTAAGT	ACTCATAGAG	21360
CCCTCACTAT	TTGAAAATGA	ACTGCCTCCT	AATTGTTATT	GTGCAAATGT	GATACATTAA	21420
ACTTAAGCTA	TTTTAATAAA	ACATCCATTT	TCGGAAGCTG	TAGTAGGTTC	TCCCAGGTCA	21480

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GATTTGATAA	GCCATAAAGA	ACAAATGCCA	ACTCCTATTT	TTCTATGGTG	CTGGGAAATA	21540
AGAGAGAAAT	GTGTAATTCA	AAGCAATCAT	TTAATTTTAT	CCAATAGCTT	GATTCTCCTC	21600
TCTCTTCTAG	CCTTTTAGCT	AAGCTGTTAC	CAAGTAACCA	CACTAGTTGG	CTTGAGTCTT	21660
ACCACTGTTT	CCCTGACCCC	ACAGTGAGGA	GACTGCATCT	GTAAAGAGC	AGTTATGTAA	21720
CCATGGCTAT	GCTGAGCTGG	GATTCCTAAG	GCTTAGGTTC	TTTCTGTGAA	TGACCTTCAC	21780
CAAGACACCT	GAGGTCTGTG	TGGAACCACA	GGCTTGTCAT	CTCTAAGGCA	GAGTTGATAA	21840
TTCCATCTGT	TTCTTGAGCC	CACACTGAGA	AAAAGATTAC	ATGACTGCAG	TTATTTGAAT	21900
GCCTCATGGA	AAGACGTCTT	ATAAATATTA	TAATTAATGT	TATCATTAAG	TAATGCTTCA	21960
ATGCAGATCT	TCCAAGTATA	AATATCAGCT	GAGTAAGAAG	TCAATCTTCC	CTGAAGCAAA	22020
ATTGAAATTT	GTAAATGCGA	TTTCTGGGAG	CTTATTTTGT	AATACATGAT	TCCAGAGTGT	22080
CCATAACACA	CACAATTGTC	TTTTTTCCCC	TACATGGGCT	ATTTACAACA	AAATTGGACT	22140
TATAATGTTT	ATTTCCAGGG	ATGACTAGAA	CTTTAATAAC	AAACCTTGGG	CCAGGCATAG	22200
TGGCTCATGC	CTATAATCAC	AGCACTTCGG	GAGGCTGAGG	CTGGTAGATT	ACTTGAGGCC	22260
AGGAGTTTGA	GAACAGCCTG	GCCAACATGG	CAAAACCCTG	TCTCTACTAA	AAATATAAAA	22320
ATTAGCCGGG	TGTGGTGGCG	CATGCCAGTA	ATCCCAGTTA	CTAAGTAGGC	TGAGGTACGA	22380
CAATCGCTGG	AACCTGGGAG	GCGGAGGTTG	CAGTGAGCTG	AGATTGCACT	ACTGCACTCC	22440
AGCCTGGGTG	ACAGAGAAAG	ACTCTGTCTC	AAAAAAAAAA	AAAAAAAAATA	ATAATAATAA	22500
TAAACCCTGA	TGAAAGGTTT	CTAAAAATGTT	TTCATCTAAT	GGTTTTCTTG	ACAATTAAAT	22560
TTTCTATATA	ATGTCAGTTC	ATAAAAAAAC	TGAGAACGAC	CACATGTCAT	ATCGACTGCT	22620
TAAAAGAAAA	TACGTATATT	TACAAACATA	TACACGATAC	TGTCTTTTGT	CTGGTTAGTT	22680
TAGAGGTTAG	ATAAACTGCA	GTATGTTGTA	GTGGACAGAT	CATAGAACTA	GGAGTCAGGA	22740
TGTCTGGATT	CCTAGGAAGC	AATGAATAGG	TTGCACGGTG	CAGACCAGCA	TCATGAGTAT	22800
CCTCAGGGAG	CTTGTTAGAA	CTGCAGATCC	TTTAACTCAT	TGAATCAGAA	TCCCTAGGTG	22860

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TGGGGCCCTG	AAATCTGTAT	TTTAGCAGGC	TCTCTGGGAT	TGTGATGTGC	CTTAGAGTTT	22920
GACAACCACT	GGGTAGCTGA	TCCTGACTTA	GACTTATCAG	GCATGTGATC	TTGAACAAGT	22980
CACATAATCT	CACTGAGTTC	AGTTTTCTTA	TGCTTAAAAT	AGGCCCAATA	ATATCTATTT	23040
CACATGGACT	GCTTTGAGGA	TTAGGCAAGA	GATCTGTAAC	AGACACTGTA	GAACAGTGTC	23100
TCTGGTCTAC	AGCTGACCTT	CCATAAATGG	TAGTTGCCTT	GATCTCTGCT	CTGCCACATA	23160
ATAGCTGGTT	AACTATGAGC	AAGTAATTTA	GTTCTTCTCA	GTTTAGTTTC	TTCACCTGTA	23220
AAAGAAGGAA	AATAACTGTT	ATACTCAATT	TCTGAAGTGG	CTATAAAAAT	CAGTTTAAAT	23280
TATGGGCATT	GAAGCTCTTT	GTACACTGTA	TAAGGACTGT	ACATCTAAGG	GATTAATGAG	23340
ACCAGGCTTA	TGATTTTAAG	CATGGAGTAA	ATAGTAACAC	TGACTCTGTT	CTATGAACCA	23400
CATGGAAACT	CTAAAGAATA	TGCACATTTG	AAACACAGGT	ATCATCTGGG	GAAGGTGATC	23460
TGCTCACCCA	AACCAGTTCA	TGAACATCAA	TCTCCAGTGG	CGTGCTGGAG	CTAGCTGTAC	23520
CAGCTCATGA	GGGCCAATTG	TTTCATTTTT	AGGAATTTTG	TTTGCTGGTT	AAAAATAGTC	23580
ATTATTTAAA	ATTAAATTAT	GTAAACAATA	ATATTAGATA	AAATAAGTTA	AAATAAAAAC	23640
AAAGGAACTA	ATTATCCCCA	AACTCTTCCC	CACCTAATTA	TTTTACTATC	TGTGCCTTGG	23700
GATTATTTAC	ATTGATTTTA	TCCATATGGT	GACAATACTA	TTCATATATA	AATGGTGTGC	23760
TTCTCTTCAT	AACTCTACAT	AGCCTGATGT	CAGGCTAGTA	GCTTGAAATT	GGCCACAGTG	23820
GGAGTGTGAG	CATTTGTACC	ATGAGGCTTG	GCCAAGGCTA	CAAATCCAGA	CTTTTGTTTT	23880
TCCCTCCTGG	AGAGCTGTCT	GTAAAAAATT	TACCAACACA	CCACTGGTCT	TACCTTTGTT	23940
AATTTACCAC	AGTCCAGGTT	CTGACCTAGA	CTTAGAAACC	TGGATTTGTC	AGCAAGCTGA	24000
GGATAGAGCC	ATTATTTTTA	AGAAGGACTC	ACATTACCCA	AGTGCAAAGC	CTGATATATA	24060
CCTTCAGAAT	ATCAATTTAT	TAATTTACAG	TGAAGAAAGC	CACCCCAGGG	CATTCCCCAG	24120
GGGAAGGCAA	AAAGAGCTAG	TTGCACATTT	TGAATGTTTG	ATGACATTAG	GGTAAGGTGA	24180
CACAGAATAT	CCATTTCCAC	AACTGAGATA	CCTGCTGCCT	TAAGGAAGGG	ACAGGCAAGT	24240

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CCTTGGGCAG GACCTTAGAT TGTCACGTGC CATCTTGCTC TAGGACTCTC CTTTCCAGGC	24300
ATGACGATGG CCAACTCTGT CCTCCTACCC TACTGATGGG ATTATCTTTT CTTGACACAT	24360
GGCAATGCCT CCAATCAGAG GCTGGTAGCT ATTTTAAATC TTCAGGGCAG TATTTTTC	24420
AGGGAAGTTC ATGGACCATA TGCATCTGTA TCATTTAGAT GTATATTAAA AATGCTTAGT	24480
CTTCCCCAGT TATACTAGAT CAGAATCTCT GTTGGTGGGG CCCACGAATC GGTATTTTCA	24540
ACAAATCACT AGGTAATTTT TGTATATACT ATAGTGTGAA GACCACTGCT TGAAGGTTTC	24600
TTTGCATATC TCCACTAAAT ATAAAAATA TTGACTTCTA GATTTAACCT CCAAAGCACT	24660
TGCATTTTTA AGTTTCTGGG GGCATTATAT TGTGGTACCC CTATACCACT CACACTCTAG	24720
TCAGGAGGTA TATTATGGAC TGAATGTTTG TGTCCCTCCA AACTCATAT GTTGAAGTCT	24780
TAGCTTCCAA TGTGATAGTA TTAGGAGATG GTGCCTTCTG GAGGTAAAAT CAAGCCCTCA	24840
TGAATGGGAT TAGTGCCTTT AGAAAGAGAG CTCCGTCCT GTCTTTCCAT CAATGAAGA	24900
TGCAGTGAGA AGCTGGTAGT CTTGCATCTG GAAGAGGGCC CTCACACAAC CTGATCATGC	24960
TGGCACCTGG TCTCAGACTT TCTGCCTCCA GAACTATGAG ATGATAAATT TCTGTTGTTC	25020
ATACCCCACT CAGGCTACAA TATTAGGTTG CTGCAAAGTA TTTGTGATTT TTGCCTTTAC	25080
TTTTCAGGGC AAAAAGTGCA ATTACTTTTG TGCCAACCTA ATATTTTGTT ATAGCAGCCC	25140
GAACTAAGGC AAGGGAGACT ACATCAGACA GTGTAGCTAT GTAAGTACAA ATGTATCCCT	25200
GTTGAGGAAA ACTAAGTTCT AACCTGACT TCAGGCCAGT AGCCACCTTT TCAATCTCTT	25260
TCATGAAGGG ACCATTATCA TTATCACTGG TGGCAAAAAT AGAGGCACGA GAATGGAATT	25320
TGCTTTTCTG TGAAATCTCA GTGTATACAG ATTGAAGAGC AAGGGTTTGC TTTCATCTCT	25380
AAGAAGCAAA AGTGAGTACG GACTGGCACA TTATCAGAGA AAGAATCATT CTAGCTCGGT	25440
GGGTCTTAAC CAGGAGTGAA TTTGACTCCA GGAACAGTT GGCAATGTCT GGAGACGTTT	25500
TTATTTGTTA TAGCTGGGGG ATGAGTGGGT GGGTTGCTAC TGGCATCTAG TGGGTGGAGA	25560
CCAGAGATGC TGTAAACAT CCCGCAAAGC ACAGGACAGT CCCCACAAAC AAAGAATTAT	25620

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CTGGCCCCAA ATATCAATAG TGCCAAAGTT GAGAAACCTC ATTCTAGCTT CCTTTTCCCT	25680
TCTACGTTCT AATCAACTGT TGTTCTTTCA GCATTAGGAT TCATCCAGCA GTCTCTTTCC	25740
CCAGCAATTT GTTGAAATTT TTTTAAAAAT GGACTCATT TTAGTGTCACA AGAAAAAAT	25800
ACATTACAG GAAAGGATGG GTCATTTTGT TTAATGATGT TTTGCCTTTC ACATAGCAAA	25860
AGCTTAATAA AGTATTTTTA AATAAAATGG TGAATAGATC AAAACATTAA TTTCACATGT	25920
GTTTTAATAA ATAACAGGAA GATGGCTATA TTATATAAAT TGTCTTGTA TATGTCTGA	25980
GTGGATCATC AAACACAAAC GTATCTACAT GCCTTTTCTT GTGAATAGAT CTAATAATAA	26040
CGCTCTCTA AAAACAAAT AAATGGATAT TATTTGCTGA GAATGTAATG CTTGTGTGAA	26100
TAGAAGCCAG CCCTGAATCC AAGCCCCCAG ATCTATTTAA AGAATTTGAA GAATGTCAGA	26160
AAAGCACGTG GCTTCAAGGT TAATGTGTAA GACTCACAGA AACTTGAAAA ATCACTATGA	26220
CTAAAAAGAA AGTATGAGCT CCCTGCATGC CTGTAAATTG GAATGACAGC CAAAACCACT	26280
TAATTATAAA AACAGCTAAT TTAACAGGTT TTCAAATTTG TTTCTTTCTC CAAGTAGCAT	26340
ATAGTCAATA ATCCTTAAAG AGAAAGCAAA GAAGGGGAAG CACTGAACCA AATTTGCTTT	26400
TTTGACCTG CTCAGCTCAA ATGCAGAGTT CTCTACCTGG AAATTGACTG CTTCCATAGT	26460
TTGATAGCCA CAGAGAGATG GGAACAGAAG GAGAGGTATA ATCCCAGACT TGATTCAGCT	26520
ATAGAGAATG ACAATAGTGT CAGAGGCCTT CCAACCAGAG CGACTCCATC TTGAATACGG	26580
GCTGGGTAAA ACAGGGCTGA GACCTACTGG GCTGCATTCC CAGGAGGCTA AGCATTCTAA	26640
GTCACAGGAT GAGACAGGAG GTCAGCACAA GACCTTGCTG ATAAAACAGG TTGTAATAAA	26700
GAAGCCAGCC AAAACCCACC AAAACCAAGA TGGCCATGAG AGTTATCTGT GGTGGTCTC	26760
ACTGCTCATT GTATGCTAAT TATAATGTAT TAGCATGTTA AAAGACACTC CCACCAGTGC	26820
TATGACAGTT TACAGGTACA TTGGCAACTT CCGGAAGTTA CCCTCTATGG TCTAAAAAGG	26880
GGAGGAACCC TCACCTCCCA GAATTGCCCA CCCCTTTCCT GGAAAACTTG TGAATAATTC	26940
ACCCTTGTTT AGCATATAAT CAAGAAGTAA CTGTAAGTAT CCTTAGGCCA GAAGCTCAGG	27000

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CCACTGCTCT	GAATGTGGAA	TAGCCATTCT	TTTATCCTTT	ACTTTCTTAA	TAAACTTGCT	27060
TTCAC TTAC	TGTATGGACT	CCCTGTGAAT	TCTTTCTTGC	AAGAGATCCA	AGAACTCTCT	27120
CTTG GGTCT	GGATCAGGAC	CTCTTCCAG	TAACAATAGT	AGTAAGGGGT	CAGGGAGACT	27180
GGACAAAGGA	GTTTAAGAAG	CCTTAGATAA	AGGGTCCTCA	TCATTGTCAT	AACATAAAAT	27240
CATGGACTCC	TAGAATTTTA	TAGCTGATAG	GATTAGAAAT	TTCAAAATTC	AATTTTCATTA	27300
ATTTTCATCT	GCGAAAACAG	ATGGCCAGAG	AGGCCAAACA	ATTTGTTAAG	GAGCACTGAG	27360
GGCAGACCAC	ACTGGAACGC	AAACCTCTTA	GCAGAGTATA	CAAGGCCTTT	GATCTCCTCA	27420
GTCAGAATGA	ACTAGAGCTT	TCCAGGGTAC	CCTTTCTGAC	TGTTTAGCAT	GTTTGCCAGT	27480
CTGACTAATT	TTGAAGTTGC	TTAAATATCT	GTCATTTCCA	CTGTATCATA	ATCTCCTCAT	27540
TCATCTTCAA	TCTCCAATGC	CTTGA ACTCA	GTAATGTTA	GTTGAACAAA	AGTAAATTGA	27600
ACCCAGAATT	TCTGATCATA	ATCTGGAGCA	CTTTAA AAT	GTCAGCTTAC	TGGGAAACGG	27660
GATAACATGT	GATTTGTCTT	TGATTTTTTT	TTTCTCATAT	GCTTTTTCCA	CCTATAGATG	27720
CTACACGAAT	GTTTTTAAAA	TCTGATATAA	AAATTAAAAT	TAAAAAATTA	AAAAAAGAAA	27780
ATTTGATACA	ATGCTACATT	TAGAGTGTG	TGATTAGATT	CCTTAAGTGT	ATCATGGTGA	27840
TCTCTACATC	ACGTGGTGAT	CAAATTGCTT	TGGGTTTTAA	CACATAACTG	ACAAAGGCTT	27900
GGGGACATGT	AAGATCCCAA	ATACATTTTT	ATTGATTTTT	TTTTCTTGTT	TGTCCTCTTT	27960
TAAATAACTT	TTTTTTGTTA	TAAGAATAAT	TCATGTT CAG	TGGAGAAACC	ATAGAAAATA	28020
GTGACAAGTG	AAGGAATAAA	TTTAAAATGA	CCCATAATTG	TACCATACAT	TCTGATTTTT	28080
TAAACGCTGA	ACAAATTAGC	CTTGGGTAAG	TACCAGGAAT	AGAGTGCAGC	ATTGAAAGTT	28140
AAAGTTTGGG	GAAGGATAGC	TGACTTAAGA	AATTATCTAG	TTAGACATTT	TTTGATGGGG	28200
TAATTTTGCA	GATGACATTA	GTGAGAGAAA	GGACTTGCCA	CTCTCACACA	GCTAGTAGGG	28260
GTGTGGGAGG	ATATTGGAAC	CAAGTTTCAA	GTCTTCAGTG	AAGAATCAAG	GGAGAAGTTC	28320
TAAAACCTAA	CAATATCCCT	CTGGATGGAC	ATTTATTTTA	TTACTACAAT	AAGCCACACG	28380

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GTGAGTCATA AGGAGCATTT CATTCTTCTA ATATGTCTCT ACTGTATTTA GAATCTGATA	28440
AAGCCCCTAT TAGAATTCAT CTCTTTAAGA ATAAAAGAAG CTGAGGAACT AAAGAGAGGG	28500
TTGGAATAAT CCACTAATTA TATCCGTAA GCTTCAGTTA CGCTAATAAG GAATATCACA	28560
TGACTGTGGT GTGTGCTTGT TCTGAACAGT AAAGTACATG AGGAAAGATA AGATTCAGGG	28620
CTGAAATGTC CTTCAGCATA TGTAGGTAGT GGTGATGAAA GTCATTAAAA GAAAAATTGA	28680
TTGAGGTATT TTAGTAAACA AAAGAACTCA CCACTTACCC ATCAGGAAGT GTATTGTTAA	28740
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TTCTTATCCT GTCACCTTTC AGGCAAAATT AAAAAAAAAA AAAGATTGAA AACGATGCTC	28860
CTATTTTATT TGCTTCAAAA GAAACAGGCT GTTGCATTGT GCTTGGAACA GTTTACTCTT	28920
GGCCTTGATG TAAGTGTGAA AGGAAGCCCA TGTAATTGAC TAGGCAGTAT CTGAAGAAGC	28980
AGGAAATACA GTGTAAAGAA AATGAACAGG CATGAAAACC ATGGCTATTT GATAAAAGTA	29040
AATAATTTCT GCAGTTCACA TGTTCCTCAGC ATATTTTCTT TGATACTGAC TTGCTTAATA	29100
TGACAATAGC AGAACCATGG TAGCTGTAG GCATTACTTT TCTTTTAATT TCTTTTACAT	29160
TTTGAATTTA CCAGCACTCA CATTTGTATT ACTTTTGGGT TATACTGAGG ATCTATAACT	29220
TATAGATCAA ATACCTGACA TATATATGCA TTCTCTGAAG TCTTAGGGCA GAACTAGAAC	29280
ATTCTTGTTA ACATCAGTAT AAGATATTAA AATGGAAGTT TTGCCTAAGA CTGAAGACAA	29340
TAAAAATATC ATAGTCTGAA ATGAATGCCA GCACACCATA CAGGATTTAA ATATCTATAC	29400
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GGGGGAAATC AGTTTTACAA TTATTAAGTA TTTCACCCTT GACAAGAGTA TATATATTGG	29520
AAATCAGTTG GAGAGTATTT TCAAAGATAA ATGTTAGTGT GCTATGAATG AATCCACCCC	29580
TACCACCACT GAGGCAGGGT AGGAGAGGCC TGTGCTCCTC AAGCATAGTT GGAAAAGGAC	29640
CTCAACAAGA CCACTTCAAG AGTCTAATGT GTGGAGACTG TTGCTTAGGG AGACCTTATG	29700
GTCTAGCTTC TGACTCACAG CTAAGTCAGG GAGACAGGTT GGCTGCTCTG ATCGTGGAGT	29760

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CCAAAAGATG GCCTGCACTG AAAAGCCTCA TGAGTGTTGA CTTAGGGCTA GTCTAAGAGG	29820
TCCCTGGAAG AAGAAACACT CAGTAGGAGA GAAGCTGGAG GTACCTTCAG TGCTGAATTG	29880
GAACCTAGAT TCATTCCCCC GTGGAGCAAA TTACATAGGA AAGATGCCCA GTGATGGAGA	29940
GTGGGGGTGT CTCTAACAAT TACCCACCCA CCTGCCCCCA CCCCTAAGAA AAAGAAAATC	30000
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CAGGGTACCT GGCAAGTAAG AACATTCTCTG ATTCCCTTCC CTCCTCTTCC TCTTTGCCCT	30120
CCAACCTTAG TGGCTAGCAA GATGGGGAGA GGAGGAGAAG CTGTAAGTGG GGAAAAAGA	30180
GCAGCTTTCT CTCCTTTTCA GCTGCTGGAT TCTCCCTCAT CATAGGCCTG AGCTGGGGAA	30240
TCAGGAAGAA GGATTCTTTT TAAAACTGAA GTAACGTTAT CATTTAATTT TAAACATTT	30300
TAAATTTTGA CAATGTTGAG ATTAGATATA CTAATTATTA AACTAAGATT ATGTTTTCGA	30360
GCTTGAAGTG ATAAGAAAAA CCTCTTATCT AAGAGCATCC AGGAAAGTCG GGGGTTTCCT	30420
GAACATCCTT TTAAATCCTT TGGAAGTCAG CTTTCAGAGA GGATTTAAAG TGTAGACTGG	30480
GCCTTCAGAA ACTTG GTTAA TGTAGGGGTT TCCTATGCAG ACTTGGGGAC TATACCTTGT	30540
GTGGAAGAGA GAAAATAAGA TTATCTTACA TTTTTCCTAT TCCTTTTCA AAAAGAAAGC	30600
TCAGCTAGCA TGAAAGTTAA ATTCAAAACG TAATGGGTAT TATTTGCATA TTCAAATCTA	30660
GTGCATATCA TGTAAGTACT GAATTATGGT ATTCATTATT TCAAATGACA AGCTGGATTT	30720
TTTTTTCTTT CGAATTTTAC AAATTAATTT TCCTTGGAAC CTTTGGTTT GGGCTTTAAG	30780
AGTTTAGGCT TTCATCACAA AGAGAGGACA GCCTTGAAGA TTAAAGTGTG TGGCTCTTCT	30840
CAAGATGTTT TTAGTCCAGC AAAGGATTCT ATGCATATTT GGGCTTCCTT CTGTCTCATA	30900
ACCTGTATTT CTGATATTC TATTTATATT CTGTAAGATT TTTTTTTTAA AGGAAAAATT	30960
CTTCCATGGT TGAAGGACAT GTCAAAAATA GAGGATACAG TTTTATATCA AAGGAAGTTT	31020
CATGATATGA CTGTAGAAGC TCATTTGACT TAAGACACAT CATTCCTCA TGGAAGTGTT	31080
AAACAGATCT GTACAATAAG GTTGGCAATC TTTGTGTAAA ACAGTTTTTT TTCTCCTGCT	31140

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CTAAAGAAAG TGTATATTTC AAAATGTGAA TGTCAGCAGT CAGAAAATAG TATTTTTTTA	31200
ACTTCGTTTT CAAAGTCCTC AAAAACCTGT ACCTAATCAT GAATTTTTTT TCCCACAGAT	31260
TGTTTCTTCT TCTCCCTCCC AGAACTTTG AAGTTTTTCT ACATGACACC AGGACCTATG	31320
TCTTTTTTTA ATTACACAGA AATGAAAGAA AAAAAGTGTG TTGTATCGTT AACCAAATAT	31380
ATGAAATCTT TAAGCTGTAT TTTTATTTTT AACTTTGTTT TGCAAAGAGG CCATTCCCTT	31440
TGGTTAAATA ATTTGTTATT CACAGTTTCC TTGTCCTCAT ATTATCAAGG GGAAAATTGT	31500
AGAAATTTTA AAGGAAGCTC TAGGCAATGT TTTCATCCCT GAATCTTTGG AGAGTTATAA	31560
AAACAAACAG ATTACTGAAC CTGTAAGAGA ACCAATCGTG AAGTCATTAC ATCTAAGCAT	31620
AAGCAAAATC TCCTCTTGGA TCATTAAGTT ATAGAAGAAA AGAAAGCCTG CACTTTGAAA	31680
TTTAAATAAA GCTTGGTAAC TTGTAAGTCA AACACGTAAA ATTTTACAAT TCAGGAATAT	31740
CGATAGCAGT TGAGTTTAAT AGACTTCTCA CATTCCAAAT TTAAAGCTTC CTTCTCTGTG	31800
CTAATAGAGA TACAATAGCA GTAGGCGTTT AAGAAGAATG AATCAACAAT TTAAACTAT	31860
AATGTGTTTT TTATTCATCT CCCTTATTCA CATATATTTG TTTTGTTTTG AGAAGGAGTT	31920
CTGCTCTGTC GCCCAGGCAG GAGTGCTGTG GCACGATCTC AGCTCACCGC AACCTCTGCC	31980
TCCCGGGTTC AAGCGATTCT CTTGCCTCAG CCTCCTGAGT AGCTGCGATT ACAGGCGTGC	32040
GCCAGCAACC CCGGCTAATT TTTGTATTTT TAGTAGAGAC AGGGTTTCAC CACGTTGGCC	32100
AGGTTGGTCT CGAACCCCTG ATCTCAAGTG ATCAGCCCGC CTCGGCCTCC CAAAGTGCTG	32160
GGATTACAGG CGTGAGCCAT CACTTCTGGC CCTTATTCGC ATACAATTTA AAAATCATCA	32220
CAGAAGGTTT GAAAGAAGGA AGGGGCAGAA AATTACCTAC TTTCCCTCTC CCCAGCGATC	32280
TCCTTCAAAT CTGTGCCTTT TCCTCAGGCC CAGGCCTCAA TTTACTGAGC AGTCACACCT	32340
CACAGAGGGA GGTCTGGGCA ATCCACTCTT GGTCACAGGA AAGCCATTGA CCCTCCCACT	32400
TCCTCTCCTC CACCTTGTTT TCAACTCTTG ACTTTGGGCT TTGTTTCTGT TCAAGTCCTA	32460
GGAAGTGGTT TCTTTTATCA GGTAAAGTGA TTAGTTCTCT TTCCCTCTAG TTGCTCTCAC	32520

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TCCCTGACTC TTGCCTTCTG TAACAACTGG AGACAACTCT TTCAAAACCA GCTCCAAGCC	32580
CCAGACTTCT CTCTGGGCTT TAGTTCGTAA GGCAGGTGCC CTACTGAGTG AGCCTAGATC	32640
AGACAGAAAC ATAGCTGTTG GCAATGATTT AGGTGAATTT CCTTCCATTG TTTTCTAAT	32700
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GTGAACTCC ATCTCTACTA AAAATCAAAA ATTAGCCGGG CATGGTGGCA GGCTCCCAGC	32940
TACTCAGGAG GCTGAGATGT GAAAATCGCT TGAACCCGGG AGGTAGAGGT TGCAGTGAGC	33000
TGAGATCTTG CCATTGCACT CCAACCTGGG CAATAAGAGC GAAACTCCAT CTCATGGAAA	33060
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AAGTAGCAGA CACCTGTCAT TCTGCCCCACT CAGCACCTCT CTTTCTTTTA GGGAAATGCT	33240
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GCTTTTTATA TATTTTATAT AATTTCTCAG AAGTGGAATT ACTTAGTCAA AAGGTATGAA	33780
CATTTTCTG ATTCTTAATA TAAATTGTGC AAATGCTTTT TAAGAGGATT ATACCAGTTT	33840
ACATTTTGTG TTATATATAA CAGAAAGTAC TACTGAAAAA ATATTACAAA AATTGTCTC	33900

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TCTGTTTCAGG	AGGACCTTGT	AATAGATGAT	AAAGTACTTG	AAATAGGAAC	ATAGAGCATT	33960
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TTATAGATGA	TCTGTACCAA	ACCTAGGTTG	GTTACATAAA	TTGCTTATTC	AACTGGCTTA	34080
AATCTATAAT	AGAAAGATGA	CACTTACTGA	ATGTTTAATA	TACACTTTGT	CAGGGGCTTT	34140
GTATTATTCT	ATGACATCTT	CAAAATGACC	CTACTTTCCT	ATTTTATAAG	TAAGGACAGG	34200
AAGGCTTCAA	GAACATGACT	AATTTTCCCA	AGGGCTGTAC	CAAAGCCAGA	ACCCAAATCT	34260
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TAAGGTTAGA	AAGCCAGATT	GGAGTCCCAA	TTTCACTACT	TAGTAACCAG	ACAAACTTGA	34380
GGAATTCACT	CAACGTCTTT	GAATCTTCAT	TTTCTAATCT	TTAAAACTAA	AACAATAATA	34440
CTTGCTCTAC	CTATGTCCTA	AGATTTCGTG	AGGCACATAG	AGATAGTGTG	GAAGAGTGCT	34500
GTACAGATGT	CAAGTGTTAG	CGTGATTACT	TAGATCCCCTG	AACACCATGG	ATGAATGTCT	34560
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ACACACCTGT	AGTCCCACAT	ACTCAGGAGG	GTGAGTTGGG	AGGATAACTT	TAGTCCAGGA	34800
GTTTCAAGGT	GCAGTGAGCT	GTGATTGCAC	CACTGTACTC	TAACCTGGAC	AGCAGAGTGA	34860
GACCCTGTCT	CTAAAAAAAA	AGAAAAAAAA	ATAATAATAA	TAAAGAATAA	TGGGGCCTTG	34920
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CCAATGGATG	AGGTTGAAAA	TATCAACTGG	ATTGGAATGT	GGCTTACTTG	CGTGGCCACA	35040
ATGAGCTTCG	TAACACTTCC	TGACAGGGTG	AGAAGACAAA	CTTCCTCACC	CAGTCACTGG	35100
CAGAGCTGGA	CACTCTGTGT	CTCTCCCACA	GAACAACCTC	TTACTGCATG	GAGGTGGATG	35160
AAAAAGTCAA	CCGAGAACAG	GCTACTCCAA	AAAGCAGAGC	ACCAAAGGCA	CCAGCTGGTC	35220
AGGTCCCCCT	TCCTAAGTAA	ACAATCACGT	AATTCATTCT	GGACAAAGCC	AGAGAGGTGG	35280

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TGTGGAGAAA	GAGAGGGCAG	TTTCCTCCCA	AGTTTTTCCT	GGAATTCCTT	ATGGGAATAT	35340
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AGGGTCCCAT	CCAGGCCAAA	GTGAGTGCCA	GCCTCATTTG	GGCAGCAGAT	GCCCTGTGGA	35760
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TGGTTCTTAA	GTGGTTAAAA	TCCCTAGCTG	GTCTTTAATC	TGAGCCTGGA	GAATTTAGTT	36000
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TGAGTAGCTG	GGACTACAGG	TGCATGCCAC	CACGTCCGGC	TAATTTTTGT	ATTTTAGGAG	36660

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AGAGAGGGTT TCACCATGTT GCCCAGGCTG GTCACGAACT CCTGAGCTCA GGCAATCCGC	36720
CCTCCTCGGG CTCCCAAAGT GCTGGGATTA CAGGAGTGAG CCACCTCACC TGGCCCCGAC	36780
CTACTAGTCT TTAGTGTTTG CTCCTTCTA TTGGGTAATT GTCTGTTTAT ATGCATGTCT	36840
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TATTGTTTCA AACCCTTGGA TTGCAAGTGA CAGAACTCA ATTCAAACCA ACGTAAGTCA	37440
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GTTAGGATGA AGGTAGGGCT AAGCAAACAA GGGCAAGGGC CACTATATCA TGCTAAAAAT	37680
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CAGCTTACTC ACTGCTTGTA CCTGAGGCCA TATGCCCTGT AAAAGCTTCT GCAGGGTTTC	37860
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TGGGTTTTTT CCTGGGGACA ATGTCTTCAG ATTATCCTAG ACCAAATAAA CTACAGCCAC	38040

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TGGGCCAGGC	TCTTCCTCCT	CCAACTGGAC	CATGTTCCCA	GGGCTCTTCA	CCTTAGTTTA	38100
GGTCAAGCAT	TCTTGGCAAA	AGAAAGGCCT	AGTTAACAAT	AGACATTCTA	GCAATTGATT	38160
CTTTTTGACA	TGTTGTAAGA	TCTATTCACA	TTTGTAATT	AAAGCATTC	CCTATGGAAA	38220
CCAACACGAA	CTAAGCTGCT	CCTGGAATGC	AGGGTGGCCT	CCTCAATACA	GGATGTTCTA	38280
GAGAGCTGTA	TTTTGGGCAC	TTAACTATTC	TCCACTACTT	AGGGCACAGC	ACTGAAATTA	38340
ACACCACTAA	GTTTGTCTATG	TCCATGTAGT	TAGTCTCAGG	CAGTGCAGCC	TCAGGAGTGG	38400
AACTGACCTC	TTATGTGTGT	CCAGCCTTTC	TTCCCTTCAGA	AGTCAGCTGT	GTTTTCTGCT	38460
GACTCTCCAT	AGGAACATCA	GTCCTGAATC	CTCAGACCAC	CATCTGGAGT	AGTAAGTGCT	38520
CCTGACAGTC	CTAGAAGTTG	TCTACCGCTG	GATCTCCAAA	GCGTGTGACA	CACCGTGAGA	38580
GAGAAATGAG	AAAGCTGGGC	TCTTCAGGTA	AATCTTGCTT	TTTCAACAAGC	CCCCTAATTT	38640
TACTGCATAA	TTATTTTGAA	TTCACTGATA	ATTTCTACAA	TTTTCCCAT	AGTCATCTAC	38700
ACACAATACC	CTCTCATGCA	ACACTTGGCT	TTGCTAATAC	ATATCTATTA	TGAGAGCTGT	38760
GCTTCTTAAG	CGTAAATGTT	TTATATGCAC	TAAGGCTCTT	GGCTTACATA	TAAAAGGGGT	38820
ATTGAGCAAT	GTGATACAGA	AGTCTTTTCT	CCACAGGTCT	CATATGTAAA	GAATTCATTA	38880
GATTGGCTGA	AATAGACTGA	TCTGTCCATT	TCTCTGCTCA	CTTATCATAA	GGAAGTCATT	38940
AGCTAAGGAA	CAAAAACCTAC	AATCTATGTA	ATTAGAAGAA	CAAGCTGGTT	TTGCTCAATA	39000
TAAAAATAAG	AAAAAGAAAC	CATGTGAAAG	TCAAAATATT	TGTTTAATCA	GGTCATTGAG	39060
AATCTATTAA	AAAGTATTTG	AATCTTTTAT	GATGAGAACT	ATCTTGACTC	AAGTGGACAG	39120
TGGTGAGCTT	TTTGGCCTGT	GGTCCCTACG	TAGAAAGGAG	GCTTTGTCAT	AAAGTCTTAT	39180
ATGGTACAGG	TGCCAAGTTA	AGTGCCCAAG	CTTGCTCTTA	AAAGCATACT	GGATTTTG	39238

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(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5596 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TATGGACATA TTGTCGTTAG AACGCGGCTA CAATTAATAC ATAACCTTAT GTATCATACA	60
CATACGATTT AGGTGACACT ATAGAACCAG ATCTGATATC GAATGAATTC TTTCTTGCAA	120
GAGATCCAAG AACTCTCTCT TGGGGTCTGG ATCAGGACCT CTTTCCAGTA ACAATAGTAG	180
TAAGGGGTCA GGGAGACTGG ACAAAGGAGT TTAAGAAGCC TTAGATAAAG GGTCTCATC	240
ATTGTCATAA CATAAAATCA TGGACTCCTA GAATTTTATA GCTGATAGGA TTAGAAATTT	300
CAAAATTCAA TTTCATTAAT TTTCATCTGC GAAAACAGAT GGCCAGAGAG GCCAAACAAT	360
TTGTTAAGGA GCACTGAGGG CAGACCACAC TGGAACGCAA ACCTCTTAGC AGAGTATACA	420
AGGCCTTTGA TCTCCTCAGT CAGAATGAAC TAGAGCTTTC CAGGGTACCC TTTCTGACTG	480
TTTAGCATGT TTGCCAGTCT GACTAATTTT GAAGTTGCTT AAATATCTGT CATTTCCACT	540
GTATCATAAT CTCCTCATTC ATCTTCAATC TCCAATGCCT TGAAGTCAGT AAATGTTART	600
TGAACAAAAG TAAATTGAAC CCAGAATTTC TGATCATAAT CTGGAGCACT TTAAAATTGT	660
CAGCTTACTG GGAAACGGGA TAACATGTGA TTTGTCTTTG ATTTTTTTTT TCTCATATGC	720
TTTTTCCACC TATAGATGCT ACACGAATGT TTTTAAAATC TGATATAAAA ATTAAAATTA	780
AAAAATTAAA AAAAGAAAAT TTGATACAAT GCTACATTTA GAGTGTTGTG ATTAGATTCC	840
TTAAGTGAT CATGGTGATC TCTACATCAC GTGGTGATCA AATTGCTTTG GGTTTTAACA	900
CATAACTGAC AAAGGCTTGG GGACATGTAA GATCCCAAAT ACATTTTTAT TGATTTTTTT	960
TTCTKGTTTG TCCTCTTTTA AATAACTTTT TTTTGTTATA AGAATAATTC ATGTTTCAGTG	1020

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GAGAAACCAT AGAAAATAGT GACAAGTGAA GGAATAAATT TAAAATGACC CATAATTGTA	1080
CCATACATTC TGATTTTTTA AACGCTGAAC AAATTAGCCT TGGGTAAGTA CCAGGAATAG	1140
AGTGCAGCAT TGAAAGTTAA AGTTTGGGGA AGGATAGCTG ACTTAAGAAA TTATCTAGTT	1200
AGACATTTTT TGGATGGGGT AATTTTGCAG ATGACATTAG TGAGAGAAAAG GACTTGCCAC	1260
TCTCACACAG CTAGTAGGGG TGTGGGAGGA TATTGGAACC AAGTTTCAAG TCTTCAGTGA	1320
AGAATCAAGG GAGAAGTTCT AAAACCTAAC AATATCCCTC TGGATGGACA TTTATTTTAT	1380
TACTACAATA AGCCACACGG TGAGTCATAA GGAGCATTTT ATTCTTCTAA TATGTCTCTA	1440
CTGTATTTAG AATCTGATAA AGCCCCATT AGAATTCATC TCTTTAAGAA TAAAAGAAGC	1500
TGAGGAACTA AAGAGAGGGT TGAATAATC CACTAATTAT ATCCGTTAAG CTTTCAGTTAC	1560
GCTAATAAGG AATATCACAT GACTGTGGTG TGTGCTTGTT CTGAACAGTA AAGTACATGA	1620
GGAAAGATAA GATTTCAGGC TGAAATGTCC TTCAGCATAT GTAGGTAGTG GTGATGAAAG	1680
TCATTAAAAG AAAAATTGAT TGAGGTATTT TAGTAAACAA AAGAACTCAC CACTTACCCA	1740
TCAGGAAGTG TATTGTTAAT GCAGTGCTGT TCAGCCTTCT GGAAGAAAAG GTTCTTTCAT	1800
GCTTCTCTCT TTAGCCTAAT TCTTATCCTG TCACTTTTCA GGCAAAATTA AAAAAAAAAA	1860
AAGATTGAAA ACGATGCTCC TATTTTATTT GCTTCAAAAG AAACAGGCTG TTGCATTGTG	1920
CTTGGAACAG TTTACTCTTG GCCTTGATGT AAGTGTGAAA GGAAGCCCAT GTAATTGACT	1980
AGGCAGTATC TGAAGAAGCA GGAAATACAG TGTTAAGAAA ATGAACAGGC ATGAAAACCA	2040
TGGCTATTTG ATAAAAGTAA ATAATTTCTG CAGTTCACAT GTTCTCAGCA TATTTTCTTT	2100
GATACTGACT TGCTTAATAT GACAATAGCA GAACCATGGT AGCTTGTAGG CATTACTTTT	2160
CTTTTAATTT CTTTACATT TTGAATTTAC CAGCACTCAC ATTTGTATTA CTTTGGGTT	2220
ATACTGAGGA TCTATAACTT ATAGATCAAA TACCTGACAT ATATATGCAT TCTCTGAAGT	2280
CTTAGGGCAG AACTAGAACA TTCTTGTGAA CATCAGTATA AGATATTAAA ATGGAAGTTT	2340
TGCCTAAGAC TGAAGACAAT AAAAATATCA TAGTCTGAAA TGAATGCCAG CACACCATAC	2400

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AGGATTTAAA TATCTATACA TATATATGTG TGTGTATTAT ATATATTTAA TATATATCTG	2460
TGTGGGATAG GAAGAGGTAG GGGGAAATCA GTTTTACAAT TATTAAGTAT TTCACCCTTG	2520
ACAAGAGTAT ATATATTGGA AATCAGTTGG AGAGTATTTT CAAAGATAAA TGTTAGTGTG	2580
CTATGAATGA ATCCACCCCT ACCACCACTG AGGCAGGGTA GGAGAGGCCT GTGCTCCTCA	2640
AGCATAGTTG GAAAAGGACC TCAACAAGAC CACTTCAAGA GTCTAATGTG TGGAGACTGT	2700
TGCTTAGGGA GACCTTATGG TCTAGCTTCT GACTCACAGC TAAGTCAGGG AGACAGGTTG	2760
GCTGCTCTGA TCGTGGAGTC CAAAAGATGG CCTGCACTGA AAAGCCTCAT GAGTGTTGAC	2820
TTAGGGCTAG TCTAAGAGGT CCCTGGAAGA AGAAACACTC AGTAGGAGAG AAGCTGGAGG	2880
TACCTTCAGT GCTGAATTGG AACCTAGATT CATTCCTCCG TGGAGCAAAT TACATAGGAA	2940
AGATGCCCAG TGATGGAGAG TGGGGGTGTC TCTAACAATT ACCCACCCAC CTGCCCCCAC	3000
CCCTAAGAAA AAGAAAATCA CATACAACCA GTCAGCTGTA AACATATGCC GAGCCTAGTA	3060
AACTCAGATA CTAAGTTACC AGGGTACCTG GCAAGTAAGA ACATTCCTGA TTCCCTTCCC	3120
TCCTCTTCCT CTTTGCCCTC CAACCTTAGT GGCTAGCAAG ATGGGGAGAG GAGGAGAAGC	3180
TGTAAGTGGG GAAAAAAGAG CAGCTTTCTC TCCTTTTCAG CTGCTGGATT CTCCCTCATC	3240
ATAGGCCTGA GCTGGGGAAT CAGGAAGAAG GATTCTTTTT AAACTGAAG TAACGTTATC	3300
ATTTAATTTT AAAACATTTT AAATTTTGAC AATGTTGAGA TTAGATATAC TAATTATTAA	3360
ACTAAGATTA TGTTTTGCAG CTTGAAGTGA TAAGAAAAAC CTCTTATCTA AGAGCATCCA	3420
GGAAAGTCGG GGGTTTCCTG AACATCCTTT TAAATCCTTT GGAAGTCAGC TTTCAGAGAG	3480
GATTTAAAGT GTAGACTGGG CCTTCAGAAA CTGGTTAAT GTAGGGGTTT CCTATGCAGA	3540
CTTGGGGACT ATACCTTGTG TGGAAGAGAG AAAATAAGAT TATCTTACAT TTTTCCCAT	3600
CCTTTTTCOA AAAGAAAGCT CAGCTAGCAT GAAAGTTAAA TTCAAAACGT AATGGGTATT	3660
ATTTGCATAT TCAAATCTAG TGCATATCAT GTAAGTACTG AATTATGGTA TTCATTATTT	3720
CAAATGACAA GCTGGATTTT TTTTCTTTC GAATTCACA AATTAATTTT CCTTGAACC	3780

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TTTTGGTTTG	GGCTTTAAGA	GTTTAGGCTT	TCATCACAAA	GAGAGGACAG	CCTTGAAGAT	3840
TAAAGTGTGT	GGCTCTTCTC	AAGATGTTCT	TAGTCCAGCA	AAGGATTCTA	TGCATATTTG	3900
GGCTTCCTTC	TGTCTCATAA	CCTGTATTTT	TTGATATTCT	ATTTATATTC	TGTAAGATTT	3960
TTTTTTTAAA	GGAAAAATTC	TTCCATGGTT	GAAGGACATG	TCAAAAATAG	AGGATACAGT	4020
TTTATATCAA	AGGAAGTTTC	ATGATATGAC	TGTAGAAGCT	CATTTGACTT	AAGACACATC	4080
ATTTCTCAT	GGAAGTGTTA	AACAGATCTG	TACAATAAGG	TTGGCAATCT	TTGTGTAAAA	4140
CAGTTTTTTT	TCTCCTGCTC	TAAAGAAAGT	GTATATTTCA	AAATGTGAAT	GTCAGCAGTC	4200
AGAAAATAGT	ATTTTTTTAA	CTTCGTTTTT	AAAGTCCTCA	AAAACCTGTA	CCTAATCATG	4260
AATTTTTTTT	CCCACAGATT	GTTTCTTCTT	CTCCCTCCCA	GAAACTTTGA	AGTTTTTCTA	4320
CATGACACCA	GGACCTATGT	CTTTTTTTAA	TTACACAGAA	ATGAAAGAAA	AAAAGTGTGT	4380
TGTATCGTTA	ACCAAATATA	TGAAATCTTT	AAGCTGTATT	TTTATTTTTA	ACTTTGTTTT	4440
GCAAAGAGGC	CATTCCCTTT	GGTTAAATAA	TTTGTTATTC	ACAGTTTCCT	TGTCCTCATA	4500
TTATCAAGGG	GAAAATTGTA	GAAATTTTAA	AGGAAGCTCT	AGGCAATGTT	TTCATCCCTG	4560
AATCTTTGGA	GAGTTATAAA	AACAAACAGA	TTACTGAACC	TGTAAGAGAA	CCAATCGTGA	4620
AGTCATTACA	TCTAAGCATA	AGCAAAATCT	CCTCTTGGAT	CATTAAGTTA	TAGAAGAAAA	4680
GAAAGCCTGC	ACTTTGAAAT	TTAAATAAAG	CTTGGTAACT	TGTAAGTCAA	ACACGTAAAA	4740
TTTTACAATT	CAGGAATATC	GATAGCAGTT	GAGTTTAATA	GACTTCTCAC	ATTCCAAATT	4800
TAAAGCTTCC	TTCTCTGTGC	TAATAGAGAT	ACAATAGCAG	TAGGCGTTTA	AGAAGAATGA	4860
ATCAACAATT	TAAAACTATA	ATGTGTTTTT	TATTCATCTC	CCTTATTCAC	ATATATTTGT	4920
TTTGTTTTGA	GAAGGAGTTC	TGCTCTGTGC	CCCAGGCAGG	AGTGCTGTGG	CACGATCTCA	4980
GCTCACCGCA	ACCTCTGCCT	CCCGGGTTCA	AGCGATTCTC	TTGCCTCAGC	CTCCTGAGTA	5040
GCTGCGATTA	CAGGCGTGCG	CCAGCAACCC	CGGCTAATTT	TTGTATTTTT	AGTAGAGACA	5100
GGGTTTCACC	ACGTTGGCCA	GGTTGGTCTC	GAACCCCTGA	TCTCAAGTGA	TCAGCCCGCC	5160

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TCGGCCTCCC AAAGTGCTGG GATTACAGGC GTGAGCCATC ACTTCTGGCC CTTATTCGCA	5220
TACAATTTAA AAATCATCAC AGAAGGTTTG AAAGAAGGAA GGGGCAGAAA ATTACCTACT	5280
TTTCCTCTCC CCAGCGATCT CCTTCAAATC TGTGCCTTTT CCTCAGGCCC AGGCCTCAAT	5340
TTACTGAGCA GTCACACCTC ACAGAGGGAG GTCTGGGCAA TCCACTCTTG GTCACAGGAA	5400
AGCCATTGAC CCTCCCACTT CCTCTCCTCC ACCTTGTCTT CAACTCTTGA CTTTGGGCTT	5460
TGTTTCTGTT CAAGTCCTAG GAACTGGTTT CTTTTATCAG GTTAAGTGAT TAGTTCTCTT	5520
TCCCTCTAGT TGCTCTCACT CCCTGACTCG GGGGATCCAC TAGTTCTAGA GCGGCCGCCA	5580
CCGCGTGGAC TCACAG	5596

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18443 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GAGGGCGGGA ACCCCCTTTC CAAAAAAAAA GAAACAAAGA CAGGATAAAC ATTCTAGATA	60
GTCTCTATAA TGGTCATGAT TAAGACAATA AAATAGTCTG AAATTGTCAA TATATATTAA	120
TAATAATTTA TTTGGCCATT CTGCCAAGTA GCAGACACCT GTCATTCTGC CCACTCAGCA	180
CCTCTCTTTC TTTTAGGGAA ATGCTACCCA CTCTTTGCAT GGGTTCTGGA TGGAAGTGT	240
GATCACAGTG TTTTCACTCC CCATTTTGCC TCACCAGAGG TAGACAGAAG ACCCAAGCCA	300
GGCCAGTTAC ACACAATCTT CAGATAATTA CCGTATTGAT CACAGTATCA CCCCCTCAA	360
GGCTTG GTTG GAGATGAGCA GAAGAGACTA AAGCTGGGTC ATTTTAATTA ACACCTGTAC	420
CCCAAAGAAA GACTGTCAAT GAGGCTTTTA TACCGACACT CCTGGTTTCC ATTCTTCTTG	480
ATGCCATTCA TTTGACGAAC TACCCAATCT TTCCAACAGT GTCTTTGGAA GAAAGATAGT	540

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CAGAAAAGAA GATAGAGTTG TTTTCTGTTT TTTGCAACCA AGGAACTCTA AATGATAGAC	600
TTGTTGCTAG GCACTTTGGT TATTTTATT ATCTTGAATA CTTCTGTGAT ATACTTCTTT	660
GTGCATGCCT GTTTGTACGG ATGTAGCTTT TTATATATTT TATATAATTT CTCAGAAGTG	720
GAATTACTTA GTCAAAAGGT ATGAACATTT TTCTGATTCT TAATATAAAT TGTGCAAATG	780
CTTTTAAAGA GGATTATACC AGTTTACATT TTGTGTTATA TATAACAGAA AGTACTACTG	840
AAAAAATATT ACAAAAATTT GTCTCTCTGT TCAGGAGGAC CTTGTAATAG ATGATAAAGT	900
ACTTGAAATA GGAACATAGA GCATTTTCAG TTTAAAATAA TTTCATTGGG TTATTTACGG	960
AATCCTTAGA ATTATGGCCA GACATTTATA GATGATCTGT ACCAAACCTA GGTGTTTAC	1020
ATAAATTGCT TATTCAACTG GCTTAAATCT ATAATAGAAA GATGACACTT ACTGAATGTT	1080
TAATATACAC TTTGTCAGGG GCTTTGTATT ATTCTATGAC ATCTTCAAAA TGACCCTACT	1140
TTCTTATTTT ATAAGTAAGG ACAGGAAGGC TTCAAGAACA TGACTAATTT TCCCAAGGGC	1200
TGTACCAAAG CCAGAACCCA AATCTATAAG GCTTTTAAAC CTGCATTCTA AACTGCATC	1260
TCGGCCATCT TATTCTTACA GAACTTAAGG TTAGAAAGCC AGATTGGAGT CCCAATTTCA	1320
CCACTTAGTA ACCAGACAAA CTTGAGGAAT TCACTCAACG TCTTTGAATC TTCATTTTCT	1380
AATCTTTAAA ACTAAAACAA TAATACTTGC TCTACCTATG TCCTAAGATT TCGTGAGGCA	1440
CATAGAGATA GTGTGGAAGA GTGCTGTACA GATGTCAAGT GTTAGCGTGA TTACTIONAGAT	1500
CCCTGAACAC CATGGATGAA TGTCTCTGAC TGCTATTAGA GGTCATAAAG AATATTGGGG	1560
CCAGGTACAT TGGCTTATTC CTATAATGCC AGCACTTTGG GAGCCTGAGA CAGGAGGATC	1620
ACTCGAGGCC ACGAGTTCAA GACCGGCCTG GGCAACATAG TGAGACCCCT TCTCTACAAA	1680
AAAAAAGCA GCCACGTGTA GTGGCACACA CCTGTAGTCC CACATACTCA GGAGGGTGAG	1740
TTGGGAGGAT AACTTTAGTC CAGGAGTTTC AAGGTGCAGT GAGCTGTGAT TGCACCACTG	1800
TACTCTAACC TGGACAGCAG AGTGAGACCC TGTCTCTAAA AAAAAAGAAA AAAAAATAAT	1860
AATAATAAAG AATAATGGGG CCTTGGGATA CCCACTCCTC TCTTTCTGCT CTGAGTTGTG	1920

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AAGCAGTTGA GTTACATATG CATGTCCAAT GGATGAGGTT GAAAATATCA ACTGGATTGG	1980
AATGTGGCTT ACTTGCGTGG CCACAATGAG CTCGTAACA CTCCTGACA GGGTGAGAAG	2040
ACAAACTTCC TCACCCAGTC ACTGGCAGAG CTGGACACTC TGTGTCTCTC CCACAGAACA	2100
ACCTCTTACT GCATGGAGGT GGATGAAAAA GTCAACCGAG AACAGGCTAC TCCAAAAAGC	2160
AGAGCACCAA AGGCACCAGC TGGTCAGGTC CCCCTTCTTA AGTAAACAAT CACGTAATTC	2220
ATTGCGGACA AAGCCAGAGA GGTGGTGTGG AGAAAGAGAG GGCAGTTTCC TCCCAAGTTT	2280
TTCCTGGAAT TCTTTATGGG AATATGAGGT TTAGGGGAAT AAGACTTCCC TTTAACAGTG	2340
AAGAATCCCC AGCTCTATTG GTAATAGGAA ATCGCTTACA AGGATCATGG GGAGTATTTT	2400
CTCAGCTCGT TCTGCCTCCT ACTTGGCTGA GTGGAATGGA ACCATCTGTG GCTGCTGCAT	2460
ATGATATTGT CAACTTTGTC ATTCCACACC CACTCCTTGA CGCCCTACCA TGTGGTCATA	2520
AGACTCCCTT TAAAGTGTTT CTTTAAAAAA CAAAATGTGT TTTGTTTCTA TAAAATACAG	2580
CTCAATGTCA GAACCCTTGT CTGTGTTGCT CTCTGATGTA ACCCTTTCAC AATGTTTGGG	2640
CAGCTTATTC TCTCTATTTT CCTGTAGGGT CCCATCCAGG CCAAAGTGAG TGCCAGCCTC	2700
ATTTGGGCAG CAGATGCCCT GTGGAAGGGC AGGAGGAGAC GAGAGCTAAT TGTAACTTTG	2760
TGATTAGCTG TCATGGATGC CTGGTCCTGT CAATAGCGCT CAATAAAGCC AGAAGGCCAA	2820
GCGTTCGCTT CTGCATACTG ATTGCTGAGT CAGATTTCTC AGTGCAGAAG GGCTTTCTAG	2880
GCAGTCAATT TTAGAATATT AGTCTTGGTT CTTAAGTGGT TAAAATCCCT AGCTGGTCTT	2940
TAATCTGAGC CTGGAGAATT TAGTTATGGC TGACATTCTG CTGTGATATT TTTGCCCTCA	3000
ATATATATGT CTTTCCTCCA TCTCTTAGAT CCCTGAATCA TAGAGATATA TATGTTATAT	3060
AATCAACTGT CTCCAGTCTC TAAGAGTGAT AAGTACACAT TGTGTCAGGT TGAGGGGACA	3120
GGAGAACTTT CAAAAGCCTT TCTTGCCCCCT TTTTCCTTCT CACTGCCTCC CACTAAGTCC	3180
AGCCACTTAT TATTCAGCTG ACACTATCAT CATGACCATG AGGTCTTTTG GGGCTACCCT	3240
GGTTCGGATC CTTCTGGAGG TTTGTTGCTT AACTCTGTCT TCAGTCCTAT GAGCTGCTTT	3300

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TTCAATAAGT	TTCTATTTTG	GCTAAAGTTG	GCCAGAATCT	CCTTGTAACC	AAAGAACAAA	3360
TAAAATACCA	GCTTGCAATG	TTCTATGTTG	CTTCCACCAA	ACTTATGCAG	CACTTCCATAT	3420
CTAATCCACC	TACTAGTCTT	TTTTTTTTTT	ATTTTTTTTG	AGACGGAGTC	TCGCTCTGTT	3480
GCTCAGGATG	GAGTGCAATG	GTGCAATCTC	GGCTCACTGC	AACCTCTGCC	TCCCGGGTTC	3540
AAGCAATTCC	CCGGCCTCAG	CCTCCTGAGT	AGCTGGGACT	ACAGGTGCAT	GCCACCACGT	3600
CCGGCTAATT	TTTGTATTTT	AGGAGAGAGA	GGGTTCACCC	ATGTTGCCCA	GGCTGGTCAC	3660
GAACTCCTGA	GCTCAGGCAA	TCCGCCCTCC	TCGGGCTCCC	AAAGTGCTGG	GATTACAGGA	3720
GTGAGCCACC	TCACCTGGCC	CCGACCTACT	AGTCTTTAGT	GTTTGCTTCC	TTCTATTGGG	3780
TAATTGTCTG	TTTATATGCA	TGTCTTGTTT	CCTCAAATAA	AATGTGGTCT	TCTCAAGGGT	3840
ATTGGCCCAT	GTTCTATCCA	TCTGTAGATA	TCACAGCACC	TAGCAGTGTC	TTTCACAGAG	3900
GAAGTACACA	ACTGGCATTG	TTGATTCATT	GCTCCATTTT	TTCTTCTTTT	ATCCCCAGCA	3960
TTTCTCAATA	ATTTCAAACA	TCTCCATTGG	AGTACCGGAG	AAAGCAGGTA	GCTTTACTTG	4020
CAGCTATGTT	TCTATCCCCA	TAGTAACTAA	AAGAGGACCC	AGAGAAACAT	GTTTAAATGC	4080
TGTCCTGTGA	TCAGGACCTC	AGCCTTCTGA	TGCTCCGTGG	CTTGGGGGTT	ATTGCTTGAT	4140
CATCTCCTCC	CCAACCTACA	CTGTGTACCT	ATGCTAGTCT	CTTCATGAGG	ACTAAGCCCC	4200
ATAGTAAAAG	GGCTAGATAA	ATAGAAAATC	ATTTTATGTA	ATTATAAGAA	TGAGAATACT	4260
GAGTATTCTG	GTGTTTGTTT	AGGATAAGCA	CATCTTTATT	TGTATGAGAA	AAAGAAAAG	4320
AGAGTGAAAA	ATATATTAAC	GTGCATATTG	TTCAGAACCC	TTGGATTGCA	AGTGACAGAA	4380
ACTCAATTCA	AACCAACGTA	AGTCAAAAGG	AAAATATATT	GGCTCATGTA	ACCTTCTCAC	4440
AGAGAGGGCA	GGATGGAAGG	GGCTTTGGGA	ACAAGAGAAT	TGTTCTCAAA	TTCTAGGAAT	4500
ACTAGGATTA	GTCCAGGATG	GGTCACCTTC	CTGTCCCTGA	GGTGGTGGTA	GCGATGGTAG	4560
AGTCTTATGG	GAGGAAAGAG	TGCATGTTAG	GATGAAGGTA	GGGCTAAGCA	AACAAGGGCA	4620
AGGGCCACTA	TATCATGCTA	AAAATGGTTT	TTTTTGATGT	CTTCCTTAAT	TTCACAAATG	4680

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CTTCCAACAA	AGTAGCACAC	AGGAAAAAGA	ACATAGGGAC	TCTACTGGTG	GGTGCTTTTA	4740
TCTTAAGCCT	TGTACTTGCT	TTTCACAGCT	TACTCACTGC	TTGTACCTGA	GGCCATATGC	4800
CCTGTAAAAG	CTTCTGCAGG	GTTTCTACTA	AGCTGGGTTC	CTTATATGGC	TCTCTCCCAT	4860
TTCTGTTGCC	TCACTCTAGT	GATCTTTCTC	TTTTCCCTCAC	CTCTGGGACT	GGTGGCTGTT	4920
TGTATGGACT	GCCTTAGCTT	TGCTTTGGGT	TTTTTCCTGG	GGACAATGTC	TTCAGATTAT	4980
CCTAGACCAA	ATAAACTACA	GCCACTGGGC	CAGGCTCTTC	CTCCTCCAAC	TGGACCATGT	5040
TCCCAGGGCT	CTTCACCTTA	GTTTAGGTCA	AGCATTCCTG	GCAAAAGAAA	GGCCTAGTTA	5100
ACAATAGACA	TTCTAGCAAT	TGATTCTTTT	TGACATGTTG	TAAGATCTAT	TCACATTTTG	5160
TAATTAAAGC	ATTCCCCTAT	GGAAACCAAC	ACGAACTAAG	CTGCTCCTGG	AATGCAGGGT	5220
GGCCTCCTCA	ATACAGGATG	TTCTAGAGAG	CTGTATTTTG	GGCACTTAAC	TATTCTCCAC	5280
TACTTAGGGC	ACAGCACTGA	AATTAACACC	ACTAAGTTTG	TCATGTCCAT	GTAGTTAGTC	5340
TCAGGCAGTG	CAGCCTCAGG	AGTGGAAGTG	ACCTCTTATG	TGTGTCCAGC	CTTTCTTCCT	5400
TCAGAAGTCA	GCTGTGTTTT	CTGCTGACTC	TCCATAGGAA	CATCAGTCCT	GAATCCTCAG	5460
ACCACCATCT	GGAGTAGTAA	GTGCTCCTGA	CAGTCCTAGA	AGTTGTCTAC	CGCTGGATCT	5520
CCAAAGCGTG	TGACACACCG	TGAGAGAGAA	ATGAGAAAGC	TGGGCTCTTC	AGGTAAATCT	5580
TGCTTTTTCA	CAAGCCCCCT	AATTTTACTG	CATAATTATT	TTGAATTCAC	TGATAATTTT	5640
TACAATTTTC	CCATAAGTCA	TCTACACACA	ATACCTCTC	ATGCAACACT	TGGCTTTGCT	5700
AATACATATC	TATTATGAGA	GCTGTGCTTC	TTAAGCGTAA	ATGTTTTATA	TGACTAAGG	5760
CTCTTGCTT	ACATATAAAA	GGGTATTGA	GCAATGTGAT	ACAGAAGTCT	TTTCTCCACA	5820
GGTCTCATAT	GTAAAGAATT	CATTAGATTG	GCTGAAATAG	ACTGATCTGT	CCATTTCTCT	5880
GCTCACTTAT	CATAAGGAAG	TCATTAGCTA	AGGAACAAAA	ACTACAATCT	ATGTAATTAG	5940
AAGAACAAGC	TGGTTTTGCT	CAATATAAAA	ATAAGAAAAA	GAAACCATGT	GAAAGTCAAA	6000
ATATTTGTTT	AATCAGGTCA	TTGAGAATCT	ATTAAAAAGT	ATTGAATTC	TTTATGATGA	6060

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GAACTATCTT GACTCAAGTG GACAGTGGTG AGCTTTTGG CCTGTGGTCC CTACGTAGAA	6120
AGGAGGCTTT GTCATAAAGT CTTATATGGT ACAGGTGCCA AGTTAAGTGC CCAAGCTTGM	6180
TCTTAAAAGC ATACTGGATT TTGTTT TAGA CTTT TAGTGA ACTGAAGGGA ATAAACAAAT	6240
CCCTCTGGGA GAACTTCTCC TCCATCCTTG GTGAAGTCAT TCTGCCAGAA TTCTATCTGG	6300
TAGTTACCTT CTCCGATTCA TTAAATGTTG TCCCATGGTC CGACATGGGT AATTTTTCTC	6360
TCATTGTGA TTAGTCCAC TACAAGGAAT TAAATATCA ACTTCTTGCC TTCTGGGATA	6420
TACTCAGCCT TATCACAGAG CTCCTCCAGG GAAGGAAGTT AGATTCTTTG AAGAACTTCC	6480
CTGCTCTTAC CCAAACCGAT TCAGTTGTTA ATTCTGTCCA CCTTGCTCCA TTTTCAGTGC	6540
AGGAGAAAAA GCATTTGTGG CAAGTCGAC CTTACAAAGG CTCGTTAATG CTCAATAACT	6600
GTGAGGACCT GCTATAAGTC ATGCCTTTTA AGAAAAATA CACACATGCA CACACTCAG	6660
ACAAGACTGC AACACAACTG TGATGGCAGC TTGCATATTG AACCAGCTGT TTCCCTAAAA	6720
CATTTGATTC GGCATCCTTT GTAGACAGTA AATGCAAAAG ACTTAGGTTG GAAAAGTGCA	6780
TTAGGTTT TG ATTAACGATT GGATGAGGGC CAGTTAAATT TTAAATCTG AATGAGCTTG	6840
CTGACTCAGG AGCCTTAGCA GCATAATGGA CAGACAGTCC TCAAAGCTTT CATTAAGG	6900
GTTTCTGGTA ACTGATGTCT ARAGAAATGA GTTGAAATAC AATTCAGTGA ACCACTCAGC	6960
TTTCATCTAA AACAGAATAT GTAATCTCAA AGAACTCAAC TGGTCTCTTG AAATATTCAG	7020
GTAAATTA ATGTAAAGAA GCTAGAGCTT AAATATTTTG AGGAAAGGAA GCCTCCTGTA	7080
GCTTTGTGAC TATATCACTT TATCCTTTTG AATGCCGTAT TTAATTATGT TAATTGCATT	7140
TTAAGTATAG CTGGAGTCAC CGATCTGCTG AAAACAACT CTASAATGGT TTGTGGGAGG	7200
TGCTCAGGAT GTATCAGAGA CTGATTTGAT TTGCATTTTA TTTTAACTT TAGTTCCTCT	7260
CTGAAGTCTG CCTTCTCATG TTTGTTTTTT WTGTTGTTGT TGCTTAATAC AGTCATGTGC	7320
CACCTAATGA CAGGGATATG TTCTGAGAAA TGCATTATTA GGTGATTTTG CCATTGTGCA	7380
AACATCACAG TGTAATTACA CAAACCTAGA TGGCATAGCC TACTACACAC GTCTGCTATA	7440

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TGGTAGAGCC TATTGCTTCC AGACTACAAA CCTGTATAGC ATGTTACTGT ACTAACTACT	7500
GTAGGCAGTT GTAACACTGG TATTTGTGTA TCTAAACCTA TCTAAACATA GAAAAGGTAC	7560
AATAAAAATA CAGTATTATA ATCTTATGGG ACCACTGCTA TATATGCAGT CCATCATTGA	7620
CTGAAACATT ATGTGGTGCA TGACTATAAT AGGATCAAAC TATGCCTTTG CAGAAATCCC	7680
CCTGGAAAGC CTCTGAAACT ACCCTGATCT TAGAGGCAGT TTTATAAATC ACGCCAATG	7740
ATTCTCAGCC TTTGGGTGT GCCAGAGATG TGTCCGCTCT CCTTTTGCAA TGACCCTAGA	7800
GGTAAAGGTG CTCTTCTTC TTCTGCTTCT CATGAAAAA TGTAATGTT GTATTTTAGC	7860
TTCTTTTCCC AGTCTAGTAA TATCTTGTTA AATTTACAAG ATGTAGCGG TGCCTCCAAA	7920
AGGGGATAGC AATAGTTACT TTGAAAATGG GTGAGTTCTT TGCAACCATC TCTGAGTTGA	7980
ACAGTTCTTG TATAATCTGT CTTCCCAGTT AGGCTGTGAG CCGCCTGAAG GCAGCAAGTG	8040
TATCTTTCAC TCTTCTCTGA TCTCCTCAGC CACTCTCTG CCCCACAATT CAAAAATCA	8100
GTTACCAAGC CATTGTAATT CCTTTTCTGA AATGTGTAGT AGACTCCTTT TAGGGTATTT	8160
GCCCAGTTCA CAAAGACCCC TGCCCTCTTT GGAAATCTGT CCTTGCAGCC ATATATGGTT	8220
TTTGTTTGTG TGTGTGTG AGACAGAGTT TCACTCTGTC GCCCAGGCTG GAGTGCAGTG	8280
GTGCGATCTC GGCTCACTGC AAGCTCCCCC TCCCGGGTTC ACGCCATTCT CCTGCCTCAG	8340
CCTCCCAAGT AGCTGGGACT ACAGGCGCCT GCCACCATAC CCAGTTAATT TTTTGTATT	8400
TTTAGTAGAG ACGGGCTTTC ACCATGTTAG CCAGGATGGT CTCGATCTCC TGACCTCGTG	8460
ATCTGCCCCG TTTGGCCTCC CAAAGTGCTG GGATTACAGG CGTGAGCCAC TGCACCCGGC	8520
AGCCATATAT GTTCTATATG ACTCTTCTG AGACAATAGC TGATTAGAAC AGTGATTAGA	8580
ACTGTGATTT CTGAGACAAT AGCTGATTTC TGAGACAATA GCTGATTAGA ACAGTTGCCA	8640
CGAGCTGGAC CAATCATATT AATATTCTCT ATCTCTCTCT TTTGCTCTCG AAATCTCAAA	8700
TTGAGATTCA GAAACAGCTA TGTAGTCTCT GTTTGTGGCT AGAACTGTAA CATATGAACC	8760
CAGAGCTAGA GAGATGCAAT ATTCTATCAA GCAGAGAGAG AAGCAGAGGA AGCCGGTCGG	8820

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CACAGACGGA ATGCAGTAGC ACACAGAGAG AAGCAGACAC TCGGAGATGT CTGACACCTT	8880
TC TGCTTAGA TTCCAGTCAG TTCAGAGGCC CAGACGCATT CCTGTCTGGA AGCATTCTGA	8940
TCCTGTTTTG TAAATCAACA ATAAATCCCT TGCCACCCTC TTTGCGTGTT AGCTTAAGTT	9000
GTCTTGCTCT TAAAAATCTA AAGAGTTCTA AATGATATGA AATGTCTGTT ATACAGAAAG	9060
TAGAATGACA ATTGCCAGGG GCTGAGAGGA GAGGGAAATG GAAAATTGCT CAATGGTTAT	9120
AGTTTTAGCT TTGCAAGAGG AAAAAGTTGT GGATATTGGT GGCACAACAA TGCGAATATA	9180
CTTACCACTA CTGAGCTCTA TGCTTAGATA CGGTTAAGAT GGTAAATTTT ATGTTATGTA	9240
TATTTTATCG CTGTTTTTAA AAAAGTTTAA AATAGCCTGT TGTAGTCAGC TTCCTTGCTCT	9300
TCCTTACTAC TGCAGCCATA TTCAGGTCTC CATGGCCCAA GGTATGGACA ACTGTAGTCA	9360
CCAAACTGGT CTCCCCACTT CCACCCCTTG GAATTTGGTC CCCAGCAATC TACCCTACAT	9420
GCATGGAGCA ATCAATATTA CCCATAAAGC ACTAACGCTG TGCTGTACTC CAAAATGCAA	9480
ACCTTCATGG TGTCCCATTG AATTCAGGAT CAAGTTCATA CTCCCCAGCT TGTCATACAG	9540
GACCCAGTGA TCCTTTCCAA CCTTCTGACC TACTGATTCC CAGTAGGAAG CAAACCCTAG	9600
CAAGACTGGT CTGCCTCATC CCAGAACAGT ACTTACTCAT GCTGTTTCCT TGCCATGATT	9660
ACCTTCCTTC TCCTCACCAC ATCTTATCTT TCTTTCCTT GATCTTAGTC CAAATGCCGA	9720
GAAGCAATCT TATCTTACTT TCAAAGCCCA GGTCAGACC CATCAATTCT ATAAACATT	9780
TCTGACCACA CTAGTCCTCC ATGGACATTT ATTTGAATTG AACTTCTTAG CATTTAAATA	9840
TACACAGTTT CTTATTCATC TGTCTTGTTT TTCTGCTAGT TTATAAATTG CTTGATTATA	9900
GAACATGAGC TTGATAATCT TTGATTTTTT CTGGATACTG TGTCTTGCT AGGCTGTTAA	9960
TAATGCTTGT TGAATGAAAT GAGAAATGAA GAACGGCTGC TTTACCAGTT TGTCTCTTCT	10020
GCCAACTTTT TTACATGGAT TTTACACGTC AACTTTTTTA CACAATGATT AAATATACCT	10080
AATTTGATCA TCCCAACAAC ACTAGTAAAT ATATATGATC ATTATCCTCA TACTACAGAT	10140
GAGGAAACAC AGGCACACAT CGTTTGTTTG TTTTTTTTTT TGAGACGGAG TCTTGCTCTG	10200

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TTGCCCAGGC	TGGAGTACAG	TAGCACGATC	TTGGCTCACT	GCAACCTCTG	CTCCTGGGTT	10260
CAGGCCATTY	TCCTGCTCA	GCCTCCCGAG	TAGCTGGGAC	TACAGGCATG	TGCCACAATG	10320
CCTGGCTAAT	TTTTGTACTT	TCAGTAGAGA	TGGGGTTTCA	CTATGTTGGC	CAGGCTGATC	10380
TCGAACTCCT	GACCTGATGA	TCTGCCTGCT	TCGGACTCCC	AAAGTGCTGG	GATTACAAGC	10440
ATGAACCACT	GTGCTGGGCC	AAGCACACAT	AGTTAAATAA	CTTGCAAAAA	AAAAAAAATC	10500
GSTATCTATTT	GTAGGAGGCA	GAGTCGTGAT	TCTGAGCTGA	ATCTATTTGG	CTCCTAAGCT	10560
TATGCTTTTT	CTACAGTATC	ACCACATATC	CCATACTCTA	TTGTTATTGT	TGGCTTTATT	10620
GCCTGTTTTT	CCTGTGAATT	TTAACCTTCC	CAAAGCAGG	AATCTTATCT	CAGTATATCA	10680
CAGAGAATCA	CTAAGTATCT	ATAGAGGAAA	GGAAGGAGAG	AAGGAAAGAA	GAAAAGGAAG	10740
AAGGAAAGGA	GGGAAGAAAG	GAAGAAGGAA	AGGAGGGAAG	AAAGGAAGGA	AGGAAGGAGG	10800
GAAGGCAAGA	GGGCAGGAAG	ACAGAAAAGA	AGGAAGGAAG	AAGGAAGGAA	GGGAGGGAGG	10860
AAGGAAAGAA	GGGAGGGAGG	GAGGAACGGA	TAGGAGGGCA	GAAACTCTGG	AAAGGAGCTT	10920
GTCTTACTCC	TAAGCTTGGT	AAAGATCAGT	CTTGCAAGGG	GCTTGACTAG	AAAACACTGG	10980
CTTATCTCAC	TGAACCATAT	TCCCAATGTC	ATTGACTCCT	TTCCCCTGGG	GAGTAATTCA	11040
ACCATGTGTT	CACTGTATGG	ATCAGAGTTG	ATGATGAATA	TTCTCTTGCC	TCAGTCTCTT	11100
TTGGCCAGAG	TTCCCTGGCT	TCCAGCCTGC	TCCTTGCTTG	TTTTGAACGA	ATAATATATG	11160
ACTTTCCTTC	TTAACTGGCA	AATGCTGAAC	TGTGGCCTCT	CTTAACCCTC	AAGTCTCCCG	11220
ATAAAAAGCA	AAATATTAGA	TTCGCTGACC	AGCGCTACTC	CTTACCCCGG	CTGATTTTAC	11280
ATGAAGAGCT	ATATATGGGG	TGGTAACATA	GGTTTAAGGA	TGGATGTGCA	TATAACTCCT	11340
GGATACCGTT	CCTGAAAATA	TACTATTGGG	GATTATTTCT	TTGGTTGAAG	AGTCCCTTCA	11400
CTACCACATG	TCAGTCCCCT	TACCTATAAA	ATGGGAACCT	TAGGGTTGTT	ATAAGGATTA	11460
AATGAGTTAA	TGTGTATAAT	GTGCTTAGCA	CAGTACCTGC	CACTCAATGC	TATTATTGTT	11520
GTTGTTGTTA	TTATTATTGG	TAGTAGTAGT	AGCAGTAGTT	GTTGTATGAA	GATGCATGAT	11580

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TTTACTAGCC	CTTTCATGCT	ATTTCCTCAA	GGGATGGTTT	ATCAAGTTGA	GGAAGATGTA	11700
GATGTGATTT	ATGATGGATT	TGAGGTTAGT	ACTGTGTATC	CAGGTTGTGT	GTGAGAAGAC	11760
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CTAATTCAGA	CGAGTTTAAA	CCATAGGAGA	TTTTGTTACA	AAGGCACTAG	GTAAGTGCAG	11880
GGACCAGGGA	GCAGGGTGTC	CACTCTCATT	CCAGATTCTT	TTGAATTCTG	TATATTTTAT	11940
TCTCTTTCCA	CAAACAGACT	TTCTATCCAC	GGTGGTGATG	ATAACCAATA	ACATTTTCCTT	12000
CAGTCTCACC	CTGTAGCTC	TGTGACCAAA	AATGCAAAGC	TGCTGCTTCT	CCAGCTTCAA	12060
AATTTAATAA	GAATCACAGG	GCAGAACATT	TATTGGCTAG	GCCTGAGTTG	CATGTCTAAC	12120
CTTGAGAAAC	TCACTTTGAA	TAGGGGAATT	CAGAACTAGG	ATTGGTGGCT	CCACAAATCT	12180
CACAAAAATG	GAGCAAARTA	GGAATCATC	AAACAGAAAT	CAATAGATCT	CCACTGGCTT	12240
TATAGTACGT	GGTCTGGGA	ATCCAGATAT	TCAGAGCCTA	GGTGAACCTG	AACATTTCCC	12300
TTTAGGCAGA	TGAAATCCA	CGTCTTCTA	GCTAAAATTT	TTCCATTCTC	TTTGAGGGGA	12360
GTTTCCATGG	AGAGGCTAGC	TTTGTGGGAG	AGAGTGGGAA	RAAACAACTC	ATGCTGTTTT	12420
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TCCTTACTCT	TGTTGCTTCT	GGGCTTTTTT	TTTTTCCTTT	GCATGCTGCT	TATATTCCTT	12540
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AGATACAAAA	CATGAAGTAC	GAAGACCTCT	TCAGAAAAC	GCAGGCTTGC	TACTCACCCA	12720
CAGACAAATA	GAGCTGATTC	TATTAGAACA	GTGAGGAAAG	AACACAGTAA	AGAATGGCAT	12780
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ATGAGAGAAA	ACAAATGCAA	TACAATTTCA	TTGGCTACCT	GGTTAGACCT	AGCATGAACT	12960

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GGTAAGAGCT TGATTCAGGT AGAGAGAAAC AATAATTATT TTACAGTGTA CAAAGCACTT	13080
TCTTATACGA TATATTATTT TCATCCTCCC AACTAGTTTG ATAGGCAGTA ATATTATTCC	13140
CATTTACAG AGGGGAAAC CTGGGTTAGG GCCCAGGAAC TTGGCTGGTG AGTTTGAAAA	13200
GCTTGAATAG CAATGATTAT AATCTTGGTG CACAGAAGCA GCCAGTGAAA TTCTGAAATG	13260
CATATTTCTG TTCTCTACTT CCAGAGGGTC TGATTGAGTT AGCTTGGGGA AGGGCCTAAG	13320
AAATGGAATC TTTTTTATTC ACACCAGGTG ATTTTGAAGC ATGGGGTCTA CTGAGTATGC	13380
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TGTATCATAA TCATCAGCTG TAAGTTTACT ATTAACAAAA ATCAACAAAA GAACAATATC	14220
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GCTTATCCCA AAATATTAAA AGTAAAATAT GATCCAATCT GCATCTCTTG CACATGTCAT	14340

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AAGAGGAAAT CCCTGAGACT CTGTAAACCT WACCTGCAGG TATGAGAATA CAATCTGTGT	14640
TTWATTTATK GTATTCTTWA GCAAAATTAT AGTAAATTA GTATTTTTCT TTTCATTTGC	14700
TCTCGAATTA TCCTTTAGTA ACAGAGTGAA CTTGTATGTC CATATTTTGG GTTTAAAGAA	14760
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ACCTTGGGGC CAAACTGCCT AAGCTCAAAT CATGGTCCTG CCAGTACTCT CTGTTGACC	14940
TTTAGCAAGT TACTTAATCC TTGTAGACCT CTGATTTGGT CTCTTCAAAA TAGGGATAGC	15000
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CTCAATAAAT ACTTGCAGAG CGAATGAATA AATGGGAGTT CAACTTGGGT AAGGCAACTT	16440
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TCACTACCAT TTGGAATTTT CCTATAATGA ATATGCGAGG CAAAGACAGA AATGAAAGGA	16800
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TACTGCATGG CCCATTTCTC TGA CTCTTTG AATGTGGGTA TTATTCTCAT CTTTCTCCCT	16920
CCTCTTCTCT TTTTGGTTAA AAGTAAAGAG AGCTTTTGAA GCTATTATGG AACAGAACA	16980
ACAGCCTAGT TCATCCTCAC ATTTTGGAGC CTCTTATTCC TTCAAAGAA CAAACACATC	17040
TATTTAGTGG CTAAGAGTCT CTTGAGCTGA AACCATTTCAT CACCATAACT ACATTCAAAC	17100

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TGTCTGAGGT ATACATTATA ACTAAGAAAA TGGGGTTCCT CATTGGAATT TACAACTAA	17160
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GATCTTAGGG CCTCATAAAG AAATAATTAT GGCAGAATGA GCCCTAAGAA GCAAGCACTT	17340
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CTGGTCTTCA GTCTTTCCCTG TCTGTTTGCC TTTCCCTGGTG TTAATATACT TGTTCCCTAAG	17460
GTTTTCACCC TGCTGACTTT TAGCTCTTCT TGCTAAGATT CCTGGCTGTA CATTAGAAAA	17520
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GACTCTGAGG CAGTTACTAT TATTATTAAT GTACCCCTTC TACAGATGAA GAATCAAGA	17880
TACCAAAAAT CTACATAATT TGGCAAACAA GTAAATGCTA AAGTTGGAAT TCAAACACAG	17940
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GGTAAATATA TGTACCTTCT CTGATATGAA CTAGAGACTC CATCCCTTCT TTTAAGTAA	18180
TGTAAATGAT TAACCAGCTT TCTGTTATTC CTTTCAGAAT CTCATTCATA GAATAAATTC	18240
CTGGCATAAA TTAGTATCAT AAGTTTTCTA TTATTGCTCA TTAATCAGTA TGTGATGTAA	18300
GATCAAGCAG TAAGAGTTCC CCCCAACCCC AAAGAATGGT CTTTCTGTTT GTGACAAATT	18360
ATTCTTGGA ATGTAATTAG CCAGTTGGGT TATTGAGGGG GATCCACTAG TTCTAGAGCG	18420
GCCGCCACCG CGGTGGACTA GAT	18443

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(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11811 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CCTGTAAAG TTTACCTTGT ATCTTAAAC TTGCCCTAAC CGGATTAATT TTCTGGCCAA	60
ATAGGGAGGC TGAATGAAAG TTTCACATAA ACCTTAGATA CTCCTAATTA ACTGTTTTTT	120
ATGTCTGTTT TTCTAGGACA CATGTTCAAA GAGCATAATT AACTTTTTAA AAGAAGCTAG	180
TAAGTACTGA AATAGTTTTT TAAGTTTTTT CTACAAGAAT AGAGGAAGAA AGGAAACATG	240
GAATTCTGAA GGGCTACTTA GCAAGCTGCT TATGGCATAA TCTGGGGTGG GGGTGCATAG	300
TAAAGGATTT GCATTTTACT GAGACCGATA CATGTCAAGG GAATGGTATT TAAAATTAGT	360
GATATGTGTT GATTTTTCAA GGACTATAGC CCATCAACTA CAATAGGCTC CAAAAATTC	420
TGGTGAAATT AGCTTCTTGG AGCCTTCCAG TTTACCTACT ATGTTATTCC CACTATAAAA	480
TATTCTCAAC TTTTGGGGTT TTAGCCACTT AAGTTTTTTA TTTTCTCTAA TGTCTCTAGT	540
ATCTGCTTTA GTTCCTGTC AATGCTAGAC TCTGTGGTTC AGCAGTTCAT CCATTCTCTT	600
CCCAGTACTC AACCTCGTTG CTTATAGTTT CATTACATTC ATCTAGCAAA ACCTTAATTC	660
TGTATGTTTG CCATACCATT AGTGCTTAGA GCATTTTTTC AGAAAAGAAT CCTGGAAAAA	720
TGGATCTTAT CTCACCTGGG CCCTCAGGAC TGCTGGGCTG CCTGGTGTCA GCACTTCCCG	780
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TCACGCCTGG AATCCCAGCA CTTTGGGAGG CCAAGGTGGG CGGATCACAA GGTCAGGAGA	900
TCAAGACCAT CCTGGCTAAC ACGGTGAAAC CCTGTCTGTA CTAAAAATAG AAAAAATTA	960

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TCTTTTTTAT ATGCTAGATT CAATTTGTTG ATACTTTGTT ATGATTTTTG AATATATATT	2160
ATTGTGTAAG AGTGAGCCTG TGATTTTCTT TCTTGTAATG TTTCTGTCCA GTTTTGGTGC	2220
CTGGTTTTGC TCTCTCCTTA GAATGAGCTG GGAAGTAGTC ACTCTTGTTT TCTCACCTAT	2280
AATAGCATCT GGGTCCAGTG TTTTTTATGT GGGACAAATT TGAAGTTGTG GTCAACCTCT	2340

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TTAATTGTAA GAATATTCAG GTCTTTTGTT CTTCCCTGGGC TAGTTTTTTA TTCTTTTCT	2400
AGAGATTCGT TCATTTTCT TAGTTTATT TGCCTATAAT TGTGGATAAT CTGTTTTTA	2460
TCTGCTACTT CTGTAATTAT TTCCACATTT GATTTATAAT ATTAACCTGT GGGCCAGGCG	2520
TCGTGGCTCA CACCTGTAAT CCCAGCACTT TGGGAGGCCG AGGCGGGCGG ATCACGAGGT	2580
CAAGAGATCG AGACCATCCT GGCCCATGGT GAAACCCCGT CTCTACTAAA AATACAAAGA	2640
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AAAGTGCAGT GGGGCGATCT CGGCTTACTG CCAGCTCCGA CTCCGGGGTT CACACCATTC	3360
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GTGAATAACT CACTCATAAT CTAGCTGCCT CCTTTATGTC GCTCTCATAG GACTTTGACA	3660
CCTCTCTGCT ACAATCCACC TGCCCTGTTT ATTTCAAGAT CAGGTACCAG GAAACTCGGG	3720

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ACATCCCTAT GCTGCAGAAC TCACTGAAAT TATTCAAACCT AGCCAGTCCT AAACATGCTT	3780
ACCCTGCCTT GCCCATTCCT TCCGCTGAAA CCACATAAAG GCTCTTGCCC ATGTTTTTCAT	3840
CCCATTCAT TGACCTCCTT ACTGACCCTA GCTAGTGCTT CCTCATGTGG CCCCTGCATG	3900
GCATGGTGTG CACCTTCCTC TTCGGAAGTG CGAGTAACTG TCTTGTCAGC GGCAATCATC	3960
TTGTGATCTG TTGGCCTCAT CATATTTGAA TAACAATAAA ATCTGTTTTA AGGCTGGGCG	4020
CGGTGGCTCA TGCCTGTAAT CCCAGCACTT TGGGAGGCCA AGGCAGGCGG ATCACGAGGT	4080
CAAGAGATTG AGGTGAAACC CCCTCTCTAC TAAAAGTAGA AAAATTAGCT GGGCATGGTG	4140
GTGCGTGCCT GTAATCCCAG CTA CTCAGGA GACTGAGGCA GGAATCTCT TGAACCCAGG	4200
AGGCAGAGGT TGC GGTGAGC CAAGATTGCA CCACGGCACT CCAGCCTGGT GACAGAGCGA	4260
GACTCCATCT CAAAAAAGA AAAAAAAAAA ACTGTCAAAT GATACTCCAA AATGGTTGTA	4320
CCATTTTATA TTTGCAACAA CAATGTCTGA GGGTACTGAT TGCTCCATAT CCTTGACAGC	4380
ACTTGGTATA GCTGATCTTT TAATTTTAGT CACTTTAGTG GGCATATACT GGTATTTTAT	4440
GTTTTACTTT TTATTTTCCT AATGATTAAT AGTTTGAGC ATCTTTCATG TGCTTATTTT	4500
CCTTTCATAT ATCTTCTTTG ATAAAAATAT CTGTTCAAAT ATTTTGCCCA TTATTTTGTT	4560
GGAATACTTA TTTTCTTACT GTTGAGCTTT GAGAGTTCTT TATATATCTG GATACCAATC	4620
CTTTGTCAGA TATATTTTTT GCAAAATTTT TTCCAGCCT GTGATTTAGT TTGTTATTCT	4680
CATGTCTTTT AAAAAAATT GTAGTTAAAA TATACACATA ATACAAAATT TAACATTTTA	4740
ACTCTTTGTA AGTATACAGT TTTGTGGTAT TAAGCATAGT CACATTGTTG TGCAACCATC	4800
ACCGCCATCC ATCTCTGGAA CTTTTTCATC CTCCCTGACT GAAATTCTGT ACCCATTTAA	4860
ACACTAACTT CTCATTCCCC CTTACTCCAG CCCCTGGCAA CCATCGTTCT GTTTTCCTTC	4920
TCTATGAGTT TGA CTGCTCT AAGTACTTCA TATAAGTGGA GTCATACAAT ATTTTCATTT	4980
TGTGACTGGC TTATTAGTAT AATGTCTTCA AGTTTCATCC ATGTGGTAGC ATGTGTCAGA	5040
ATTTCTTCC TTTTAAAGGC TAACATTCCA TCCTATGTAT ATACCACATT TTATCCATTC	5100

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ATCTGTTGAT GGACATTTAA GTTGCTTCCT CCTTTTGGCT ATTGTGAATA ATGCTGCTGT	5160
GAATGTTGTT GTATAAATAT CTGTTTCGAGT TCCTGCTTTC AATCTTTTGG AGTATGTTCC	5220
CAAAAGTAGA ATTGCTGGGT CATATGTTAA TACTGTATTT AGTTTTTTGA GGAATTGCCA	5280
TACTGATTTT TATAGTAGTG GTACCATTTA CATTCCAACC AGCAGTGTTT AGGGTTCCAA	5340
TTTGTTAACA TTCTTGCCAA CCCTTGTTGT TTTCTGGATT TTTTPTATTT TGGGGTTTTT	5400
TATTTTATTT ATTTATTTTT TTTTGGAGGC AGAGTCTCAC TCTGTCACCC AGGCTGAAGT	5460
GTAGTGGCGC AATCTCGGCT CACTGCAACC TCTGCCCCC GGGTTCAAGC GATTCTCCTG	5520
CCTCAGCCTC CGAGTAGCTG GGAATACAGG CGCGCGTTAC CACGCCTGGC TAATTTTTTG	5580
TATTTTTAGT AGAGGTGGGG TTCACTGTG TTAATCAGGA TGGTCTCGAT CTCCGGACCT	5640
TGTGATTCAC CCGCCTCAGC CTCCCGAAGT GCTGGGATTA CAGGCGTGAG CACTATGCCT	5700
GGCCATTTTT TATTTTTTAA CAATAGCCAT CCTAATGGGT ATGAAATAGG TTTTTTGGTG	5760
TTTTGTTTTT TTTTTTTGAG ACAGAATCTT GCTGTGTTGC CCTGGCTGGA GTTTAGTGAC	5820
GTGATCTCGG CTCACCTCAA CCTCCGTCTC CTGGGTTCOA GCACTTCTCC TGCTCAGAC	5880
TTCCAAGTGG CTGGGACTAC AGGCGCCCGC CACCACACCC AGCTAGTTTT TGTATTTTTA	5940
GTAGAGATGG GGTTCACCTG TGTGGCCAG GCTGGTCCAC GATCCATCCA CCTTGGCCTC	6000
CCAAAGTGTT GGGATTACAG GGGTGAGCCA CCATGCACAG CCAGGGTTTT GTTTTGTTTT	6060
GTTTTTACTA TTTTTTTTTT TTTTGTAGAG CAAGCTGTCT CCCAAGCTGT AGTGCAGTGG	6120
CACCATTTCGT ATCTCACTGT AACCTCAAAA TCCTGGACCC AAGCAATCCT CTGCCTCAG	6180
CCTTCCATGT AGCTACCTCT ACAGGGAATT GCGCCCATAC CCGGGGAAAT TTTTTTTTTT	6240
TTTTTTTTTT GAGAGTTTTG CTCTGTGTGC CCAGGCTGGA GTGCAATGGC ATGATCTTGG	6300
CTCACTGCAA CCTCCTCTT CTGGGTTCOA GTGATTTTCC TGCTCAGCC TCCTGAGTAG	6360
CTGGGATTAC AGGCGCCCGC CACCACGCCT GGCTAATTTT TTGTATTTTT AGTAGAGATG	6420
GGGTTTCACC ATGTTGGCCA GGCTGGGCTC GAACTCCTGA CCTCAGGTGA TCCACCCACC	6480

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TTGACCTCCC AAAGGGCTGG GATTACAGGC GTGCGCCACC ACACCTGGCC CCCAGCTAAC	6540
TTTTAAATGT ATTTTGTAGA GATGAGGTCT CACTGTGTTG GCCAGGCTGG TCTTGAACCT	6600
CTGAGCTCAA GTCATTCTCC CACCTCGGCC TCCCAAAGTG CTGGGATTAC AGGCATGAGC	6660
CACCACACCT GGCCCCCTTG CCCATTTTAA AAATTAGGTT GTTTTTGTTG TTGTTGAGTT	6720
GTAGGAGCTC TTTGTATATT CTGCATTTCTG GTTCCTTATT GGATATGTGA TTGGCATACA	6780
TTTTTTCCCA TCCATGGATT GCTTTTTTCAT TCTGTTATAG TATCCTTGAT TCACAGAAGT	6840
TTTTAATATT GATGAGGTCC TGCTTAGTCT GTGTTTTGTT TTGTTGCTTG TGCTTTTGGT	6900
GTTATATCCA AGAAATTTTT GCCAAATCCA AAGTCATGAA GCTTTGCCCT CTGTTTCCTT	6960
CTGAGTTTTA TAGTTTTAGG ACTTAAATTT AGGTTTTCTGA CCCATTTTTA GTTAATTTTT	7020
GCAAGTGGTA TAAGGGAGGG GTCCAGCGTT ATTGTTTCAC GTGTAGATAT ACAGTTTTCT	7080
GAGTACCATT TGATGAAAAG GCTGTCCATT GAATTGCTTT TGCAACTTTT ATTTGGGCAT	7140
ATTTATGTGA GTCTGTACT GGTCTATAT TTTACTCCAT TGATCTATGT GTCTATTCCT	7200
CTGCTAATAC TGTCTTAAAT ATGGTAGCTA TATAGTAAGC CTTAACACTG AGTAGATAGA	7260
TTTCTCCCCT TTTTTTGTTT TTTTCAAAA TTGTCACTGG TTTGTTTTTA TTTTTACTT	7320
TATGCAGATA ATCTGTACTA TACTTTGGTT TCATGTATCA AGTAGTTTGT TCCAAGTTGT	7380
GCTTTAAGCA GAACAAATAA ATTTTCATAT TGTTCTTTGT GTTAATCTGC AATATAAACC	7440
TATACCAAAT TCTATTTTGT GTATTTGTTT ATTGTAGTAA TCTGACTGAC TCTTTTGCCT	7500
CCAGACTCAT CTCTTCAAG GTCCCCAACT GAATCTTGTT TTAGGTGGAA CTTAGAAGCA	7560
GTAGAAGTTA AGAATCTATT TCACAGCCTT AGTAGTCTAG TTTCATTCTC TATATAATGT	7620
TGTCTATGCA AGTGAGCTGC TCTCCAGTGC CTTAGTTTCA CTAATGTTGG GGAAGGTCTC	7680
TTCTCTTGTT TTGGACTTCT CTATCACATT GCCTTTCTCA AGAGAAGACA TATAATGAAA	7740
GTGATATCT GGTGTTCTAG GACTTCTTCA GAAGCTTGCC AGTTTTTCAA GCTGATTTCT	7800
CTCACTGGCA ACTCTCAGA GTGCTGTTCC TACTCCACCC TCCCCTGGTG GTATGTATCA	7860

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GTTTTCTACT CATCAGCACC CACCTACTCC TGCCTACTGT GTTTCCTCAGA TGTCTGCTGC	7920
CTGGCTAGCT CATTGCTGCT TTTGTCACTC ATAGAGCTGT CTTCTTCCCT TTTTTTGGCT	7980
TTCTGCCTGA CTTCCAGGGC AGCTGCTCTG TCATTGCCTG TCTGCCATTC TGTCTTTTTT	8040
CCCCCTACCC CCCACAGATA CAACATCTAC TCTAATACCA CACATTCTCC ATGTTCAAAC	8100
TAACCTCATC ACTTTCCCA CCACATTCCC CAAAAGCTGGT CATCCTCCAG CTTATAGCAT	8160
TGCAGTTCAC TGAAGTTAGA CATCTGGGCC TTGCTTACCT CCAACATCTC ATTAGCCTTC	8220
GATTCTACCC CTATAAATCC TCTTCTCAGT CTCCTTTAGA TATTCCTGCC CTGCTGTGAG	8280
ATCCATCTGG TTTATTGGCT AGATTACTTC AGAAAGCTTC AGTCAGTGAC CCTCCTTACT	8340
TCAAACCCCA CCAGTTGATC CTTCACTCTG CCATCAGTCA TTGCTTCTAA AATCTAAATT	8400
GTTCCATTTA ACCTTGCTGT GATAAAACCT TTGGTAGTTC TTCAGTGTGT TCAGTGGTAA	8460
GTTAAAACTT TCACTGTAAT GTACAGGCC CTTCAATGATA TGATCGCTGC CTCCTCGAGC	8520
CTCATTGTGT GCATTTCCCC GCCCCACCCT TTCCTCACCC ACCCTAGTCT TTCATGTCTG	8580
CCATTTTTAC ATTCATTTAG CAGATATTTA TTGAAGCCCC CTGTGATGTC CTTACCTAGG	8640
TCTTTCTTGT TGCCAGGACC AGACAGGCTT TTTCAAGCTT CCAAGTCATC TCAGTTTGAA	8700
AGACTATGTC TGACCCCTGT CTTGGCCAAT TACTCTTTAT CCTTCCAAGT TCAATGATTG	8760
TCCCCTGCA CTCCAACCAG AGTGAGAGAG CAAGACCCTG TCTCAGTAAA TAAAAATAAA	8820
TAAATAAATA AATAAATAAA TAAATAAATC AGCCATAATT TATTTAATCA TGTCTCTCTC	8880
CCCCATTGAT AGACGTTAAG GGTATTTCCA GTATTCTTCT CTTGAAAACA ATGCTACATT	8940
GAATAACCTT GTACATGGGT CACTTTGAAA GTATGGATAT GTATCCGTGG AATAAGTTTC	9000
CAGAAGTGGA ATTGTGTCAG AGGGGTGTG CATTTGTAAT TCTGATGAAT ATTTATAGAT	9060
TATATGAGAG TACCTGTTTA CTCAAATCT TGCCAATGCA GCATTATCAA AGTTTTTTAT	9120
GTTCGCCAGT GTGATAGATT AAAAAATGGT ATCTCAGCCA GGCGCAGTGG CTCACGCCTG	9180
TAATCCCAGC ACTTTGGGAG GCTGAGGCGG GCAGATCACG GGGTCAGGAG ATCGAGACCA	9240

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TCCTGGCCAA CACAGTGAAA CCCTGTCTCT ACTAAAAATA CAAAAAATTA TCCAGGCGTG	9300
GTGGCGGGCA CCTGTAGTCC CAGCTACTCG GAAGGCTGAG GCAGGAGAAT GGCATGAACC	9360
TGGGAGGCGG AGCTTGCACT GAGCCGAGAT CGCGCCACAA CATTCGAGCC TGGGCGACAG	9420
AGCGAGACTC CGTCTCAAT AATAAAAAAA AAAGATGGTA TCTCAGCATT GATTTCTTTG	9480
ATCATCAGTG AGGTTGAGCA TCTTTTCATA GATTTAAGAG AACTGTATGG TTTTTTGTGA	9540
GTTATGTTTC ATATCGTTTA CCCATTTTAC TTTTAGGCTG GAAGCAGCTG TTTTAGTGGA	9600
ATGGTGGAAC AAGAAGCCAG ATTGCCATGG AGAGACAAC TTTCTAGAG ATTTGGCTAT	9660
GAAGCAGAGT AGAGACAATG ATAGCTGAAG GATTGATGTA GATGCAAAGA AATTTTTCAT	9720
CTTCTTTGAA AACTTAATTG TGTTAAAAAC TGGTATGAAA GGGAGGGGTT AAAGCTAGAG	9780
ATGGTGGTAG AAAAAATGC AGGGTTCCTA AAGGACTGAG ATTCTGGAT GGAATTTTCAG	9840
GGAAGGGGAA AATTTCTGGA TATAGTGA CT GGGGAGTTAA GGGTGTCTAG TCCAATGGCT	9900
TTTATTTTCT TGGAAGGGTA GGCAAGGCCA ACAGCCACAT GTGTGGGAGG AGATGGTTAG	9960
AGGGGAGAGG AGGTTTGAAG GCACCGCTAT GGAGAATTGG AGAGAGCTAA GGAAAGACAG	10020
AAAGACTGCA GAAAGTGCTT AGGGTTCAC TGAAGCGGAA ATAGTGATTT GTAGTGATAC	10080
AACCCTTATG AGTTATTTGA TTTTTTTTTT TTTTAAAGCA GCATCTGGCA GTCCAAGTAT	10140
AGGGCTGACA GTTTGGGATT TTTCTTTCCA TGTGGTGTA AAAGAAGAAC AGTGTAGTGA	10200
AGGAAGTTAG GACAAAAGAA TGATTGAACT GACACCAAGT TTTCTTGATT TGGTAGAAAA	10260
GGAAATAAAG ATAGAGCAGA GATATTGAAA AGAATTAGAG AGGGGTTCAG GAGACTGAAG	10320
GCCTGGGTGA GGTGAGAGAG CAGGTGTGGT AGACATAACA GAGAGAACTA CAAGGATAGA	10380
AAGTGTGGTT GGAGAGTGGG AAGGCAAGAT TTATTCAGTA TGGGGGCTTT TCTGGGTGAT	10440
GACAGCATCT GGAGTACAGC CATTGTCGTG AGTGGCCCAA GTGTAGCAGA GATAAAGCGT	10500
TGTTGGAGTG AAGGAAGTCA AGGAACTGAG AGGCTGGCCT AGATGGGGAT TTTGGTTGTC	10560
ATCCATGAGG ATATTGAAGT CATCCAGGAG AATAGCAGGC CTGGGGGACA GGAAGGAAAC	10620

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TGAGCCACTT	ACAGTGTCTT	CAGTGATAGG	AAAGCACAGG	GCAAAAAGCT	TTCAAGAACA	10680
GGGACTGTTA	AGCCGGGTAC	AGTGGCTCAC	ACCTATAATC	CTAGCATTTT	GGGAGGCCAA	10740
GGCGGGTGGA	TCACCTGAGG	TCAGGAGTTC	AAGACCAGCC	TGGCCAACAT	GGTGAAACCC	10800
CATCTCTACT	AAAAATACAA	AAATTAGCCA	GGCATGGTGG	CACGCGCCTG	TAATCCCAGC	10860
TACTTGGGAG	GCTGAGGCAG	GAGAATTGCT	TGAACCTAGG	AGGCGGAGGT	GGCAGTGAGC	10920
CTAGATCGCG	CCCTTGGCTG	CGATCCAGAC	TTCACTCCAG	CCTGGGTGAC	AGAGCAAGAC	10980
TCTGTCTCAA	AAAAAAAAAA	GAAAATCAGA	CTCTTAATAT	TTGTAAAGAA	GTAGTCCTTG	11040
AGCTACTACT	TAAGTCTAGA	AAGAGTTGAT	ATTCTTGTTT	TAAGAGTGTT	AGGGCACTTT	11100
GGGAGGCTGA	GGCAGGTGGA	TCACCTGAGC	CCAGGAGTTC	CAGACCAGCC	TGAGCAATAT	11160
GGGGAAACCT	TGTCTCTACT	AAAAATACAA	AAATTAACCA	GGCATGTGGT	ACGTACCTGT	11220
AGTCCCAGCC	ACTTGGGACG	CTGAGGTGGG	AGGATCACCT	GAGCCCAGGA	AATGGAGGTT	11280
GCAGTGAGCC	AAGATTGCGT	GA CTGTACTC	TAGCCTGGGC	AACAGAGCAA	GA CTCTGTCT	11340
CAAAAAAAAA	AAGGGCGGGG	ATTATCATAG	TGCCATTATT	ATTATGAGTT	TATGATGGCT	11400
TTCTCTAAGC	ACCTTTTACA	TCGGGCATTT	ATTCAGTACC	TATTAAGCAT	CAAGGAGTCC	11460
AGAAAAAATT	TTATATATAA	ATATATATAA	AATATGTAAA	TATATATATG	CATATGCTTC	11520
CCTATCTCAG	GAAGGAAATA	TGTGAACATC	AGGAACCGAA	GTCTACTCAG	TTACATGCCA	11580
TTGGATATAT	CACACAAAGT	GCTGAGGGAA	CTCAGAAGGC	TCATTATATC	TGGGGAGTGG	11640
GAAGGAGGCA	CAGAGATGTG	CTTTGGGAAG	TTTAAATTAA	AATAGCAAAT	GGGGAAAATG	11700
AAGACACACC	AGACAGGGCA	CAAGCAAAGA	GACATGAAAG	AGTAAGTCAT	GTGTTTGAGG	11760
ATCTGGGGAT	CCACTAGTTC	TAGAGCGGCC	GCCACCGCGT	AGCAGTTACG	G	11811

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(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

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TCGTGATGCG GTATTTTCTC CTTACGCATC TGTGCGGTAT TTCACACCGC ATAGATCCGT      60
CGAGTTCAAG AGAAAAAAAA AGAAAAAGCA AAAAGAAAAA AGGAAAGCGC GCCTCGTTCA      120
GAATGACACG TATAGAATGA TGCATTACCT TGTCATCTTC AGTATCATAC TGTTTCGTATA      180
CATACTTACT GACATTCATA GGTATACATA TATACACATG TATATATATC GTATGCTGCA      240
GCTTTAAATA ATCGGTGTCA CTACATAAGA ACACCTTTGG TGGAGGGAAC ATCGTTGGTA      300
CCATTGGGCG AGGTGGCTTC TCTTATGGCA ACCGCAAGAG CCTTGAACGC ACTCTCACTA      360
CGGTGATGAT CATTCTTGCC TCGCAGACAA TCAACGTGGA GGGTAATTCT GCTAGCCTCT      420
GCAAAGCTTT CAAGAAAATG CGGGATCATC TCGCAAGAGA GATCTCCTAC TTTCTCCCTT      480
TGCAAACCAA GTTCGACAAC TGCCTACGGC CTGTTGAAA GATCTACCAC CGCTCTGGAA      540
AGTGCCTCAT CCAAAGGCGC AAATCCTGAT CCAAACCTTT TTA CTCCACG CACGGCCCCCT      600
AGGGCCTCTT TAAAAGCTTG ACCGAGAGCA ATCCCGCAGT CTTCA GTGGT GTGATGGTCG      660
TCTATGTGTA AGTCACCAAT GCACTCAACG ATTAGCGACC AGCCGGAATG CTTGGCCAGA      720
GCATGTATCA TATGGTCCAG AAACCCCTATA CCTGTGTGGA CGTTAATCAC TTGCGATTGT      780
GTGGCCTGTT CTGCTACTGC TTCTGCCTCT TTTTCTGGGA AGATCGAGTG CTCTATCGCT      840
AGGGGACCAC CCTTTAAAGA GATCGCAATC TGAATCTTGG TTTCATTGT AATACGCTTT      900
ACTAGGGCTT TCTGCTCTGT CATCTTTGCC TTCGTTTATC TTGCCTGCTC ATTTTTTAGT      960
ATATTCTTCG AAGAAATCAC ATTACTTTAT ATAATGTATA ATTCATTATG TGATAATGCC      1020

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AATCGCTAAG AAAAAAAG AGTCATCCGC TAGGTGGAAA AAAAAAATG AAAATCATTA 1080
 CCGAGGCATA AAAAAATATA GAGTGTACTA GAGGAGGCCA AGAGTAATAG AAAAAGAAAA 1140
 TTGCGGGAAA GGACTGTGTT ATGACTTCCC TGAATAATGC CGTGTTCAAA CGATACCTGG 1200
 CAGTGAATCC TAGCGCTCAC CAAGCTCTTA AAACGGGAAT T 1241

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1701 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATAAAAAACA GTTAATTAGG AGTATCTAGG TTATGTGAAG CATTATCAC CYYCCTAYTG 60
 RCAGAAAWTW TCGWTAGGCA AATTTTATAT TWTAAGTAAC TTTAACATGA ACACTTCTTA 120
 AACTTTGGCT CATAATTTCA CAAAAATTAG GCTGCAAGTC ACCATATTCA TCAGATACTG 180
 GCAGACACTA ACTTCTGCGG CTATGACACC AAGCAATACT GAAATCTCTT ATCTTTCCAG 240
 GGGGGTTGTT CATGTATTCA GTGTTTGCAA AGAGTTCCTG CTGAGCTAAA CACAGTCCAC 300
 TGTGCACTCT ACGAAAGAGT CCATGAGACA AGCATGGGGG AGGGTAGGAA GTTTAATACT 360
 TTCACAATGC CTGTGGAGAC GCTGGCAGTG ATGAAAGCCT AGAAACTCA TGAAAGGACC 420
 TTTTATGAGC AGGGTGAATG TAGAGCACA AAGCAAAGTC AGATGACCCA CTAAAGCTT 480
 TGCCTTTACT GATGAGAATT CATTCTCATT CCAGATTAGT CTCTCTCTAG AAAAAGCAAA 540
 CCTTATATAA GAGTTGGAAA ATTAAGATAC AGGAAGTATA ATTCTACTAA ATTCCAGTTT 600
 TTCCTTCTCA AATATCAGCC TAAGTCCTAA GGTCTGTGGC CAAAGACAGA AAATACAAGG 660
 CGCTGAGAAA TATGCTATTT ATCTTGGTGT AACAACTCTT GACTGTTGGG GTTTGAGGAA 720
 ATTTAAGCTC TACAATCCAT AGATCAGACC AGAAGTTTAG GGTAGTAATA TTATGAGAGG 780

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AAATAGTTTC TTTCTGGAAC TTATATAAAG CAAATAACTG GTAAACCTGA TTTGCAAGGT	840
AATGACAGTC CAAGTTCCTT CAAAGCAGAG AACCCTTAT TTGCTCATTC ATTCAACTAA	900
GTTCTTGTC TTGTGCCAGG CTGGAGAGAG AAAGCAGCTC CTGTCCTCAA GGAGCTCACA	960
TCTCAGGCAT CTTCTCACCC TCCTTTCTCA TGTTAACCAA AACATTTAG GTTCATCAAT	1020
GAAACTCTTC ATCCAGGAGG CAGATAAAAT GGCTTCTCTT CATTTTGATT CATTTACTCT	1080
TTCTTTTATT TATTTTATTA TTATTATTTT TTTTTTTTCT GAGAAGGAGT CTCGCTCTGT	1140
TGCCCAGGCT GGAGTGCAGT GCGTGATCT CGGCTCACTG CAACCTCTGC CTCCCGGGTT	1200
CAAGCGATTC TCCTGCCTCA GCCTCCCAAG TAGCTGGGAT TACAGGCATG CGCCACCACG	1260
CCCGGCTAAT TTTTGTAATT TTAGTAGAGA TGGGGTTTCA CCATGTTGGT CAGGCTGGTG	1320
TCAAACCTCT GACCTTGTGA TCCGCCTGCC TCAGCCTCCC AAAGTGCTGG GATTACAGGT	1380
GTGAGCCACC ATGCCCCGCC TACTCTTTCT TTAAACAGA GAAATAAGAT GGAATATTTT	1440
TATCCCATCT TTTCTTCTGT AATTAAAAA GGAATACGAA GAACTTGAC ATAGTCTCTC	1500
TCCTCATGTG CTCTCTTACT TCCCATCCA ATTCCATGTT TGCTCTCTTT TTCTCTCTC	1560
CTTCTGTTTT GTTGGAATG AAGAATTAGG TAACTAGTCC AAACTACAG AGCTACACCT	1620
GGAGCCTAGA TTCCTGGTA GCAATCACT AATTTTCTGA AGGTAAATGG GAGAAAATGG	1680
GGGTGGGGG AACTCATTA A	1701

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1293 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGAGATAATA AGTATACACT ATGTGTGAAG GGGGTGTCTC TATTGTTGTT GTGGCGATTA	60
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GGTGAGTAAT TTTACACCTG GTTGTGAATA AAGTCCGAGA TTGGGGGACT CACGCTTTGT	120
AGAGTCTCCC AGGACAATGG GTTTTGCCCC CGTGCCCAAT TAATAGTTAA AGGTTGGGGG	180
CTTTTCGATT CCCTTATTCC AACTGGATAG GGCTCTTGAA ATGCCCCCAA AAAAGGTTGA	240
CCCTTTCCCC ACACGTCAAA GAGGGAATTC TCCCGCTAGA CTACCCTTGA ACCTGAAGTG	300
CAGTCCCTAC AGGGTATTCT AGCTTGTTAG CATCCCCAC TGTGAATCAA TCCCTTAAAA	360
TAAACCTATA TAAGATGTAT GTAATAGAGG ACTAATCTTT AATATAATAA GCATATATTT	420
AATATAATTT CGGTACTACC CCCTTATCTG GGGGGGGGGT GGGGGGATAT GTTCCAAGAC	480
TCCCAGTAGA TGCCTGAAAC CACAGATGGT ACTGAACCCT ACGTAAACTG TATTTTCATTC	540
CTATACATGC AGGCTATGTG TTGTAATCTG TAGGGTAACC ACTAAAAGAA CAGGGTCTAT	600
AACTTGGCAA GAGGGAAAAA AGCTAGGATA GTAAAAAAGT CTATCAATCC AAAAAGCAAG	660
AAAAAAGAGA AAAAGGAACA TGCTGGCATA TTATTATAAG TATTGTATTT TATTATTAGT	720
TATTGTTAAT TTTTACTGT GCCTAATTTA TAAATTAAAC TTTATCACAG CTATGTATGT	780
ATAGGAAAAT ATATATCTGT GGTTTTAGGC ATCCACTGGG GTCTTGGA TATAATGCTT	840
CCCCCAGATA AGAAGGTACT ACTGTAATTA TATTATATGT CATATTAAGT ATACATTAAT	900
TCTACTAGGT AGTAGCCACA TTATATATTA ATTATATTAA ATATATATCA TATAGAATTA	960
TTTTAAGGAA TTGACTCATA ATAGAAGAGG CTGGCAGGCT GGAGATTCAG GGAGGAGTTG	1020
CATTTCAAGT GCAAAGGCAG ACTGCCAGAG AATTCCTCT TGCTTGGGG AGGTCAGCCT	1080
TTTGTTCTAT TCAAATCTTT GAGGAAAATA GAAAGCAAAG AATATATTAA CTATATTAAA	1140
CAAACTAAAT GTTCCAATTA AAATACAAAA ATTATAAAGC CTAATAATAA AAGCCCTCAA	1200
TTATATGCTG TTTAAAAGAG ACATTTTAA GCTTAAGGAT ATAGAAAAGT TGAACATACA	1260
AGCATGGAAT AAAATAAGCA TGCAAAATAC TAG	1293

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(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 529 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GCTGAGGTGC ATCGCGGTGG CGGACGCTCT AGAAGTAGTG GATCCCCAAA CAAAACCTGT	60
CCCTGCTAAT GATGGTAGAC CCAATCAGAT CCCCGGAGAA GCCGAAATAC GGAAACCATA	120
TCAGCATACG CATGGCATAC ATAGAACCCC ATACATGGAT TGCTTACTCA GCCAGATATA	180
GAAATCTATC TTCACGATAG AGATATATAT ATATAGACAC ACTGCATATA CAGATGTGAG	240
ATGGAGGCTC ACTCTGCCAC CCGTGCTGGA TCTACAGTGG CACAAGCTCA GTCCACAGTC	300
ACGTCGATCT GCCGGGCGTG ACCGACTGAG ATGCAGCGGC CTCGGGCGTA GCTGTGAGTA	360
CACGCACCAG TCATCGCGAC TGGCTGCAAG TGGTATAAGC GGAGGGGACA GGGTTACAGC	420
ATGACGGCTA GGCAGGCCGC AAAGTGAGGA CCACAAGAGT GCCACGCTGC CCGAACGCAT	480
GCAGTGGCGA GATTACATGG GGCAGCCACT AGAGCCGCCG TATCAGAAA	529

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18073 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

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AGCGCGTGCG CCGCTCTAGA ACTAGTGGAT CCCCCGAGGA GTGAGGAGGA CCTCAACCCCT	60
ACTTCCTGAA ATGGAGCTCT GAGATGTTGG AGTAGAAATT TGGAAACCAG AGAGAGAAGT	120
AAGGGTAGTG TTGTTGCAAC ATGCATTGTA TATGGGGGGT CGGGAAGTCA CAGGAGTTTG	180
CCTCAAAGTC TTTCTCGAG ACGGATGAGG TTTTCACTGT GATTTTCCTG GTCGTGGTCT	240
ATGGATATAG TACCTGTTAG TGACATGGAT CTTCTTAACT TCTGATGTGT CTTTTCCTCC	300
CTAGTGACG CATAACCAAT CTCTCCACAG CTTCCATCAC CATGCATTTG TTCTTTTCCC	360
TTGTTCTTGT ATTACCTTTC TGGAAAGGAA TTTTATTGT AGGCTAATTG TTACTIONCAC	420
CAGTATTTAA CCACTGGATA TTTTATATGA TTGATCTCTT CTGATTTGGA AAATAAAAAAT	480
GTAATCTCAT TATATTCATT TGATTAGTGG GGACAGTCAA CACTTCTTTG TGTATTTTCT	540
TAGCTGTTTCG TTTTCTCGT CTGTAAATTA TCTGTTTAGG TCCTTCAGAT TTTTCAAAAT	600
TGGACTGTTA TGTTTTTCAGT ATTGTTATGA GTTCTTGTTT CAATTATTTA TGACAGTTCA	660
TTTTCTTTTT TAAAATAGAC TTTTTTTTTT TTAGAGAAAT AAGAAAAAAT AAAAATTAAA	720
ATAGACTTTG TGTTTTTAGAG AGTTTCAGGT TCACAGCAA ATTGATCAA AAGTATGGAG	780
AGTTCCGGCC AGGCGCGGTG GCTCACACCT GTAATCCCAG CACTTTGGAA GGCCAAGGTG	840
GGCAGATCAC AAGGTCAGGA GTTTAAGACC AGCCTGGCCA ATATGATGAA ACCCATGTC	900
TACTAACAAT ACACAAATTA GCTGGGTGTG GTGGTGCACA CCTGTAAGT TACCTACTCA	960
GGAGGCTGAG GCAGAAGAAT CTCTTGAACC TGGGAGGTGG AGGTTACAGT GAGCCACAGT	1020
CATGCCCTG CACTCCAGCC TGGGCAACAG AGTGAGACTC CGTCCTAAAA AAAGAAAGAA	1080
AGAAAATATA GAGCATTCCT AAATACCACC TGTCCCCAAC ACCTGCACAG CCTCCTCATT	1140
ATCCACATCC TACACCACTG TGGTACCTTT GTTGCAATTG ATGGACCAAC ATTGACTCCT	1200
CATTATCACC CAAGCTTTGG TGTTGTACAT TCTGTAGATT TGGACAAATG TATAATGACA	1260
TGTGTCTACC ATTGTAGTAT CATAAGAAG AATTTGACTG CCCTGACAGT CCTCTGCTCC	1320
ACCTGCTTAC TCCTCTCTCC CTTTTCTTAA CTGCACAACC ACTGATTTTT TTTTTTTTTT	1380

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TTTGAGAGGG GGTCTCACTC TGTCCCCCAG GCCGGAGTGC AGTGGGGCCA TTTGGGGTCA	1440
CTGAAAGCTC CACCTCCGGG GTTAATGCAA TTCTCCGGCC TCAGCCTCCC GGGTAACTGG	1500
GATTAAAGGG GCCC GCCACC AAATCGGGGT AATTTTTTGA ATTTGAAGTA AAAAGGGGGT	1560
TTCCCCATTT TAGCCAGGAT GGTCTCGATC TCCTGACCTC GTGATCCGCC CACCTCGGCC	1620
TCCCAAAGCT GGGATTACAG GCATGAGCCA CCACGCCCTA CCTTTTTTTT AAAAAACAAG	1680
GTCTTGCTCT GTCACCCAGG CCTGAGTGCA GTGATGATCA CTCCTCACTG AAGCGTCGAC	1740
CTCCCAGGCT CAAGTGATCC TCCCACCTCA GCCTCCTAAA TAGCTGAGAC TACACACACA	1800
CACCACCATG CCCAGCTAAG TTTTGTATTT TTTATAGAAA TGTGGTCTTG CTGTGTTGTC	1860
CAGGCTGGTC TTGAACTCCT GAGTTCAAGC AATTTCGCTG CCTTGGCCTC TCAAGGTGTT	1920
GGGATTACAG GCATGAGTCA CCGCACCTGG CCTTTTTTAT TTTCTTTTTT TTTTTTTAAC	1980
CAGTGATCTT TTA CTGTCTC CATGGTTTTT CACATTGGCT TCTGTCACTT AGTAATATAT	2040
GTTTAAGTTT CTCTACGTA TTTTCATGTT TTTAGCTTAT TTCTTTTTAG CAGTGAGTAA	2100
TATTTTCATTG TCTGGATGTG CCATCACTTA TTTATCCATT CGCCTGCTGA AGGATATCTT	2160
GATTGCTCCC AGTCGTGGCA ATTATAAATA AAGTTGCTGT AAACATCCAT GTGCAGGTTT	2220
TTTTTAAGTG GCATAAGTTT TCATCTCATT TGGTTAAATA CCAAGGAGCA CAATTGCTGG	2280
ATCATATGGT AAGAGCTTAT TTATTTTTTT GAGAGACTAC CAAGCTGCCT TCCAAAGTGG	2340
ATGTACCATT TTGCATTCCC ACCAGCAGTG AATGAGAGTT CTGCTGCTC CATATTCTTA	2400
CAAACATGTA GTATTGTCAA ATGTTTTGGA TTTTAAAACC AAAATCCATT TTCATAGATG	2460
TGTAGTGGTA TCCCGTTTTA ATTTGCAATT ACCTAATGAC TTGATGTTCT GTGTCTTTTC	2520
AGATGCTTAT TTGCCGTACT GTTTATCTTC TTTGGTGAGG TGTCTATTCA GGTCTTTTGC	2580
CCATTTTTAA TCTGGTTGTT ATTTTCTTG TTGAGTTTAA GAATCTCTG TCCTTTGTCA	2640
GATCTATCTT TTGCAAATAT TTTCTCCTAG TCTGTGGCTT ATCCTCTGAT TCTCTTGGCA	2700
TTGTCTTTCA CAGAGTAGAC ATTTTATATT TTAATGAAGT CCAGACTATC AATTATGTTC	2760

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TCATGGATCA	TGCCTTTGAT	GTTATATCTA	AAAAGTTCTC	GCCATACCCA	AAGTCATCTA	2820
GATTTTCTCC	TGTTATCTTC	TTGGCATTTC	ATAGTCTTAT	GATTGATATT	TAGGTCTATG	2880
ATTCATTTTT	AGTTAAATTT	TTGTGAAAGA	TAATAAGGTC	TGATATGGAT	TAATTTTTCT	2940
ATATGTAGCT	GTCCCGTTCC	AGTATCATTT	GTTGAAAAGA	CTATCTTGCT	CCATTTTATT	3000
GCCTTTGCTC	CTTTGTCAGT	TGACTATATT	TATGTGGGTC	TGTTTATGAT	CTCTGTTCCG	3060
TTCCATTGAT	CTGTTTGCCT	TTTCTTTTGC	TAATACCACA	GTCTTAATTA	CCATAGCTTT	3120
AAAGTAAGTC	TTGAAGTCCA	ATAGCATTAA	TCTTTGACTC	TTCTTTAATA	TTGAGTTGCC	3180
CCTTCAGAAT	CTTAATGTCT	CTCCATGTAA	ACTTTAGAAT	CAGCATTTTT	ATATTCACAA	3240
AATAACTTGC	TGAGATTATG	ATTGAGATTG	CATTGAATCT	ATAGGCTTAT	TTGGGAATAA	3300
CTGACATCTT	GACAATATTG	AGTCTTCCTG	TCCATAAACA	TTATTTATGA	TGGGCTTCTT	3360
CTTTATGTTT	AGGAGCTTTT	GTTTTTCTG	TCAGATATTC	CACTTCTACC	TTTATGATTT	3420
CTTAATTGCC	TTTTATGCTT	AGAAAGTTTT	TCCTCATCCT	GAGCTCACAT	ATTCATTTAT	3480
TTTCTTTTAA	AATGTGTTTT	CAAGCATTTA	ATTTTAAAC	CTATGTGGAA	TTTATTTTGG	3540
TATATGGAAT	GAGGTGGTGG	TCTAACTCCC	TCCTCTCAAA	TATGTAGTTA	TTTTTCCCAA	3600
AACCATTTTC	TATTAATTTA	TCAAGAATAG	ACATGTATAC	ATATACATAT	ATAATAGTCA	3660
GCCTTCCACT	TGTTGTTTGA	CCCTGTGAA	GGAAATTGTA	TGAGTTTCCA	ATTTTGGATT	3720
AGGCTCAGGT	AGTAATTGAG	CTGGGTCTG	CCAGAGATCC	ATGTTAATTC	ACTATCCAAA	3780
CAGAGTTATA	AAATGTAAGT	TTTATGAAAA	TCTAACAGTA	TATCACTGGT	TTAATGATCA	3840
CAGCCTAGGA	AGAATGGGGA	AATTGTCAAA	ATCTTCTGTG	GATGCACCTG	AAGGCCACTG	3900
CTGAACCCAT	TTCCCTGCTA	GGCACGGCTG	CTGGTACCAG	GGGCAAACCTC	CTGGAGTATA	3960
TATGAACCAC	CTACATCTCC	TTCTCTTCCC	CCCCTACCCT	TGAGATTTTC	ATGTGTCCCT	4020
TAAGGATGTG	TGTCCTACTT	CCCTTGGAGA	GTCACTACCA	CATTGAACAC	TTTAGACTGT	4080
GAGTCCTGTG	AAGATGGGGC	TCATGAGTGT	ATTGCTCCCC	AGTTGTTTCT	CTAGCACTAG	4140

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CTCAGTATAG	GGCATAAAAA	TCTGAATGGA	TGAACAAACC	ACTATTACTG	GTGGGGACAT	4200
GCTACTATCT	TACATGGTTC	GAGGTGGAAT	AAAGGTTGAG	AACAGCTATA	TAATGTGTTC	4260
CTTGAAGGGC	AGCAGTACAT	CAGTGCAATC	AGCCTACCTT	CTCCATACTT	CTCACTCTGA	4320
AAACTGTAAA	GCTGCACCTA	GCAATCAACT	TGGGAGCTTT	AAAAGGGACT	GCTCCCTAGC	4380
TCTCACCCAC	AAAGCTGTAG	TCTAGCACAG	GTGACTTTTT	TAAAAAAGTT	TTTTGGTCCA	4440
GATGTGATGA	CTCACGCCTG	TAATCCCAGC	ACTTCGGGAG	GCTGAGGCTG	GGAGGTCACC	4500
TGGGGTCAGG	AGTTTGAGAC	CAGCGTGACC	AACATGGAGA	AACCCCATCT	CTACTAAAAA	4560
TTTGCCGGGC	ATGGTGGCAC	ATGCCTCTAA	TCTCAGCTAC	TCGGGAGGCT	GAGGCAGGAG	4620
AATTGCTTGA	ACCCGGGAGG	CGGAGGTTGC	CGTGAGCCAA	GATCACACCA	TTGCACTCCA	4680
GCCCCGGCGA	CAGTGCAAGA	CTCCGTCTCA	AAAAAAAATA	AAAAAGGAGT	CCTATTAAGA	4740
CTTATTTTTA	CAGGTTGGAT	ATCTCTAATC	CCAAAATCTG	AAATGCTCCA	AAATTTGAAA	4800
CTTTTTGAGC	GCAGACATGA	TGCTCAAAAA	AATGCTCACT	GGGACATTTT	GGATTTCAAA	4860
ATTTGGATTA	GGGACTAGGT	GTGGGAGCTC	ACACCTGTAA	TCATAGCACT	TTGGGAAGTT	4920
GAAGCAAGAG	GATCAGTTGA	ACCCAAGAGT	TTGAGAGCAG	CCTAGACAAC	ATAGTGAGAC	4980
GCCGTCTCTA	CAGAAAATTT	TAAAAATTAG	CCAGGCATCG	TAGTACATGC	CTATAGTCCC	5040
AGCTACTCAG	GAGGCTGAGA	CAGAAGGATC	ACTTGAGTCC	AGGAGGTAGA	GGCTGCACTG	5100
AGCTATGATC	ATAACCACTG	TCTCCATCCT	GGGCAACAGA	GCAAGACCCT	ATCTCTTAAA	5160
AAAAATCTGA	AACACTGCTA	GTCCCTCAAGA	TAAGGGATAG	TCAGTCTTTA	TAAAGACTCA	5220
ATTAGTTATT	GGATATCTGA	GGAAGCATGC	ATATCAGGCT	CCCAAAGAT	CATTGGTTTA	5280
GGCACACATT	TTAATAGCTT	GGAAATCCAG	AATACTCTTC	TGGTGACCAG	CTCAGACATA	5340
GTCCTGATAA	TATAGGACCT	CATCTAACAT	GACTCCCTAT	TTTCCAGATA	AGCATGGATT	5400
CCTGGTTCAT	TCTTGTTCTG	CTCGGCAGTG	GTCTGATATG	TGTCAGTGCC	AACAATGCTA	5460
CCACAGGTAA	ATTGTCATTT	GATAAGGCTG	CTATTTGAAA	TGAAATTTTG	CTTTCACATT	5520

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TAATGAGCCA	CATTTGAAAA	CCGAGATGGT	ATTTGAAGAA	AGGAATATAA	AAATTTTATT	5580
CAAAGTGATG	GTAAAAATAGG	TGTCTTCAGA	AATCTTGGA	TTGAATGCTC	AGCATTGTTT	5640
TTCATACATA	CATAACTGCT	TTAAATAAAT	CAAAGAGATT	ATGTGTTCTT	TCCTGAAAAG	5700
TAAAATAAAT	TGTTGACATT	TACAACTCTA	TATATGGTTT	CTGAGGAACT	AACTGAAGAA	5760
TCTTGTGTCT	TTCTCCCTTA	AACCGTAGTC	CTTTGGAGGA	GGTAGGAAAG	GTCCAGCATG	5820
AGATAAAAAC	GTAGGGGGTG	GGTGGTGTTG	AGGGGGATTG	GTCTTTGCTT	GGTCTCCATA	5880
TGTTTGAGAG	TTTATTAAGG	CTTGCTGCTT	TGTGTCTCAC	AGCTTTTTAG	CCTCACATTC	5940
TTCATGTGCT	ATTCCTTGT	TTTTTGGTGT	TTGTAGTTGC	ACCTTCTGTA	GGAATTACAA	6000
GATTAATTAA	CTCATCAACG	GCAGAACCAG	TTAAGAAGA	GGCCAAAAC	TCAAATCCAA	6060
CTTCTTCACT	AACTTCTCTT	TCTGTGGCAC	CAACATTCAG	CCCAAATATA	ACTCTGGGAC	6120
CCACCTATTT	AACCACTGTC	AATTCTTCAG	ACTCTGACAA	TGGGACCACA	AGAACAGCAA	6180
GCACCAATTC	TATAGGCATT	ACAATTTTAC	CAAATGGAAC	GTGGCTTCCA	GATAACCAGT	6240
TCACGGATGC	CAGAACAGAA	CCCTGGGAGG	GGAATTCCAG	CACCGCAGCA	ACCACTCCAG	6300
AAACTTTCCC	TCCTTCAGGT	ACTAGAGATG	ATTCTGTTTG	TTCTTTTGCT	CTTTGAGTTT	6360
AGTCTTCCTT	TTATTATCTT	GTTTGTGTTT	TCTAGCCTTA	AAATTTCTTC	AAATAAGTAA	6420
AATTGCTCAA	GTGAAGTAAT	GAAACCTGTA	TGTGGAATTT	TTGGGTAGC	ATGAGTGAAG	6480
AGGAAAGAAG	AAAGATTCTG	GAGAATATCT	TTCTGCTAGG	TGGGATCCTG	GTTAGATTGA	6540
GAGGACTTAA	ATGTGTTTAA	AGGTAGAGAA	GAAGGCTTAA	AAAGACAAGA	GAAATAGAGG	6600
AGCTCATTGA	CGATGCAAGA	GACTGAAGAT	GAAAAGATAC	AGAGAATGAG	TAATAAGATT	6660
AGGTTTGGA	AGGGAGGGAT	CCGTGGAGAC	CATGGAAAGG	AGAATGGGTA	TTGATGTCCA	6720
TGACAGTTAG	ATGTGAGATA	CAGAGAATGA	GTAATAAGAT	TAGGTTTGGA	AAGGGAGGGA	6780
TCCATGGAGA	CCATGGAAAG	GAGAATGGAC	ATTGATGTCC	ATGACAGTTA	GATATGGAGT	6840
GGCAGGCCAG	TGGCCAGGGG	TGGCATCAGG	CTCTGGGAAA	TGGTTACATT	GCAGTGCCAG	6900

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TTGTTTCAGGG CCTCAGGTTG AAGCAGTAGT CCCAAGGAGA AAATCAGAGA CGTGGATCTG	6960
AGACCAGGGC AGGTAAGACA AGTTTCTGAC CTCTTTGAAC CTTAGGTACC TTGTCTGTAA	7020
AAGAGGATTA GAGATACCCT CAAAGGGCTT CTATGAGGAG TAAAGGAAAT AATCATTACC	7080
TGATTGCTAT GTAACGTCA TCCCTTTTCT AGCAAAAATC ACTCTTTCCT CTCTGTGT	7140
CCCAGTTAGA TGGTGAGTGC CCCTAAGCAG AATCACATCT CGCTCATGTG GAACATTACG	7200
GAAGTGTGTTG CTCAGTTGAT TCTCATTTGT TACTACAGAT GATATCTTTT ACTGCGCCTT	7260
ATAACTCAGA CCCTTCACCT GCCAGCTTTT CCCCATATTT TCTACCGTAA AGACAAGACA	7320
GCATTTGCAG TTAAGAGCAC AGTCTTCAGT GCCACACTGA GTTTGAATCC CAGCTCTTCC	7380
ATAAACCAGC CATGTTTATG GCATAGCTGG CTTACTTTAT CTCTCTACCT CGGTTTGTTT	7440
ATCTGTGAAA CAAGAATGAG TGATAGTAAT AGTTCTTACC TCATAGAGGA GATATTAGGA	7500
TTAAACAAGT TAATATGGGT AAAGCACTTA TAAAGGTGCC TACACATGGT AAGCACTATT	7560
TTTAAGTGTG AGCTGTTAGT ATTGTTGTGG TTATTGCTCT GATAGTTACC AGTAAAATAT	7620
ATGAAGGTAC CTTTAATGCA GATGGCATCC CACTATTCTT GATGAGATAG GGGACTGCAG	7680
ACAAATAATG TCTGATACTT GCTTTGTGCT TTAGAGTTAA TGTAGTTTTG TCATAGTTAT	7740
TACTGTGTGC TAGGCATCGT ACTAAGAGTT TTCTAGAATA ATCCTATGAA TTAAGTTCTA	7800
TTTTATGTTT TATAGGTGAA AGTATTTTAC AATGATGAAA CCATAATTG TGGAATGTTT	7860
TTCAGTGTAC AGGTCATGAC ACAATTCATG AAATCACTTT AGCAGGCCAC CACTAGTTGT	7920
TTGTTTTGTT TTATTTTAAT GGATGATCCA GTTCCATGTT TATCTTTTA ATGTTACATA	7980
CAATTTTTTG AAATTTTAGT AACACATAA AATGTTGGGT TGTGGCCATT GCTTAGGGAG	8040
AAAGGCAGGA TAACTTGATC AACTGTATG AGTGAATGGA AAAGGTGGAG ACTGTAACAC	8100
AGGCCTGACT GACTGAACAG CCCATGTTCT ATTGTGTACT GTCTTTCATT TAACAGTTCT	8160
GTGACATGAC CATGGATAAT CATCTCCTTT TAACAGATGC TTGATTTTAC ACTGTATATA	8220
GAGGTAAAT GATTTGTTTT AGATCTCAAG GCTGACAAAT TAGGCCTATT TCTCACTTTT	8280

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GCGGTCTTTC	CACTCTGCTT	GTAGGGAAC	TAGTTTTCCA	TAAACTGACT	TAGGTCCAAA	8340
TTGTGCCACA	GCTAAGAATC	TAGTTATTGT	ACATTTAACA	CAGTTCACGT	CATAGGAGGC	8400
TGAGACTATG	TTTCTCTAGT	GGCGTTTATT	CAAGATGAGT	AAAACACAAG	AAACCATTAT	8460
CGCACATGGG	AATTTTCATAG	TCTTAAACCC	CACATCCCAC	TTATCACCAC	CATTTACCAG	8520
TCCTCCTGTA	ACAGTTACAA	TTTTTTATTA	AATCAGTATT	TGATGTATAT	TATTGTAATT	8580
ATGAAATATT	CATTGCTGAG	CTATAAGTAT	AAATGGATTG	TTTTTCTTGT	ACAGTTTTTT	8640
TTCTGGATTT	AATACTTACC	TTATTTTTTG	TTTATTTAGT	TTTCTATTTA	GTCAGGCCAG	8700
GCACACTGGC	TAACACCTGT	AATCCCAGCA	CTTTGGGAGG	CCAAGGTGGA	CAGATCACTT	8760
GAGCTCAAGA	GTTTGAGACC	AGCCTGGGGA	ACATGGTGAA	ACCCCATCTC	TACAAAAAAT	8820
ACAAAAATTA	GCTGGGCATG	GGTGCATGTG	CTTGTAGTCC	CAGCTACTCA	GGAGCCTGAG	8880
GTGGGAGGAT	TGCTTAAGCC	CAGGAGGTTG	AGGCTGCAGT	GAGCTGTGTT	CATACCACTG	8940
CACTCCAGCC	TGGGTGACAA	AGCGAGACCA	TGTCTCAAAA	AAGTTATTGC	TACTCAATTC	9000
TTACCATGCT	CTCCAGAGCC	TCTCAAAACA	GCTTTCTACA	AAGTGAGATC	TGTTAGATAA	9060
TCTATTTCTT	TTTTACCTCT	AGAAATTCCT	CCTGAGCCCT	CCATTGTCTT	ATTCCAGTCT	9120
AGGCTTGTCG	ATCTCTAGGG	CTACTACACA	GATACATCAG	CCTGAGATTT	CCCTTCTCTG	9180
TCATTCTGGG	AATTCCCCTT	GCTGCTGCTT	CCTGACTTCC	ATATTGTCTT	CCTTTTGTGC	9240
TTCTCATCAT	TCGGTAGATT	CCTGAGAAAA	GGGGTCCATG	GGAGGCAAAT	TGCATCCTTA	9300
CATATCTAAA	AATATCTTTA	GGGCTGTGCA	TAGAATTTGA	GGAATATTTT	TCCCCCAGAA	9360
TTTTTAAAGT	AATGCCCTAA	CTGACACCTG	TTTACCAGGT	TTGGAGGATT	TTACTGCTAT	9420
CTTAATCCCT	AATTGTTTGT	ATGCTTTCTA	GGATCTTCTC	TTTATCATCA	GTATCCTGAA	9480
ATTTACACAGA	GATGTATCTT	GATGTGGGTC	TTTTTCGTTC	ATTATTATGG	ATACTTAATA	9540
GGCCCTTTAG	AGCCTTGATC	TTGCATTTCT	GAAAATTTTC	TCCCATTCTT	TTGAAACCTT	9600
CTCCCCCTCT	TCCTTTTTTT	TTTTTCTCAA	ATTCTTAATA	TTTGATATT	GGATGTATCC	9660

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TGAATTAATT CTTTAATCTT TAAAATTTTT CCTTTCTGTT GATCTTTGCT TTGAGTCTTT	9720
TTCTCCTTTT AAAAATAAAC AAAGGCCAGC TAGGCACAGT GGCTTATATC TGTAATTCCA	9780
GCACTTTGGG AGGCTGAAGC AGGAGGATCG CTTAAGCCCG GGAGTTTGAG ACCAGCCTAA	9840
GCATCGCAGC AAAACCTCAT CTCTACAAAT GATTTAGAAA TTAGCAGGGC CTAATGGCTC	9900
ATGCCTGTGG TCCCAGCTAC TCAGGGCTGA GGCAGGAGGA TTACTTGAGG CCTGGCAGTT	9960
GAGGCTGCTG CAGTGAGCTG TGATCGCACC ACCGTACTCC AGTCTGGGCA ACAGAGGGAG	10020
ACCTCATCTC AAAAATAAAT AGGCCTGGTG TGGTGGCTCA CTCCTGTAAT CCCAGCACTT	10080
TGGGAGGCCA AGGCAGGTGG ATCACTTGAA GCCAGGAGCT CAAGACCAGC CTAGCCGACA	10140
TGGCAAAACC CTCTGTCTAC CTAATAAAAA TAAAAAATT AGTCAAACGT GTTGGCATAT	10200
ACTTGTAATC CCAGCTACTT GGGAGGCTGA GACATGAGAA TTGCTTGAAC CTGGGAGGTG	10260
GAGGTTGCAG TGAGTCAAGT CCCTGCACTA TAGCCTGGGG AACAGAGTGA GACCCGAGAC	10320
TCTATCTCAA AAAAAAAAAA TCAGTGACAA GTAAAAAGGT AGAATACCTT TTTTTTTTTT	10380
TTTGAGACAG TCTCACCTG TCGCCAGTC TGGAGTGCAA TGGCGCAGTC TCGGCATACT	10440
GCAAACTCTG CCTTCAGGT TCAAACAATT CTCCTGCCTC AGCCTCCTGA GTAGCTGGGA	10500
TTACACATGC CCACGACCAC ACCCAGCTTT TTTTGTATT TTTAGTAGAG ACAGGTTTCA	10560
CCATGTTGGC CATGCTGGTC TCGAACTCCT GACCTCATGA TCCACCTGCC CCGGCCTCCC	10620
AAAGTGCTGG TATTACAGGC GTGAGCCACT GCGCCAGCC TAGAATACCT TTTAAAAATA	10680
AATAAATAGG CCGGGCGCGG CGGCTCATGC CTGTAATCCC AGCACTTTGG GAGGCTGAGG	10740
CGGGCAGATC ACGAGGTCAG GAGATCAAGA CCCTCCTGGC TAACATGGTG AACCCCATCT	10800
CTACTAAAAA ATACAAAAAA AAATTAGCTG GGCGTGGTGG CAGGTGCCTG TAGTCCCAGC	10860
TACTCTGGAG GCTGAGGCAG GAGAATGGCG TGAACCCAGG AGGTGGAGCT TGCAGTGAGC	10920
CGAGATTGCG CCACTACACT CCAGCCTGGG CAACAGAGCA AGACTCTCTC TCTAAATAAA	10980
TAATAAATAA ATAAATAAAT AAATAAATAA CTCCTTTTAC AAAAGCATAT ATATTCAATT	11040

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TTTCCATTTA	TAATATAAAT	AATAGATATG	CTGAGTTGAT	TTCTGCATAT	TGCTTTTTC	11100
GTTACCCCTAT	CATACTTGCT	CTTTGTTTTA	GTAAAGAGCT	GCTGTATTGA	AGGATATACC	11160
TTAATCTCTT	TATCCAGTTT	CCCCATCAGT	GGACACTAAG	ATTGTTTTCA	GAGTACTCTT	11220
ATAACAATA	CAGTTTGTC	TTTCAGACAC	ATATGAGAAT	ATTAGCAGGA	TGAATTATTT	11280
TAAGTCTGCA	TTTATAAAT	TATGGATATT	GCCACATTTA	CCTCTGCTAG	GAAGTCTATT	11340
CCTATTAAACA	ATATGTCAA	GTGCCTATTT	TTCTAAACTC	TCTTCAGTGT	GGTGAATTGT	11400
TAAACTTGGG	GATCTCTGCC	AATCTGACAG	GTGAAAAATA	ACATCTCAGT	GTAAGTTTAA	11460
TTTGCATTTT	GCTGAGATTG	AGCAATTTTG	TGTAATTTAA	AAGATCATTT	ATTTTCTGA	11520
GCATTCTCTG	TTGATATTCT	TTACCCATTT	TTATTAGAGT	GTCAAGGTTT	TCCTGACTCG	11580
TTTGTAGATG	TTCTTTGTAC	GTTTGGGAAA	TGAGTCCTTT	GCCTATGGTA	AACTGCAAAA	11640
TGTTGTTCCC	TAGGTGGTCA	TCTAGATTTT	CTGCATTGCA	GAAGATATCA	TTAGCTATTT	11700
TTAATTTTTT	TAATTTAAAT	ATTTCTCAGT	TTAGGTTTTT	TAGGAATTGG	GTCATATCTA	11760
GGAAGGCTTT	CCTTACTCCA	AGATTATAAA	AATAATTTTC	TTCTGGACTT	CTATGGTTTC	11820
GTGTGTGTGT	GTGTGTGTGT	GTACACGCAC	TTAAGTCTGT	CTCGAATTTA	TTCTGATGCA	11880
GAGTGAGCTA	TGGATCTGTT	TTCCCCAAA	TATCTAACTT	GTCCCAATAC	CCCTTAATAA	11940
TTTATTTTTT	CTCATTGATT	TGAAATGCCA	CCTATCTTAT	ATATTGAATT	CAGATATTTA	12000
TTTACCTCTT	CATATGTATT	TGAGTATTTG	GGAACATTCA	TTTATTTTTT	TATTAATCTT	12060
TTTCTCTGTC	CATGTGCAAA	GCCTCACTGT	CTCAATAAAT	GTAACCTTGT	AAAGTATTTA	12120
ATATCCAGTA	AAATGAGTCA	TTCCCTTGTTA	ATTTTATTTT	TCAGAATTTT	GTTAGCAATT	12180
CTTATTATAA	ACATTAGAAT	TAACTTGTCT	AGCAGGAAAA	AAAGTTTGTA	TTGATCATGT	12240
TAAATACGTA	GATTAAACAGA	GAAAATGGCA	TCTTACAGAT	GTTGAGTCTA	ACTATCCAAG	12300
AATGCAATAT	ATTCCATTTT	CTGAAGTCTT	TTTTTTTTAA	ATCTTCTGTT	TTTGTAATTA	12360
TAAATGGAGC	ATTTTCTTCC	ATCAGATCTT	CTAACTGGCT	GCTGTTGGGG	ATATGAAGGC	12420

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TACTGATTTT	TGTAGAGACA	TTTGTACTG	GCCACCTTAA	ACTCTCTTAG	TATTGGAAGT	12480
AATTTTCTTC	ATTAATTTTT	ATGGCTTCAA	GTCATCTCAT	CTGCATATAT	CTTCCAAATT	12540
TTTAGAACTT	TCTTTTTCTT	CTGTTTAATC	GCATTGATGA	ATACCTCCAG	AACAAAGTTA	12600
AGCAGCTGGT	AAATGCAGAC	AGCATTCTCT	TGTATCTGAC	ACTAAGGAGG	ACACTTTCAG	12660
TGGTTTTTCA	TTATACGTGG	TACTGACTCT	TGAGTTGAGA	TAAACATATT	TTATTGTGTT	12720
CAGGATTTAA	TGAGCGTTTA	TGTTAGGAAT	GGGTGTTAAA	TTTGCCAGT	TGCCTGTTCA	12780
GGATCAATGA	GAAAGATCTG	AATGATTTTT	TTTCTCTTTT	GGTCTGTTTC	TATGGTGGAT	12840
TCTATTCCTA	GGTTTGTTTG	TTGTTTGTT	TATTTTGAGA	TGGAGTCTGT	TACCAGGCTG	12900
GAGTGCAGTG	GCGCCATCTC	AGCTCACTGC	AACCTCCACC	TCGCGGGTTC	AAGTGATTCC	12960
CCTGCCTCAG	CCTCCGAGTA	GCTGGGACTA	CAGGCACGCA	CCACCATGCC	CGGCTAATTT	13020
TTTGTATTTT	AGTAGAGACG	TGGTTTCACC	ATGTTGGCCA	ACCTGGTCTC	GAACCTCTGA	13080
CCCCATGATC	CTGCCTCAGC	CTCCCAAAGT	GCTGGGATTA	TAGGTGTGAG	CCACTGCGCC	13140
CTGCCAGTTT	TTATTTATTC	ATTTTTTAGA	GACAGGGTCT	TGCTCTGAAT	TAATCTTTTA	13200
ATCTTCTTAA	TTTTTCTTTT	CTGTTGACCT	TTGCTTTGCT	TTAAGTCTTT	TCCTTTGAGT	13260
CATCCAGGCT	GAAGTACAGT	GGCACGATCA	TGGCTCACTG	TAACCTTGAA	CTCCCAGACT	13320
TAAGCAAACC	CCACCTCAGA	CTTCTGAGTA	GCTAAGGACT	ATAGGCGCAT	GTCACCACGC	13380
CCAGCTAATT	TTTAAATTTT	CTCAGAAACA	GGGACTCACT	GTGTTGCCCA	GACTGGTCAT	13440
GAACTCCTGG	CCTCAAGCAG	TCCTCAGCCT	TAGCCTTCCA	AAGCACTGGG	ATTATAGGCA	13500
TGAGCCAAGG	CCGCCCAAAC	ATATTGTATC	GTTCTGTAA	CAAGCTGTTG	CAGTCTATTT	13560
GATATTATTT	CTTATTTTTT	TCATTTAGAA	TTTTCTCTGT	CTAGATATTC	TCAAATTATC	13620
TCTAAATGAG	ATTGATCTAT	GTTTTTCCTT	TGTGTGTGTA	TTCTTTTGA	TAAGTTT TAG	13680
TTTTTAGTGT	TTTGTTTTGC	TACATGGAAA	GGATTGAAA	GTTTACACTA	AAAAATATGC	13740
TTTTTTTTTT	TAAGACAGGC	TTTTTCACTG	TG CCTAGTG	CTGGAGTGCA	GTGGCATGAT	13800

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CTCGGCTCAT	TGCGGCCTGC	ACCTCCTGGG	CTCAGGTGAT	CCTCTCACCT	CAGCCTCCCA	13860
AGTAGCTGGG	ATTACAGGTG	TGTTCCACCA	TGCCCAGCTA	ATTTTTTGTA	TTTTTTTGTA	13920
GAGATGGGGT	TTCGCCATGT	TGCCCAGGCT	GGTCTTGAAC	TCCTGGGCTC	ACATGATTCT	13980
CCTGTCTTAG	CCTCCCAAAG	TGCTAGGATT	ACAGGTGTGA	GCCACCACAT	CTGGCCATTT	14040
CATTCATGTT	TTCAAATGTA	TTTGAATGAG	GAAAAGTTCT	CCCTTGATG	TATTTATTAT	14100
AATAGCCTAC	AGAGCTATTA	ATTTTTAAAT	TTTGTTTACT	TTATGTCTCC	TTTTTTTTTT	14160
TGTTTAGGCT	GAATAACCAT	TTATTTTATA	GGTTTATTGC	CTTTTTTCTT	CCAAAGAACT	14220
TGCTATTGTG	CATTTATAGT	CCTTTTATGT	TTACGTTTTC	TATTTTATTG	ATTTTAACTT	14280
TCTACCTTCT	TTAGATTTAT	TTTGTTCTTT	TTCTATCTTC	TTGAATTGAG	TGTGCTTTAA	14340
TTGCATTCTT	TCCAGTTAAT	TAACATATTT	AGTGCTGTGA	ATTTTGAACA	AGCACAGCTT	14400
TAGCCACATC	CCATAGGTGT	TTCTATAGGC	AGTTGTATTA	GGATGCGCTA	TAAGCTGCTC	14460
TGACAAAGAT	ACCAAAATTC	AGTGACTTAA	ATAAGACCAA	AGTGTCTTTC	TCTCCCCAGT	14520
TACATTCCAG	AGGTAGACAG	GGCCTTCGTC	TCAGTAGGGA	CCAAATTCCT	TTCTCTTGTT	14580
GGCCCTGCCA	TCCTAACAAT	ATTGCCCTTA	TCTGTTTGGT	TAGAGATAGT	TCTCACCATT	14640
GGGTTCTAGT	TCCAACCACT	GCGAAGGACA	AACAAAGGGA	ATAGGGGCCA	TTTCTCTTCC	14700
AAAAGATGTG	ACCTGGAAGT	TACTCACATT	GCTTTAGCTC	ACATCCCGTT	GGCTAGAATT	14760
CATCACATGA	CCACACCTAG	CACAAAGGAG	TCTCAAATAT	AGTCTGCCAG	GAGAGCTTGG	14820
TGCTCAGCTA	AAAAACAAAG	GTTCTGTATC	AAGGCAAGAA	GAGAAAGAGA	CTGATCTGAG	14880
GGGAGGAGAG	TTGGCAGGTT	CTGTCACAAA	ACTTCTCGTC	ATTGTTATTT	TTAAGGTATT	14940
TTTCCATTTT	GGGTTTTTTG	TTTGTCTGAT	TTTTTTTTTT	TTTTTTGAGA	TGGAGTCTCG	15000
CTCTGTTGCC	CAGGCTGGAG	TGCAGTGGCG	TGATCTCTGC	TCACCGCAAG	CTCTGCCTCC	15060
TGGTTCACGC	CATTCTCCTG	CCTCAGCCTC	CCAAGTAGCT	GGGACTACAG	GCGTACACCA	15120
CCACGCCTGG	CTAATTTTTT	TTTTGTATTT	TTATTAGAGA	CAGGGTTTCA	CTGTGTTACC	15180

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CAGGATGGTC TCATTCTCCT GACTTTGTGA TCTGCCCACT TCGGCCTCCC AAAGTGTTAG	15240
GATTACAGGC GTGAGCCACC GCGCCCGGCC GTCTGTTTGA TTTTGTAGAT GGAATCTCAC	15300
TCTGCCCCC TTCTGGAGTA CAGTGGTGTG ATCTTGGGTC ACTGCAACCT CTACCCTCCC	15360
AGGTTTAAGC AATTCTTGTG CCTCAGCCTC CCAAAGTGCT GGGATTAAAG ACGTGAGCCA	15420
CTGTGCCCAG CCCATTTTGG TTTTGATTTT TTTTTTCTT TGAAATAGAG TCTCGCTCTG	15480
TTACCTAGGC TGGAGTACAG TGGCATGATC TCGGCTCACT GCAACCTCCC CCTCCTGGGT	15540
TCAAGTGATT CTCGTGCCTC AGCCTCCCAA GTAGCTGGGA TTATAGGCAC CCACCACCAC	15600
GCCCAGCTAA TTTGTTTTGT ATTTTGTAGTA GAGACGGGGT TTTACCATGT TGGCCAGGCT	15660
GGTCTCGAAC TCCTGACCTC AGGTGATCCA CTGCACCCGG CCTCATTTTG GTTTTGATTT	15720
TTATTTTCAA ATGTTTTCTT ACTTTGTCAA TTTCTAATTT TATTGCATTG GGACAAAAGA	15780
ATATTGTACT CTTTCTACTG TTGGGGTTTA TAAGGGCTGT GGATATTTCA CTCGCCTTTG	15840
AAAAGAAGGT TTTCTCTGTT AGTCTGTAGA GTTTGGTATG TACCAATTAG ATTTTATTAC	15900
TTATCATTTT GGTCTTTTGT ATCCTTACTT AATTTTGTCC TCTTGAATTT TAATGGAGCA	15960
AAAGACATAA AGTCCTCTAA TAACATGCGT TCTGTTTGCA TTCTCATACT TTTTATGAAT	16020
ATTGATGCTG CACTATTTGT GTACCCAGGG AGAAGGCCAG ACCACTGTCC AAAGTTTAGT	16080
GAATCTGGGC AGCCTTGTTT CCCAGTTGTT GGAGGATGCC TCATGGAGGA AAGCATTCCT	16140
AATCCTGGAG CTTGTTTTGT TGTACTCTAA TTGAATTGTA ATGTGTTTCT TTAACCTGAA	16200
TGAATGTTTC TATTTTTTAC TTATTACACA GGTAATTCTG ACTCGAAGGA CAGAAGAGGT	16260
GAGCTGCTCA CCTTATATCT GTTGTTCTT TTACACAGTG TACAGTATTC ATTTATTTCC	16320
TCTGCTCACA GTCTGTGGTA ACCGTGTGCA TCTGTGGCTG TGTGTTTGT TTACTTTCCC	16380
TTAAGTTATT TCCATGTTAA TCTCATGGAG AAGAGCAATA GAAACAAGTA CTGTATTCAG	16440
TATGTTTTTT AATATAGACT ATGGATTCTA ACAGCTATGA TGTATTTTAA CAAGTAACAA	16500
AATATATCTT ACTTTGACAT GTCACTTTGT TAACATTACT TTTTGGTGAT ATTAGGTCAT	16560

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AATTTCTATA CCATTAGTTA CTTCTGATTT CTAGGCCACA GTTCCCTTTA AATATTCTTT	16620
GTGTTGTTTT TCCCCTAGTG TATAAAATGT CAACCCTTTG TGGCTTTATA TGGATTTTAT	16680
GGATTTTCAG CCCTTAAATG TAAAGTCTCT ATGGCCTGAG ATGTTGTGTC TGTGGTTTAA	16740
GCTGGACTGC TGAGTCCCTG GTCACTAGAG AGTAGGGGGA CATGGGTACT TGTCTGCAGA	16800
AGTGTGGCAC ATTTTGCCTA GAATGACAGT AAGGCTGCTA TCAAAGAGCA TGAGAGAAAG	16860
AGAAAGAGAT CATCTAACAT TCTAAGAAGT GATTATTACA TTTGAGTTTT AAAAATGTTA	16920
CTATTGGAAG CAGTGTTTTT ATCATAATTT TCTATTTTAT CAAATCAGAC TTGAGTTTTT	16980
TTTCTGATTC TGTTATTTAA CCATACACAA TTTTCCCTGT GTAATTAAGT AATGGAACAC	17040
TTGGAGGCAT ATGAAGTCCC ACTAAGTAGG GAGCATTTGA GTCAGAAAAG TGGGTACTCT	17100
CTTCCTTTAT GTGATGTCCA TCTGCCATTG TATTTGGTAA GGAATAGTGA GGTGTTACCA	17160
TACTGTGTAC AGATTTCCCT CACTTTTCCA CCTCTCACTT TCCTAAACTT GGGAACATAA	17220
CATTGGATTA ATACAGTGTC TTTGCTGTTC AGATTCACTT GCCAGATTTT ATCAAATGTA	17280
GACTTAAATA GGTTTTATTG TGATAGATAT TTAATTGCTC CCTAAACTG CTCTCTTAAC	17340
CAGCCTTACA ATAAAGTCAA AAGTCAAAGT GGTAGGCTTC AAGATGAAAC ATAAGATCTG	17400
TTGACTCCTT CCTCTATTTA GTATATATTT TCATAATATT CAGCCTTTTC TTGCCCCAGA	17460
TATCATATCT ATTTTACCTA CCCAATATTT AAGTAGTTTC CATGTTGTGA TTAAGAAAAC	17520
AAAATTACCA TAATTACCTA GATTATTGCT AATTGTGACA TATGTAAAGT CTATTAATGT	17580
AATAAATCTC CTTTCTTAAG TCAAAAAATA ATTTTGTGTA ATTCCAAACA GGAAACTGAA	17640
AAGGCATAGG TATTCTCAGC AGTCTCTAAA GTCCCAAAAT CTAATGGCAA TTTTACCAGA	17700
GCAGATCTTT AGAAGTATTG CTATAAATTT GGATATCCCA TTCTAATTTT AAGCCAAATG	17760
CTTTTTGAGA AATAAGCCAG CTGTTTGGA ATGCTTGTAT TATAATCGGT TTGATAAGCA	17820
GTTATGTCTT ATGCAGATGA ATTAGGGGCT ACCTGTTTTT ATGCACTGGT CTTTGGGGTG	17880
CTTTTGAACA GTAGTGTCTG ATGTTTTAAT TGTCAAAGCA AAAAGAAATG AGAGGGAGGG	17940

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CAACTTTTCT TCCTCTTCTG AATTCCAGGA AACTGGTTAT TTTCTCATGC CATATGATTT 18000
TAAAATATAT TCCCAGCCAG GTGCAGTGGG TCACGCTTGT AATCCCAGAT TTTTGGGATG 18060
CCAAGCGGGG GGA 18073

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7505 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TCCGAGCTCC ACGCGGTGGC GGCCGCTCTA GAACTAGTGG ATCCCTCTGG TGGCCCATTG 60
AGAATCAAAA CTTGCAGTGA GTGACTCTAT AAAATGGAAT ATTGAATCAA GTCTGAAAAT 120
GATCCACATA GTTCTACAGC AGGGCTGGAC ACCGTGGTCA GGACCTCAAT ATATTCTGCT 180
TCCACAGAAT TCAGACAGTT CAGAGTTTGG TGAATTAACC TCAAAGGCAG CAAGATATCT 240
GTCCCGGGAG TCAGCAGGTA AGCATAGCAG AAATGGCTGG AGCAGCGGGA GCCTGCTTTC 300
CTTCTGTTGG CTGCTAGCGT CCACTCCATT ATAGCTCCTG ATGGAAGATT TCTACAGAGT 360
GATGCCTCAG AATCTTCCTT ATACCTTTCT TCCATGATCC TTGCACCTCT TTTTCTAGAT 420
TTGCCCACAT TCTTATGTGC AAGTAACTAG ATATACATTA TCAGACAAGC TAGCAGACCT 480
GCATATATCC ACTTCCCTAC TTTTCCTATA ATTTCTTCAC CTGAACCTCT ATCATTCCTC 540
TCTTTCTGTG TTGACTCTGG TGTTAACCTT GCAGGCAAGT TGAGCGTGGG TTTGGTGTCA 600
CAGTGAAGGA CTAAGGGAAT AGTTAGCCTT CTATTTATTA ACAAATCTTC CCTTTGATGT 660
CTGGATCAGT GTCTCTCTAA TAGGAATTAT TGGCATGTTA AGGCAAAGAA CATATGCTTA 720
TTGAGTGCTG ACTGATTGGG GTTAATACTA ATTTGATACT ATTAAGGTGT GGGGCCAGG 780
AATGCCAAAA TTCTACCTCA ATGTAGAGCC ACCATTCCCC TTGAGGTAAC CTAGGTGGGA 840

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TAGATATACG TGTAAGGGCT AATGGAAGAT AGGGAATCAA AGTATCACTT TATTTTTTAT	900
TTTTATTTTT TATTTAATTT TTTTGAGATG GAGTCTTGCT CTGTTGCTAG GCTGTAGCGC	960
AGTGGCACAA TGAAAGTATC ACTTTATTAT TATCTGAGCT TGTGCCCTAA ACTTCACTGC	1020
AGAATATGCT GGTAAAATGG ACTGGATTAC AGGATTTAGA GGCAAGGTCC ACAGGTCAGG	1080
ATAAGAGGTA AAGAGGGAAA TCTTTCTCTC TTCCTAAGCC CAAACCCTCC ATGACAATTG	1140
AGATTAAAAA AAAAAAATAA ACTGATGAGA GAATCCAAGC ACAGTTGATC AAAGAGGAAA	1200
GAGAAATGAT GATGTTTCCC TCTTTCTTTT TCATGAGAAA GTGGCTCTCT TATTGATCGG	1260
CTACTTGATT AGAGAAACAG TGGGGGAAAG AACTGCCATA TCCACATGTG CAATTTTTTA	1320
AAACACACAG TGATTCTGAA CACTAGTATA AATTCCCAGT CAGTGTTCTG GCCATCTGAC	1380
TACTCAGGTT ATAATACCTA ATTTTTACAA GGGAGTTGGG AAGTGTGCCA AACCTGTAGA	1440
AGTCTATATC TACTGTATTC AGATTTTATA TGCATTATTT TATATAACCT TTTGACCTCT	1500
CTCCTCTATC ATCACTTGAG TGATTTTCATC CAGCGTCATC ATTTAACATA TTTTAAATAA	1560
CTCTATATAC TGATAATTCC CAAATTTATA TCTCCATCCC CGATTGTTCT CCTAACCTCC	1620
AGCCTCTAAT ATCCAACCTGC CTACTCAAGC CTCAGCAATG GTGAGCGCCC CTGCCCCAGC	1680
CTCGCTGCTG CCTTGCAGCT CGATCTCAGA CTGCTGTGCT GGCAATGAGC GAGGCTCCGT	1740
GGGCGTGGGA CCTTCCGAGC CAGGCGCAGG ATATAATCTC CTGGTGTGCT GTTTGCTAAG	1800
ACCGTTGGAA AAGCACAGTA TTAGGGTGGG AGTGACCCAA TTTTCCAGGT GTCGTCTGTC	1860
ACAGCTTTGC TTGGCTACGA AAGGGAATTC GCTGACCCCT TGCACTTCCT GGGTGAGGCA	1920
ATGCCTCGCC CTGCTTCGGC TCATGCTCAG TGCCTGTCAC CCACTGTCCT GCACCCAGTG	1980
TCCGACGAGC CCCAGTGGGA TGAACCCGGT ACCTCAGTTG GAAATACAGA AATCACCCGT	2040
CTTCTGTGTC CCTCATGCTG GGAGCTGTAG ACTGGAGCTG TTCTATTTG GCCATCTTGG	2100
AACTGCCTTG CATTCAGTTT TTAATATCCA ACTGCCTATA CGATATCTTC ACTTGATTTT	2160
TGAATAGGCA TATCAAACCT GTCATGTTCA AAAGTGAGGT TCTAATCTTC CCTCCCAAAC	2220

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CTGCTTCTCC CATGGCTTTC CCCATCTCAG TAAATAGGAA TTTCATCCTT CCAATTGCTC	2280
ATGCCAAAAA TTTGGGAGTT ATCCTTGACT CTTCTCTTTC TCACACCCCA CATTCAATCC	2340
ATCACCACAT TCTGATGCCT CTATCTTCAA GATATACTTA GACTTTCACC ACTTTTCTTC	2400
ACTCTGCAAT TACCACTTTG GTCCAAGCCA CTGTTATCTC TTTCTTGGAT TATTGTAATA	2460
GCTTCCTAAT AATTTGTCCC CTTTCTTCCA CCTTTGTTTC CCCTACAGTA TAATCTTAAC	2520
GAAGCAGCCA GAATGGTTGC CTACAAACCT TTAATATGGT AAGCCAGAAC ATGTAGGTAT	2580
ATTCAAAACC TTCCAATGGC TTGTCATGGA ACTAAAAGTC TCTACATTGG CCTATAAGAC	2640
CCTATGTCAT CTACCCCTAG TCTCCTCCTT TCTAACTTCA TCTCCTGCTA TGCTGTCTTT	2700
CAACTCACTC TGCTCCAGGT GCTCTGGCCT CCTCAAACAC ACCACACACA CTTGCAGCTC	2760
ACAGTCTTGG CACTTGCTGT TCTTCTCCTC TAGGACCTTC TTCCTCCAAC TGTCTGGTTC	2820
ACCCACCCCT TCCTTCTGGA TTTCTGCTCT GATGTCATTT TATCAGTGGG CACTTCCCAA	2880
TTTCTCTATT TAAGACCACA ATTCCAGGCC AGGGTGGTGG TTCATGCCTG TAATCCCAGC	2940
ACTTTGGGAA GCCGAGGTGG GCAGATCATG AGGTCAAGAA TTCGAGACCA GCTTGGCCAA	3000
CATGGTGAAA CCCCATCTCT ACTAAAAATA CAAAAAAAT TAGCCAGGTG TGGTGGCACA	3060
TGCCTGTAAT CTCAGCTACT TAGGAGGCTG AGGCAGGAGA ATCGCTTGAA CCTGGGGGGC	3120
AGAGGTTGTA GTGAGCCGAG ATTGCGCCAC TGCACTTCAG CCTGGGCAAT AGAGCGAGAC	3180
TCTGTCTCAA AAAAAAAAAA AAATTTGCTG TTATTTCTTA TACTATTTTT GTAAGCAAG	3240
GACCTTATTA TTTTCCTTGA TAATACCTCT CACACTTTAT AATTACATAT TTGACTTTGT	3300
TGATTAATGA ATATCCCTCC TTTATAGCAT AAATTCCACA AGAGCAAGGA TTACATGTCT	3360
GCTTCATTCT CACTGTACAC CTAAAACCTA GCACAGGGTC TCACACATAA CAGGCACAAA	3420
ACAAACAATG GATTACGTTG AGCCAAAGAA CAAAAAAA TAGTAATTTA TCACTAAATG	3480
TCTTTGTTAA ATTCCAACAA CAGGGGGCAG TATATCAGGT ATTATAAGAA AGTAATTAGG	3540
CACATCCCAG CACTTTGGGA GGCCGAGGCG GGTGGATCAC AAGGTCAGGA GTTCAAGACC	3600

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AGCCTGGCCA ATATGGTGAA ACCCGTCTC TGCTAAAAAT ACAAATTAG CGGGTGTGGT	3660
GGCACACCCC TCTGGTCCCA GCTACTCAGG AGGCTGAGGC AGGAGAATCG CTTGTACCCA	3720
GGAGGCGGAG GTTTCAGTGA GCCAAGATCG TGCCACTGCA CTCCAGCCTG GGTGACGGAG	3780
CGAGACTCTG CCTCAAAAAA AAAAAAAAAA AGAAGAAGAA GAAAGTAATT AGGCACCTTT	3840
GGCTTAAGAC ACTGGGCTAA ATCCATGAAT TTACTTCATC TTCCCCAAA GCACACTGAC	3900
ATGGTAGAAG AAATATAAAA ATACTAATGA ATCAACAGCA TATCTGAAAG GCAGCAAACG	3960
GTGGCATATG TAGATCAGAA TCTTTGAGAG ATTTCTGGAA GACAAAACAG ACCAGACTCG	4020
ATGTCCAAGA GATCAAACAG AGCCAAAGAG CCTCCAGCTG AAAACTAAGT ACTAGTTCTA	4080
CCAGTTTGGG CCTGGAAACA CCTCAAGCTC AGAGGGAATT GGGACTGGGG TTGAAAGTGG	4140
ACCTTGAGGT ACCAGGATGG TACTTAAGCA AAGGCCTGCC AACCAGCAC CAGTACACCC	4200
ACAGCCCAA TGACAAGCGG GGCTTCCCAT CTAGACTCAG CTGGAAAAAC AGTGCTCTAC	4260
ACAGAGTAGA GAGTTTGTCA CAGAGACTGG TAAGGGCTTC TTTTTTACAA AACATATGCT	4320
GCATATATAT TTTCTCAACG TCACACTAAT GACATTTTGG GCTATACAAT TCTCTGTTAT	4380
GTGGGTCTGT CATGTGCACT GTAGGACATT TAACAATATC CCTAGCCTCT AATTATTAGA	4440
TGTCTGTAGC AAATTCCCAA TTTTGATGAC CAAAAGTATC TCCAAGCATT GCTAAATGCC	4500
TTTGTGGGGG AAATAGCCCC CAGTAAGGAA CCACTGGTCT ATACTCACGC CATTCTAACT	4560
GAATTCCTTT AAGGCAAATC CGAGACCTAG CATTTCAAAT GCAATTACTT AGGTATGTAT	4620
CACCAAGAGA TCAAGATTCT TAACATAAAC ATAATACTAT TATCCAATTT AAAAAGTAAC	4680
ACTAATTCCT TAGTATCATC TAATATTATT CAGTTACTGC TTGAATTTCC CTGAGTGTCT	4740
CATAAATGCT TTTTTTTTGT TTTGGTTAGA ATTGACACCA GAGCAGGTCT ACACTGCATA	4800
TGATTGTTAA GTATATTGGG TCCACAGAAG GTCTCCTGGG GCCTGCAGAC AGAAAAAAC	4860
CATAGTAGTG CCCAAGCTAA TTCTAGGCAA CCACAAGAGA GGAAAGGAAA AAGAAAACGG	4920
CAGCTCGCCT AGAGGATAAC TGCACCCTGC CCCGATTTTC CTGAGCCATC ACTGAACCCC	4980

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TTCCTGGTTT	AGGACGTATG	TCCATGTTTG	TCTTCTGAAG	GGATGAAGGG	ACACCTATTG	5040
TGAGCACAGT	CTAAGCCACT	CAATGGTCCA	GGGCATAGCT	CAAACAGAGC	AACAGTAGCC	5100
CTGGGAAATG	GAGGTGACAA	AAGAAACAGA	ATAAATCTTT	CAAAATATAC	TGCAATTTGT	5160
GCAACAGGAT	GCCATATTGA	TTTAAAAAAA	TTTTTTTTCT	TAAATTTTTT	GTAGAGATGG	5220
GGGGAGGGGG	TCTTGTTGTT	GCCCAGGCTG	GTCTTGAACT	CTTGGTCTCA	AGTGATCTTC	5280
TTGCCTTGGC	CTCCCAAAAT	GCTATGATTA	TGTGCGTGAG	CCACTGCTGC	ATTGCGTTTT	5340
TTTTTCTTTT	CTCGAGACGG	AGTCTCACTC	CGTCACCCAG	GCTGAAGTGC	ACTGGCGTGA	5400
TCTTG GTTCA	CTGCAACGGC	CTCCTGGTTC	GAGCGATCCT	CACACCTTAG	CCTCCCTAGT	5460
AGCTGGA ACT	GCAGGCCTGG	CTAAGTTT TG	TATTTTTTAGT	AGAGACAGGG	TTTCACTATG	5520
TTGGCCAGCC	TGGTCTTGAA	CTCCTGACCT	CAGGTGATCA	GCCTGCCTCA	GCCTCCCAAA	5580
GTGCTGGGAT	TATAGGTGTG	AGCCACTGTG	CCCAGCCTAC	ATTGATATTT	TTTAAAGGCC	5640
ACTATTTAAA	AAGGAGTAAT	CTGAGTAGTA	AGAAGGAGTT	CTTTAAAAAC	TGGCCGGGCA	5700
TGGTGGCTCA	CGCCTGTAAT	CCCAACACTT	TGGGAGGCCG	AGGCAGGCAG	ATCACCTGAG	5760
GT TGGTAGTT	TAAGAGCAGC	CTGACCAACA	TAGAGAAACC	CCATCTCTAC	TAAAAATACA	5820
AAATTAGCCA	GGTGTGGTGG	CACATGCCTG	TAATCCCAGC	TACTCTGGGG	GCTGAGGCAG	5880
GAGAATCGTT	TGAACCTGGA	AGGCAGAGGT	TGCGGTGAAC	CGAGATCGTG	CCATTGCACA	5940
CCAGCTTGGG	CAACAAGAGC	AAAAC TCCGT	CTCAAAACAA	AACAAAACAA	AAATGAAAAC	6000
AAACAAAAAA	ACACCAACAT	GATTAGGAGG	GAAAAAATCT	AGATAGAAAG	GCTTAACAGG	6060
GCCGGGCACG	GTGGCTCATG	CCTGTAAGCC	CAACACTTTG	GGAGGCCAGG	GTGGGAGGAC	6120
TGCTTGAGGC	CAGGAGTTTG	AGACCAGCCT	GGGCAACTTA	GCGAGACTCT	GGTAGTCTGT	6180
CTCTACCAA	CAAACAAACA	AACACCTGAT	TAGCTGGGCA	TGGTGGCATA	TGCCTATAGT	6240
CCCAGCTACC	CGGGAGGCTG	AGGCTGGAGG	ATCGCTTGAG	TCCCAGAGGT	CAAGGCTGCA	6300
GTGAGCTGTG	ATCAGGCCAC	TGCACTCCAG	CCTGGGCGAC	AGAGCATGAG	TCTGCCCCAG	6360

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CCCTGCCTCC	AAAAAAGAA	AGGCTAAATA	GGAGAACTGA	TATAACTGAA	AACCAAATTA	6420
GTTGTGTGAA	AGAGCAACTG	TCCTGGAAGC	TCCCAGAACA	CAGAGCAATA	AGAGATGAAA	6480
AATATGACAG	CATAGAAAAG	AAAGGAACTG	GATAGGTCCA	GGAGATCCAA	TACCTGTGCA	6540
ACAGGAGAGT	CCAAAGAAGA	AACCAGTAAG	AAGGGAGAGA	AGTAATACAA	GAAAGTTCCT	6600
GAGTTATCAG	GCCAAAAGAA	ATAATCTAGT	TTGTGGAGTA	ATATTGACAA	AAAAATCTTT	6660
ACACCTAGAT	GTATTCTGAA	AAAATCTTAA	AATTCTAATT	GAAATCAACC	AACGAACCAC	6720
AGGCCAGCCT	TAGAAAACCA	TTTCCAGGGC	ATGGGGTTTT	AGGGTCTGAC	AGACCTGAAG	6780
TTCAAATTCC	TACTATCCTA	ACTTACTAGT	AGTGTGATAA	TCTCTTAGAA	CAATGTATGA	6840
AATGGAAGCA	TAATAGCACC	CTCCACCTTT	TAGAGTTAAT	GGGAGATCTA	AAAGAGGTAA	6900
CATTTGCAAA	GTGTCTGACA	TGAAGGGAAG	AGATTGGCTT	TGGCATCCAC	AAGTTCACAC	6960
ACTAGCAGAG	AACCTCAGTC	CAGCTTCCTA	CGCTCAGGCA	GTTCTTTGCC	TAGAAGAGGG	7020
GTCGGCAAAC	TATAGCCCAA	ATTTAGCCCA	CTGCCTGTTT	TTGTAAATAA	AATGCTATCA	7080
GAACATGGCC	ATGTTCATTC	ATTTACATAC	CATCTATGGC	TGCTTTTACA	TTACAAAGGC	7140
AGAGCTGAGT	AGATGAGACA	GAGACAGTAT	GGTTACAAAC	CGAAACTGTT	TCAACCCCAA	7200
CTTCATTCCA	GCAAAGTTTT	ACTTTCTAGA	TTCAGGCCAG	GGAGCAAGCA	TGAAAATGAA	7260
AACCACTAAA	ATGGTGTCCT	GGGACAACAG	ATACCTACTT	GCTATAACTT	CTTTCCTTGA	7320
AAACAAAGGG	CCATATTAAT	TGAAGGGCTC	ACCTCTAAAC	AGGTGAGTGA	CTTAAGGACT	7380
TCAGACACAC	ACTGGTCAAC	TACAACTAG	TCAGTAAAGG	AATAGCCATA	GTCTTATAGC	7440
CCCAGTTCCT	ATGGCCCAGG	GGGATCCACT	AGTTCTAGAG	CGGCCGCCAC	CGCGGTGGAC	7500
TCCAG						7505

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(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 529 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GCTGAGGTGC ATCGCGGTGG CGGACGCTCT AGAACTAGTG GATCCCCAAA CAAAACCTGT	60
CCCTGCTAAT GATGGTAGAC CCAATCAGAT CCCCGAGAGAA GCCGAAATAC GGAAACCATA	120
TCAGCATACG CATGGCATAAC ATAGAACCCC ATACATGGAT TGCTTACTCA GCCAGATATA	180
GAAATCTATC TTCACGATAG AGATATATAT ATATAGACAC ACTGCATATA CAGATGTGAG	240
ATGGAGGCTC ACTCTGCCAC CCGTGCTGGA TCTACAGTGG CACAAGCTCA GTCCACAGTC	300
ACGTCGATCT GCCGGGCGTG ACCGACTGAG ATGCAGCGGC CTCGGGCGTA GCTGTGAGTA	360
CACGCACCAG TCATCGCGAC TGGCTGCAAG TGGTATAAGC GGAGGGGACA GGGTTACAGC	420
ATGACGGCTA GGCAGGCCGC AACTGAGGA CCACAAGAGT GCCACGCTGC CCGAACGCAT	480
GCAGTGGCGA GATTACATGG GGCAGCCACT AGAGCCGCCG TATCAGAAA	529

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 635 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TACCACGCGG TAGCGCCGCT CTAGAACTAG TGGATCGGGT AATCCAGCAC TTTGGGAGGC	60
CAAGGAGGGC AGATCACCTG AAGTCAGGAG TTTGAGACCA GCCTGGCCAA CATGGTGAAA	120

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CTCCATCTCT ACTAAAATTA CAAAAATTAG CCGGGCGTGG TGGCGCATGC CTGTAATCCC	180
AGCTACTCGA GAGGCTGCGG CATGACAGTC ACTCAAGCCC GGGAGGTAGA GGTGTCAGTG	240
AGCTGAGATT GTGCCACTGC ACTCCAGCCT GGGTGGCAGA GTGAGACCCT GTCTAAAAAA	300
AAAAAAAAAA AAAGGCCCAT TAGGGGACCC AAACGGTTCC CCAGCTTTGT TGGATTTCCT	360
CAAATTTGGG GCCAATTTTT GGAGGGTTGT CCCTTAAAAA TTTAAATTTG GGGGTTTTTT	420
TCCAGGCGCC CATTAGAAAT GGGTTCCGAA AATTTTTTGG CAAAAAAAT TTGGTTTAAC	480
CGCGGACCAA AATCCTAAGG TTTAACTTTT TCCTAAACCT TTTAGAATTT AAAGTTCCG	540
GGGTTTCTCA GGAGGGGGTA ACCCTTCACC CCAATATAAC TCGGAAACCC CCCTTTTTTA	600
GGAAAAGGGG AATTAGTGGT GCTTCCGGG CAAA	635

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 938 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CCCAGGGACC AAGCGAGTGC GACCGCTCTA GAACTAGTGG ATCCCCCTTG AAGACTATAT	60
TTCTTTTCAT CACGTGCTAT AAAAATAATT ATAATTAA TTTTAAATA TAAATATATA	120
AATTAAAAAT AGAAAGTAAA AAAAGAAATT AAAGAAAAA TAGTTTTTGG TTTCCGAAGA	180
TGTATAATAG GTTGAAAGTT AGAAATTATT ATTATAATAG CAAAAAAAT TTAAAGTTAG	240
AAATTAGAAT TTAAGGCTCT ACACACGTTT ACGATGATAT TGGACGAACG ACACGATTAG	300
ACAGTTGTAG GTTGTGTGTT GTGATGTTTT TGAGTGATTT GTAGTGTTA ACCTTGTTGGT	360
TTGGAAAGGT NGTATGAGTA TTAATCTCGG GCTTATTGGG AGGTTTATGT GCAATGCATT	420
TTGTGGTTTT TTTATAATGT TGTGTTTAGG GTTAAACCT GTTGTGTATA TTGTGTTGGT	480

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TTGTTGCTTG TTTGTACATT GGTATGATGC CTNTTTTGCT TATGGGTTNG GTGTTTGATT	540
TTGGTTGTGT TTTTGTGGT GTGTTGTTG ATAGTTTATAG CGGTTGTTTT TGGGTTGTTG	600
TTTTATGTTG TGGTGGTGT TTGTGTGTAG AGTTGTGGTT TGTGTGTTTT GTTGGTTGTG	660
TTGTGGTATT GTTTATGTTT GTCGTGTGTA TGGTTTGTG TTAGTCGTTG TTGTAGGCTT	720
GTGTGTTGTG TGTTGTGTGT GCGTGTGGTC TAGTTTGGGT GGTATTGTTG ATTTAGTGTG	780
ATAGTCTGTT AGAGTTTGGG TTGTTGTGTG TATTGGGTTT GTCTGTGTGT GGTTTTTTTG	840
TGGGTGTAGA TGATGATTG TGTATGTGGG TGAGGTATAT GTTATTTGTG GTATTTCCGT	900
TGTGATGTGT TGGTTATTAT GTGTTTGTTA TGTGTATT	938

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1145 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GTCTCCGAGC TCACCGCGGT GCGGCCGCT CTAGAACTAG TGGATCCCC GCTCTCACTC	60
CCTGACTCTT GCCTTCTGTA ACAACTGGAG ACAACTCTTT CAAAACCAGC TCCAAGCCCC	120
AGACTTCTCT CTGGGCTTTA GTTCGTAAGG CAGGTGCCCT ACTGAGTGAG CCTAGATCAG	180
ACAGAAACAT AGCTGTTGGC AAGGATTTAG GTGAATTTCC TTCCATTGTT TTTCTAATAC	240
CTTTTTTTTT TTTTGAAAA TATAACCATG CACCTACACA CATATTTGAA TATCCTGCCT	300
TTTTATTAA AATGACATGA TAGGTCCGGG AGTGGTGGCT CATGCCTGTA ATCCCAGCAC	360
TTTGGGAGGC CGAGGTGGGC AGATCACCTG AGGTCAGGAG TTCGAGACCA GCCTGGCCAA	420
CATGGTGAAA CTCCATCTCT ACTAAAAATC AAAAATTAGC CGGGCATGGT GGCAGGCTCC	480
CAGCTACTCA GGAGGCTGAG ATGTGAAAAT CGCTTGAACC CGGGAGGTAG AGGTTGCAGT	540

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GAGCTGAGAT CTTGCCATTG CACTCCAGCC TGGGCAATAA GAGCGAACT CCATCTCAAA	600
AAAAAAAAAA AAAACCCAGG GATAAACTTT CCAAAAAGGCC CAAAAAGGG GCATGATTAA	660
GACAATAAAT TAGTCGAAAA TTGTCAATAT AAATGAATAA TAATTTTTTTT GGCCATTCTG	720
CCAAGTGGCA TAACCCGTGC ATTCTGCCCA TTCGGCAACT CTTTTTCCTC CCGGGGAATC	780
GCTCCCACTT TTTGCATGGG TTTTGGATGG AACTGTTGGT CACAGGTTTT TCACCCCAT	840
TTGGCCCTCC CAGAGGTGTA CAAAGTACCC CAGCCTGGCC CTTTTTCACC CAATTTTCCC	900
AGGTATATTC CCCC GGTTTTT GTTCCAGGT TTTAACCCCC CCCTCCAAAG GGCTTTGGGT	960
TTTGAAGGA TTAAGTCCTC GAAATAGGCC CCTCATAATA CCTGGGGGGG GGACCTTTTTT	1020
CAAAGTTGTG GGCACCTCTT GTGTCGCCCC CACGGGGGAC TGATGTATTT ACGCCCCNTT	1080
GGGGNNTAAT ATGGATTGNT ATGTATTGGG CGAGGAGAAA ATATTTTGA TGGGGTTTTT	1140
CTCTT	1145

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 852 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TCACCGCGGT GGCGCCGCT CTAGAACTAG TGGATCCCC GTTTTGCTCT CTCCTTAGAA	60
TGAGCTGGGA ACTAGTCACT CTTGTTTTCT CACCTATAAT AGCATCTGGG TCCAGTGT	120
TTTATGTGGG ACAAATTTGA ACTTGTGGTC AACCTCTTTA ATTGTAAGAA TATTCAGGTC	180
TTTTGTCTT CCTGGGCTAG TTTTTATTC TTTTCTAGA GATTCGTTCA TTTTCTTAG	240
TTTTATTTGC CTATAATTGT GGATAATCTG TTTTTATCT GCTACTTCTG TAATTATTC	300
CACATTTGAT TTATAATATT AACTTGTGGG CCAGGCGTCG TGGCTCACAC CTGTAATCCC	360

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AGCACTTTGG GAGGCCGAGG CGGGCGGATC ACGAGGTCAA GAGATTGAGG TGAAACCCCC 420

TCTCTACTAA AAGTAGAAAA ATTAGCTGGG CATGGTGGTG CGTGCCTGTA ATCCCAGCTA 480

CTCAGGAGAC TGAGGCAGGG AATCTCTTGA ACCCAGGAGG CAGAGGTTGC GGTGAGCCAA 540

GATTGCACCA CGGCACTCCA GCCTGGTGAC AGAGCGAGAC TCCATCTCAA AAAAAGAAAA 600

AAAAAAACT GTCAAATGAT ACTCCAAAAT GGTGTACCA TTTTATATTT GCAACAACAA 660

TGTCTGAGGG TACTGATTGC TCCATATCCT TGACAGCACT TGGTATAGCC GATCCTTTAA 720

TTTtagGCAC TTTAAGGGGG CAAATACCTG GGATTTTAA GGTTTAACCT TTTTATTTTC 780

CCAAATGGGT TAATAGGTTT TCAGCAACTT TTCAAGGGGC CTAATCCCC CCTTCAAAAT 840

AACCTCCCCT GG 852

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1854 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CCGGCACTCA CCGCGGTGGC GGCCGCTCTA GAACTAGTGG ATCCCCGAA ATGTTACTTC 60

CAACATTTTA GAACTGAAAT GATTCTTAGT CTGGTGATAA ATGTCAATTA AAATAGTTCT 120

CCTTTCACAG AGAAAATTAA GAAAAAATTA GTTCAAGAAA ATATCAATCA TGATTGCCAG 180

CGGAAATTTG TTTCTGCAGT AAAACAAGCA AAACAAATCA AATCCATTAA AACTAGCAAC 240

AGACTGTCTT CTAAAGTCAA GTTCACATCT GGAGATTTTT ATAAACTTTA TTGGAAAAGT 300

TCTGGTTATC TATATTTTTA GCATAGCAAA ATATTCTTCT TGTTGTTGA ATTTGATATA 360

AAATGTTATT TTTAGCCAAG TCCTGGGGCA ACTCCTACAT GGCTGGAAAA TGTTCCTCGGT 420

GTTAACAAG ATGCAAAGAT CTAAATATT AATGTTATCA ATCAACTGGA TACTCTTAAG 480

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TATTATTTGT AATTATGTCC AATGTCATCA CCACAGGGCT GACCAACAAG CAAAGAGCTG	540
ACAGTAGTAG CAAAATGTAG AAATCTCTGG TAAGCATGTT GTGTTTATCA ATCCTCTTCA	600
AATAGATGAA ATTAAATTGC ATTTAAAGAA TGTTACTTAT ATTAGGCATT TTTTGTGAAA	660
GACGTTTTAA ACTATGGTGT CAGAAAACAG AAATACTAAA CAGAATGCAT TTAACAGGAC	720
CTTGAAATCA CTGAATACTC ACCTGTGTAA AAGTCAAAGT TCAGATAATT GAAATGTTCT	780
TACTAGTCTC AAGATGTCTT TTGGTTACAT AGAAATTTC ATGCTGAATT TTGATTTTTT	840
TAAAAAGCCA TTAATATGAG TCAAAATCCA TTATTTTACA AGTAAATGAC CTTTTTATTA	900
AAAAAAAAAA AGAGAGAGAG AGAAGAGCAA GGAACCACCC ACATCTAACC TCTTAAATCT	960
GAGATCAATA TATCAAAATT TTAATGTACA TTGAAAACAT TTTCATTTTA TTCCACACAC	1020
TACCTTTTCT TCATAATTTT TTATTCTGGA CATATAGCAG TTTTTTTTGT CTTTTAAAC	1080
AGGAAAAATA AACAAACATG GTCTTATTAT TGTTACTAAG TCACAGGTAG TAAAGATGGG	1140
ACCAGGAGAA CCTTGAGGGA CTAGAACTT CTCAAGAGTA GTTAGATTTC ACATTCAGAG	1200
GGAGGACTCA GAGTCCTGCC TGGGACATAC ATTTGCATTC TAGGCTCAAG AGCAAATATG	1260
TCAGCTTTCC TTTGGTCAAA CAATCTTGC TACAGGTCCT AGGTAGTTAT ATCAGTGGAA	1320
CCTACTAAAG ATGATGGAAT TTGTGGTATT TCAGGGTAGG AGGTAAAGTC TTAGCAGGCT	1380
CAACTATACA TGATCTTAAA ACTAAATTTG AAATGCAGAT GTTCTATGAG TTAGTTGGAT	1440
ATTGTAGTTA TCCCATCTAT CAACTGATCA CATTTGGTAT GAGCTTGTTA GTTCTGATTA	1500
GGACTCATCT CAACATAATA AGAAGGGTGG CATTTAGGGC CCAGTGTGGG GGCCTAGTGA	1560
TCACTGCTGG GACACTGCTT CTAAATCAAC ATAATAACC TCTCTAGGAT GGCAGGCTGA	1620
GGCTGCTCAA GTACTTCCTG TCTGGCATCT GGGACAGGGC TGAGTCTCTG GGTGGGAAGA	1680
TGGGTGGGAG GACTGAGGCT GATGAGTATA TGATATAAAT GAGAGCCATT GGAATGGCTC	1740
CACATACAGG ACATGTTGAT AAATCATTTT AACATATTTT GCTTCTCTC TCTGGTGGCC	1800
CATTGAGAAT CAAAAGGGGG ATCCACTAGT TCTAGAGCGG CCGCCACCGC GGTA	1854

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(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1101 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

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CCACCTTTTC AATTCATCAT TTTTTTTTTA TTCTTTTTTT TGATTTTCGGT TTCCTTGAAA      60
TTTTTTTGAT TCGGTAATCT CCGAACAGAA GGAAGAACGA AGGAAGGAGC ACAGACTTAG      120
ATTGGTATAT ATACGCATAT GTAGTGTGTA AGAAACATGA AATTGCCCAG TATTCTTAAC      180
CCAACTGCAC AGAACAAAAA CCTGCAGGAA ACGAAGATAA ATCATGTCGA AAGCTACATA      240
TAAGGAACGT GCTGCTACTC ATCCTAGTCC TGTGTGTCGCC AAGCTATTTA ATATCATGCA      300
CGAAAAGCAA ACAAACCTGT GTGCTTCATT GGATGTTCGT ACCACCAAGG AATTACTGGA      360
GTTAGTTGAA GCATTAGGTC CCAAATTTG TTTACTAAAA ACACATGTGG ATATCTTGAC      420
TGATTTTTCC ATGGAGGGCA CAGTTAAGCC GCTAAAGGCA TTATCCGCCA AGTACAATTT      480
TTTACTCTTC GAAGACAGAA AATTGCTGA CATTGGTAAT ACAGTCAAAT TGCAGTACTC      540
TGCGGGTGTA TACAGAATAG CAGAATGGGC AGACATTACG AATGCACACG GTGTGGTGGG      600
CCCAGGTATT GTTAGCGGTT TGAAGCAGGC GGCAGAAGAA GTAACAAAGG AACCTAGAGG      660
CCTTTTGATG TTAGCAGAAT TGTCATGCAA GGGCTCCCTA TCTACTGGAG AATATACTAA      720
GGGTACTGTT GACATTGCGA AGAGCGACAA AGATTTTGTT ATCGGCTTTA TTGCTCAAAG      780
AGACATGGGT GGAAGAGATG AAGGTTACGA TTGGTTGATT ATGACACCCG GTGTGGGTTT      840
AGATGACAAG GGAGACGCAT TGGGTCAACA GTATAGAACC GTGGATGATG TGGTCTCTAC      900
AGGATCTGAC ATTATTATTG TTGGAAGAGG ACTATTGCA AAGGGAAGGG ATGCTAAGGT      960
AGAGGGTGAA CGTTACAGAA AAGCAGGCTG GGAAGCATAT TTGAGAAGAT GCGGCCAGCA     1020

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AAACTAAAAA ACTGTATTAT AAGTAAATGC ATGTATACTA AACTCACAAA TTAGAGCTTC 1080

AATTTAATTA TATCAGTTAT T 1101

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

AACTAATGTA TCCCCCGGGC TGCAGGAACA CGATATAAAG CCTTAAAATT GTGCGAATGT 60

GRTAAGTCGA TCCAATCTCA ACTGCTATCT RTGTACCAGA ATAGTTTCAT AATTACGTGT 120

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GAATTCTCTG WKATTAKAAC TATCTTGMCT CAAATTSACT TGGTGAGCTA ACCTGGCCTG 60

TGGTCCCTTG GCTTTAATGG AGGCTTTGTC ATATAGATCA TMTGTGGTAC TKGTGCCTAG 120

TTGTAGTGCC CTGCCTTGCT STTCTWGGCT TACTKGATTT WGGGGTATAC ATCWATKTAA 180

YTSAAAGGTC TTTCTCCTCC CGYYGGGAGA ATTTCTCCTC CTCCCTCGGA GAACTCTTTC 240

TSCCGAAATT CTATTCCGGG CTGGGTCTCC ATTC TGCTTA CCTCCACAC TTTTAATMAA 300

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(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 599 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

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GAATTCCTC TTGCTTGGG GAGGTCAGCC TTTTGTCTA TTCAAATCTT TGAGGAAAAT      60
AGAAAGCAAA GAATATATTA ACTATATTAA ACAAATAAA TGTTCCAATT AAAATACAAA      120
AATTATAAAG CCTAATAATA AAAGCCCTCA ATTATATGCT GTTTAAAAGA GACATTTTTA      180
AGCTTAAGGA TATAGAAAAG TTGAAAATAA AAGAATGGAA TAAAATAAGC CATGAAAATA      240
CTAGTATAAC ACTGATGTCA AAATCTGACA AAGCACACAA AAAAGAAAAT AACTTTAACT      300
GCAAAATCTT AAAATCCTAG CAAAGAAAAA GCAGCATATG TTATAATTAT ACCACAACCT      360
GATCAAGTAA GGCTTACTTC AAAAATTTAA CCATGGTCCA TTATTGGAAA ACATATTAAT      420
AAAAATCCTC ACAAAAATAA TTCAAAATAT AAAAAGCCAT ATGATAAGCC TGATGAATGC      480
TGGTTTACAG AACTGGTTTT CTTTAAAAAG GCAATCATTG GGGAAATAAC CCGCTTACTC      540
AGTATTTACT ATGTGCTAGC CCTGTTCTT CTACTAGAAA TTAGTGAACA AATTCTAAC      599

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(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

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AAGCTTTCAA GAACAGGGAC TGTTAAGCCG GGTACAGTGG CTCACACCTA TAATCCTAGC      60

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ATTTTGGGAG GCCAAGGCGG GTGGATCACT TGAGGTCAGG AGTTCAAGAC CAGCCTGGCC	120
AACATGGTGA AACCCCATCT CTACTAAAAA AAAAAAAAAA AAAAAAAAAA AAAGAAATWC	180
MAAAATTACC CAGGCATGGT GGCACGCGCC TGTAATCCCA KCTACTTGGG AGGCTGAGGC	240
AGGAAAATTG CTTGAACCTA GGAGGCGGAG GTGGCAGTGA CCTAATCACA CCACTGTTCT	300
CCATCCTGGG CAACAGAACG AACTGTTTC	330

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

AAGCTTGGGT GATAATGAGG AGTCAATGTT GGTCCATCAA TTGCAACAAA GGTACCACAG	60
TGGTGTAGGA TGTGGATAAT GAGGAGGCTG TGCACGTGTT GGGGACAGGT GGTATTTACG	120
AATGCTCTAT ATTTCTTTC TCTCTTTTTT TAGGACGGAG TCTCACTCTG TTGCCCACGC	180
TGGAATGCAY GGGCATGACT GTGGCTCACT GTACCCCCCA CTCCCCATGT TCAAGAGATT	240
CTCTTGCCTC ACCTCCTG	258

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 622 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CTCGAGTCCA CCGCGGTGGC GGCCGCTCTA GAACTAGTGG ATCCCCCGAT TTATTTAAAG	60
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CAGTTATGTA TGTATGAAAA ACAATGCTGA GCATTCAATT CCAAGATTTC TGAAGACACC 120
 TATTTTACCA TCACTTTGAA TAAAATTTT ATATTCCTTT CTTCAAATAC CATCTCGGTT 180
 TTCAAATGTG GCTCATTAAA TGTGAAAGCA AAATTCATT TCAAATAGCA GCCTTATCAA 240
 ATGACAATTT ACCTGTGGTA GCATTGTTGG CACTGACACA TATCAGACCA CTGCCGAGCA 300
 GAACAAGAAT GAACCAGGAA TCCATGCTTA TCTGGAAAAT AGGGAGTCAT GTTAGATGAG 360
 GTCCTATATT ATCAGGACTA TGTCTGAGCT GGTCACCAGA AGAGTATTCT GGATTTCCAA 420
 GCTATTAAAA TGTGTGCCTA AACCAATGAT CTTTGGGAG CCTGATATGC ATGCTTCCTC 480
 AGATATCCAA TAACTAATTG AGTCTTTATA AAGACTGACT ATCCCTTATC TTGAGGACTA 540
 GCAGTGTTTC AGATTTTTTT TAAGAGATAG GGTCTTGCTC TGTTGCCAGG ATGGAGACAG 600
 TGGTTATGAT CATAGCTCAG TG 622

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 602 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TCGGACTCCA CCGCGGTGGC GGCCGCTCTA GAAC TAGTGG ATCCCCGGG CCCTCAGGAC 60
 TGCTGGGCTG CCTGGTGTCA GCACTTCCCG CCATTTTCTA TAGCACCAGT ATTATTCTTA 120
 ATACTTTAAA AAACCACCAG GCACGGTGGC TCACGCCTGG AATCCCAGCA CTTTGGGAGG 180
 CCAAGGTGGG CGGATCACAA GGTCAGGAGA TCAAGACCAT CCTGGCTAAC ACGGTGAAAC 240
 CCTGTCTGTA CTAAAAATAG AAAAAATTA GCTGGGCGTG GTGGCATGCA CCTGTAGTCC 300
 CAGCTGCTGG GGAGGCTGAG GCAGGAGAAT GCGTGAACC CGGGAGGCGG ACTTGCA GTG 360
 AGCCGAGATT GCACCACTGC ACTCCAGCCT GGGTGACAGA GCGAGACCCC GTCTCAAAAA 420

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AAAAAAGTAA ATAAAAATAA AAAACCATAT CCCACTATCT CCCCCTTCTC TCTTTGCCTG 480
 TGACTANNNG GCATACTTAT GGGGAAATCT TTAAGATGTC AGATTTCAGT TCTCTCACTT 540
 TTCTACAAC TCTCCCCATT TTGCCTTTCT TAGGAACTTC CCTTCTTCCC ATCTGATTCC 600
 TN 602

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 546 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

TATCAAGGCG GAGTCCACGG TGGCGGCCGC TCTAGAACTA GTGGATCCCC GAACCAGGAA 60
 TCCATGCTTA TCTGGAAAAT AGGGAGTCAT GTTAGATGAG GTCCTATATT ATCAGGACTA 120
 TGTCTGAGCT GGTCAACCAGA AGAGTATTCT GGATTTCCAA GCTATTAAAA TGTGTGCCTA 180
 AACCAATGAT CTTTGGGAG CCTGATATGC ATGCTTCCTC AGATATCCAA TAACTAATTG 240
 AGTCTTTATA AAGACTGACT ATCCCTTATC TTGAGGACTA GCAGTGTTTC AGATTTTTTTT 300
 TAAGAGATAG GGTCTTGCTC TGTGCCCAG GATGGAGACA GTGGTTATGA TCATAGCTCA 360
 GTGCAGCCTC TACCTCCTGG ACTCAAGTGA TCCTTCTGTC TCAGCCTCCT GAGTAGCTGG 420
 GACTATAGGC ATGTACTACG ATGCCTGGCT AATTTTAAA ATTTTCTGTA GAGACGGCGT 480
 CTCACTATGT TGTCTAGGCT GCTCTCAAAC TCTTGGGTTC AACTGATCTC TTGCTTCAAC 540
 TTCCAG 546

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(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 498 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GTGGATTCAG ACGCGGTGGC GGCCGCTCTA GAACTAGTGG ATCCCCCGAG CAGAGGTTGC	60
AGTGAGCCAA GATCGTGCTA CTGTACTCCA GCCTGGGCAA CAGAGCAAGA CTCCGTCTCA	120
AAAAAAAAAA CAAACAAACG ATGTGTGCCT GTGTTTCCTC ATCTGTAGTA TGAGGATAAT	180
GATCATATAT ATTTACTAGT GTTGTGGGA TGATCAAATT AGGTATATTT AATCATTGTG	240
TAAAAAAGTT GACGTGTAAA ATCCATGTAA AAAAGTTGGC AGAAGAGACA AACTGGTAAA	300
GCAGCCGTTT TTCATTTCTC ATTTCAATCA ACAAGCATTA TTAACAGCCT AGCAAGAACA	360
CAGTATCCAG GAAAAATCAA AGATTATCAA GCTCATGTTC TATAATCAAG CAATTTATAA	420
ACTAGCAGAA GAACAAGACA GATGAATAAG AACTTGGGTA TATTTAAATG CTAAGAAGTT	480
CAATTCAAAT AAATGTCC	498

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CLAIMS:

1. An isolated nucleic acid molecule comprising a sequence of nucleotides derived from a eukaryotic chromosome and encompassing a neocentromere or a functional derivative synthetic or hybrid form thereof which nucleic acid molecule or its derivatives, synthetic forms or hybrid forms when introduced into a compatible cell is capable of replicating, acting as an extra-chromosomal element and segregating with cell division.
2. An isolated nucleic acid molecule according to claim 1 wherein the eukaryotic chromosome is a mammalian chromosome.
3. An isolated nucleic acid molecule according to claim 3 wherein the chromosome is a human chromosome.
4. An isolated nucleic acid molecule according to claim 2 wherein the nucleic acid molecule is capable of associating with centromeric binding proteins (CENP)-A and -C or antibodies thereto.
5. An isolated nucleic acid molecule according to claim 4 wherein the chromosome is human chromosome 10 or a modified form of human chromosome 10 or its non-human mammalian or non-mammalian equivalent.
6. An isolated nucleic acid molecule according to claim 5 wherein the nucleotide sequence corresponds to a region mapping between q24 and q26 on chromosome 10.
7. An isolated nucleic acid molecule according to claim 5 wherein a modified form of human chromosome 10 is a mardel (10) chromosome.
8. An isolated nucleic acid molecule according to claim 6 comprising a nucleotide sequence substantially as set forth in SEQ ID NO: 3 or a nucleotide sequence having at least 40% similarity thereto or a nucleotide sequence capable of hybridising to SEQ ID NO: 3 under low

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stringency conditions at 42°C.

9. An isolated nucleic acid molecule according to claim 7 comprising a nucleotide sequence substantially as set forth in SEQ ID NO: 4 or a nucleotide sequence having at least 40% similarity thereto or a nucleotide sequence capable of hybridising to SEQ ID NO: 4 under low stringency conditions at 42°C.

10. An isolated nucleic acid molecule according to claim 7 comprising a nucleotide sequence substantially as set forth in one or more of SEQ ID NOs: 5-29 or a nucleotide sequence having at least 40% similarity thereto or a nucleotide sequence capable of hybridising to one or more of SEQ ID NOs: 5-29 under low stringency conditions at 42°C.

11. An isolated nucleic acid molecule according to claim 1 wherein the length of the nucleic acid molecule is from about 50 bp to about 1500 kbp.

12. An isolated nucleic acid molecule according to claim 11 wherein the length of the nucleic acid molecule is from about 1 kbp to about 1000 kbp.

13. An isolated nucleic acid molecule according to claim 12 wherein the length of the nucleic acid molecule is from about 10 kbp to about 500 kbp.

14. An isolated nucleic acid molecule according to claim 13 wherein the length of the nucleic acid molecule is from about 10 kbp to about 100 kbp.

15. An isolated nucleic acid molecule comprising a nucleotide sequence encompassing a neocentromere or a functional derivative, synthetic or hybrid form thereof which when said nucleic acid molecule is in linear form and co-introduced into a cell together with a telomeric sequence, is capable of replicating, remaining as an extra-chromosomal element and segregates with cell division.

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16. An isolated nucleic acid molecule according to claim 15 wherein the nucleotide sequence is derived from a mammalian chromosome.
17. An isolated nucleic acid molecule according to claim 16 wherein said nucleic acid molecule is capable of associating with CENP-A and CENP-C antibodies.
18. An isolated nucleic acid molecule according to claim 16 or 17 wherein the mammalian chromosome is human chromosome 10 or a modified form of chromosome 10 or its non-human mammalian or non-mammalian equivalent.
19. An isolated nucleic acid molecule according to claim 18 wherein the nucleotide sequence corresponds to a region mapping between q24 and q26 on chromosome 10.
20. An isolated nucleic acid molecule according to claim 18 wherein the modified form of human chromosome 10 is mardel (10) chromosome.
21. An isolated nucleic acid molecule according to claim 18 comprising a nucleotide sequence substantially as set forth in SEQ ID NO: 3 or a nucleotide sequence having at least 40% similarity thereto or a nucleotide sequence capable of hybridising to SEQ ID NO: 3 under low stringency conditions at 42°C.
22. An isolated nucleic acid molecule according to claim 19 comprising a nucleotide sequence substantially as set forth in SEQ ID NO: 4 or a nucleotide sequence having at least 40% similarity thereto or a nucleotide sequence capable of hybridising to SEQ ID NO: 4 under low stringency conditions at 42°C.
23. An isolated nucleic acid molecule according to claim 19 comprising a nucleotide sequence substantially as set forth in one or more of SEQ ID Nos: 5-29 or a nucleotide sequence having at least 40% similarity thereto or a nucleotide sequence capable of hybridising to one or more of SEQ ID Nos: 5-29 under low stringency conditions at 42°C.

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24. An isolated nucleic acid molecule according to claim 15 wherein the length of the nucleic acid molecule is from about 50 bp to about 1500 kbp.
25. An isolated nucleic acid molecule according to claim 24 wherein the length of the nucleic acid molecule is from about 1 kbp to about 1000 kbp.
26. An isolated nucleic acid molecule according to claim 25 wherein the length of the nucleic acid molecule is from about 10 kbp to about 500 kbp.
27. An isolated nucleic acid molecule according to claim 26 wherein the length of the nucleic acid molecule is from about 10 kbp to about 100 kbp.
28. An isolated nucleic acid molecule or its chemical equivalent encompassing a human neocentromere or a functional derivative thereof or a latent, synthetic, hybrid or its mammalian or non-mammalian homologue.
29. An isolated nucleic acid molecule according to claim 28 wherein said nucleic acid molecule when introduced into a compatible cell is a replicating, extra-chromosomal element which segregates with cell division.
30. An isolated nucleic acid molecule according to claim 29 wherein the nucleic acid molecule is capable of associating with centromeric binding proteins (CENP)-A and -C or antibodies thereto.
31. An isolated nucleic acid molecule according to claim 29 or 30 wherein the chromosome is human chromosome 10 or a modified form of human chromosome 10 or its non-human mammalian or non-mammalian equivalent.
32. An isolated nucleic acid molecule according to claim 31 wherein the nucleotide sequence corresponds to a region mapping between q24 and q26 on chromosome 10.

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33. An isolated nucleic acid molecule according to claim 31 wherein a modified form of human chromosome 10 is a mardel (10) chromosome.

34. An isolated nucleic acid molecule according to claim 31 comprising a nucleotide sequence substantially as set forth in SEQ ID NO: 3 or a nucleotide sequence having at least 40% similarity thereto or a nucleotide sequence capable of hybridising to SEQ ID NO: 3 under low stringency conditions at 42°C.

35. An isolated nucleic acid molecule according to claim 32 comprising a nucleotide sequence substantially as set forth in SEQ ID NO: 4 or a nucleotide sequence having at least 40% similarity thereto or a nucleotide sequence capable of hybridising to SEQ ID NO: 4 under low stringency conditions at 42°C.

36. An isolated nucleic acid molecule according to claim 32 comprising a nucleotide sequence substantially as set forth in one or more of SEQ ID Nos: 5-29 or a nucleotide sequence having at least 40% similarity thereto or a nucleotide sequence capable of hybridising to one or more of SEQ ID Nos: 5-29 under low stringency conditions at 42°C.

37. An isolated nucleic acid molecule according to claim 28 wherein the length of the nucleic acid molecule is from about 50 bp to about 1500 kbp.

38. An isolated nucleic acid molecule according to claim 37 wherein the length of the nucleic acid molecule is from about 1 kbp to about 1000 kbp.

39. An isolated nucleic acid molecule according to claim 38 wherein the length of the nucleic acid molecule is from about 10 kbp to about 500 kbp.

40. A genetic construct comprising an origin of replication for a eukaryotic cell and a nucleic acid molecule encompassing a eukaryotic neocentromere or a functional derivative thereof or a latent, synthetic, hybrid form thereof or its mammalian or non-mammalian homologue flanked by telomeric nucleotide sequences functional in the cell in which the genetic construct is to

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replicate and wherein said genetic construct when introduced into a cell is a replicating, extra-chromosomal element which segregates with cell division.

41. A genetic construct according to claim 40 wherein the eukaryotic neocentromere is a mammalian centromere.

42. An isolated nucleic acid molecule according to claim 41 wherein the neocentromere is a human neocentromere.

43. An isolated nucleic acid molecule according to claim 42 wherein the nucleic acid molecule is capable of associating with CENP-A and -C or antibodies thereto.

44. An isolated nucleic acid molecule according to claim 43 wherein the neocentromere is from human chromosome 10 or a modified form of human chromosome 10 or its non-human mammalian or non-mammalian equivalent.

45. An isolated nucleic acid molecule according to claim 44 wherein the human neocentromere maps to a region between q24 and q26 on chromosome 10.

46. An isolated nucleic acid molecule according to claim 44 wherein a modified form of human chromosome 10 is a mardel (10) chromosome.

47. An isolated nucleic acid molecule according to claim 45 comprising a nucleotide sequence substantially as set forth in SEQ ID NO: 3 or a nucleotide sequence having at least 40% similarity thereto or a nucleotide sequence capable of hybridising to SEQ ID NO: 3 under low stringency conditions at 42°C.

48. An isolated nucleic acid molecule according to claim 46 comprising a nucleotide sequence substantially as set forth in SEQ ID NO: 4 or a nucleotide sequence having at least 40% similarity thereto or a nucleotide sequence capable of hybridising to SEQ ID NO: 4 under low stringency conditions at 42°C.

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49. An isolated nucleic acid molecule according to claim 46 comprising a nucleotide sequence substantially as set forth in one or more of SEQ ID Nos: 5-29 or a nucleotide sequence having at least 40% similarity thereto or a nucleotide sequence capable of hybridising to one or more of SEQ ID Nos: 5-29 under low stringency conditions at 42°C.

50. An artificial chromosome for use in gene therapy said artificial chromosome comprising a nucleic acid molecule capable of conferring a phenotypic property on a cell carrying said artificial chromosome wherein said artificial chromosome is a replicating element which segregates with cell division.

51. An artificial chromosome according to claim 50 wherein said artificial chromosome is capable of functioning in a mammalian cell.

52. An artificial chromosome according to claim 51 wherein said artificial chromosome is capable of functioning in a human cell.

53. An artificial chromosome according to claim 52 wherein the chromosome is a human chromosome.

54. An artificial chromosome according to claim 53 wherein the chromosome is capable of associating with CENP-A and -C or antibodies thereto.

55. An artificial chromosome according to claim 53 or 54 wherein the chromosome is human chromosome 10 or a modified form of human chromosome 10 or its non-human mammalian or non-mammalian equivalent.

56. An artificial chromosome according to claim 55 comprising a region mapping between q24 and q26 on chromosome 10.

57. An artificial chromosome according to claim 5 wherein a modified form of human chromosome 10 is a mardel (10) chromosome.

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58. An artificial chromosome according to claim 56 comprising a nucleotide sequence substantially as set forth in SEQ ID NO: 3 or a nucleotide sequence having at least 40% similarity thereto or a nucleotide sequence capable of hybridising to SEQ ID NO: 3 under low stringency conditions at 42°C.

59. An artificial chromosome according to claim 57 comprising a nucleotide sequence substantially as set forth in SEQ ID NO: 4 or a nucleotide sequence having at least 40% similarity thereto or a nucleotide sequence capable of hybridising to SEQ ID NO: 4 under low stringency conditions at 42°C.

60. An artificial chromosome according to claim 57 comprising a nucleotide sequence substantially as set forth in one or more of SEQ ID Nos: 5-29 or a nucleotide sequence having at least 40% similarity thereto or a nucleotide sequence capable of hybridising to one or more of SEQ ID Nos: 5-29 under low stringency conditions at 42°C.

61. An isolated nucleic acid molecule comprising a sequence of nucleotides which defines a eukaryotic neocentromere.

62. An isolated nucleic acid molecule according to claim 61 wherein the neocentromere is derived from a mammalian chromosome.

63. An isolated nucleic acid molecule according to claim 61 wherein the neocentromere is derived from a human chromosome.

64. An isolated nucleic acid molecule according to claim 63 wherein the nucleic acid molecule is capable of associating with centromeric binding proteins (CENP)-A and -C or antibodies thereto.

65. An isolated acid molecule according to claim 63 or 64 wherein the chromosome is human chromosome 10 or a modified form of human chromosome 10 or its non-human mammalian or non-mammalian equivalent.

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66. An isolated nucleic acid molecule according to claim 65 wherein the nucleotide sequence corresponds to a region mapping between q24 and q26 on chromosome 10.
67. An isolated nucleic acid molecule according to claim 65 wherein a modified form of human chromosome 10 is a mardel (10) chromosome.
68. An isolated nucleic acid molecule according to claim 66 comprising a nucleotide sequence substantially as set forth in SEQ ID NO: 3 or a nucleotide sequence having at least 40% similarity thereto or a nucleotide sequence capable of hybridising to SEQ ID NO: 3 under low stringency conditions at 42°C.
69. An isolated nucleic acid molecule according to claim 67 comprising a nucleotide sequence substantially as set forth in SEQ ID NO: 4 or a nucleotide sequence having at least 40% similarity thereto or a nucleotide sequence capable of hybridising to SEQ ID NO: 4 under low stringency conditions at 42°C.
70. An isolated nucleic acid molecule according to claim 67 comprising a nucleotide sequence substantially as set forth in one or more of SEQ ID NOs: 5-29 or a nucleotide sequence having at least 40% similarity thereto or a nucleotide sequence capable of hybridising to one or more of SEQ ID NOs: 5-29 under low stringency conditions at 42°C.
71. An isolated nucleic acid molecule according to claim 61 wherein the length of the nucleic acid molecule is from about 50 bp to about 1500 kbp.
72. An isolated nucleic acid molecule according to claim 71 wherein the length of the nucleic acid molecule is from about 1 kbp to about 1000 kbp.
73. An isolated nucleic acid molecule according to claim 72 wherein the length of the nucleic acid molecule is from about 10 kbp to about 500 kbp.

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74. An isolated nucleic acid molecule according to claim 73 wherein the length of the nucleic acid molecule is from about 10 kbp to about 100 kbp.

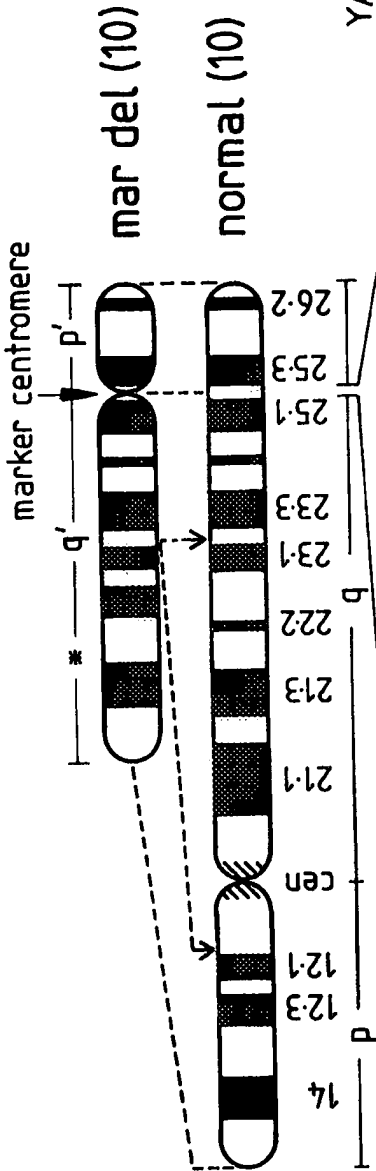


FIG 1A

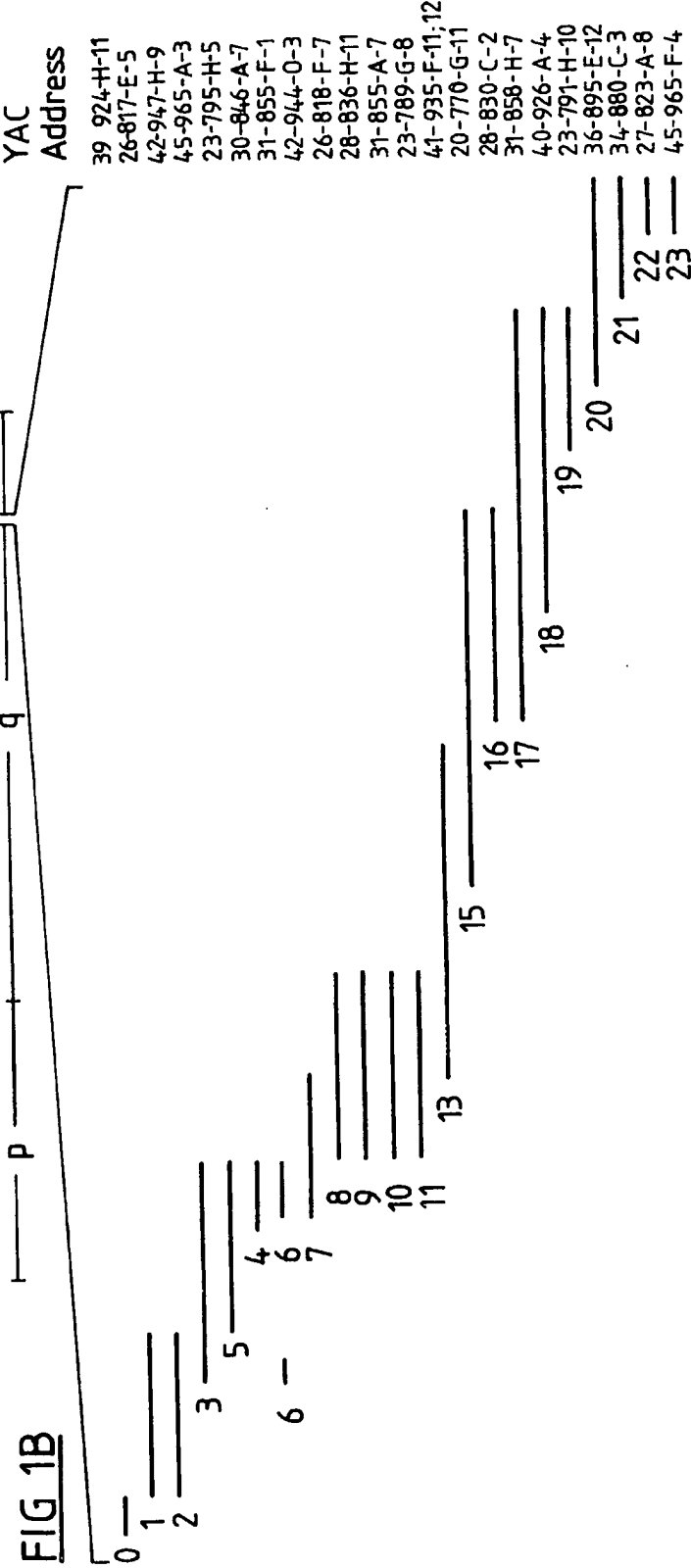


FIG 1B

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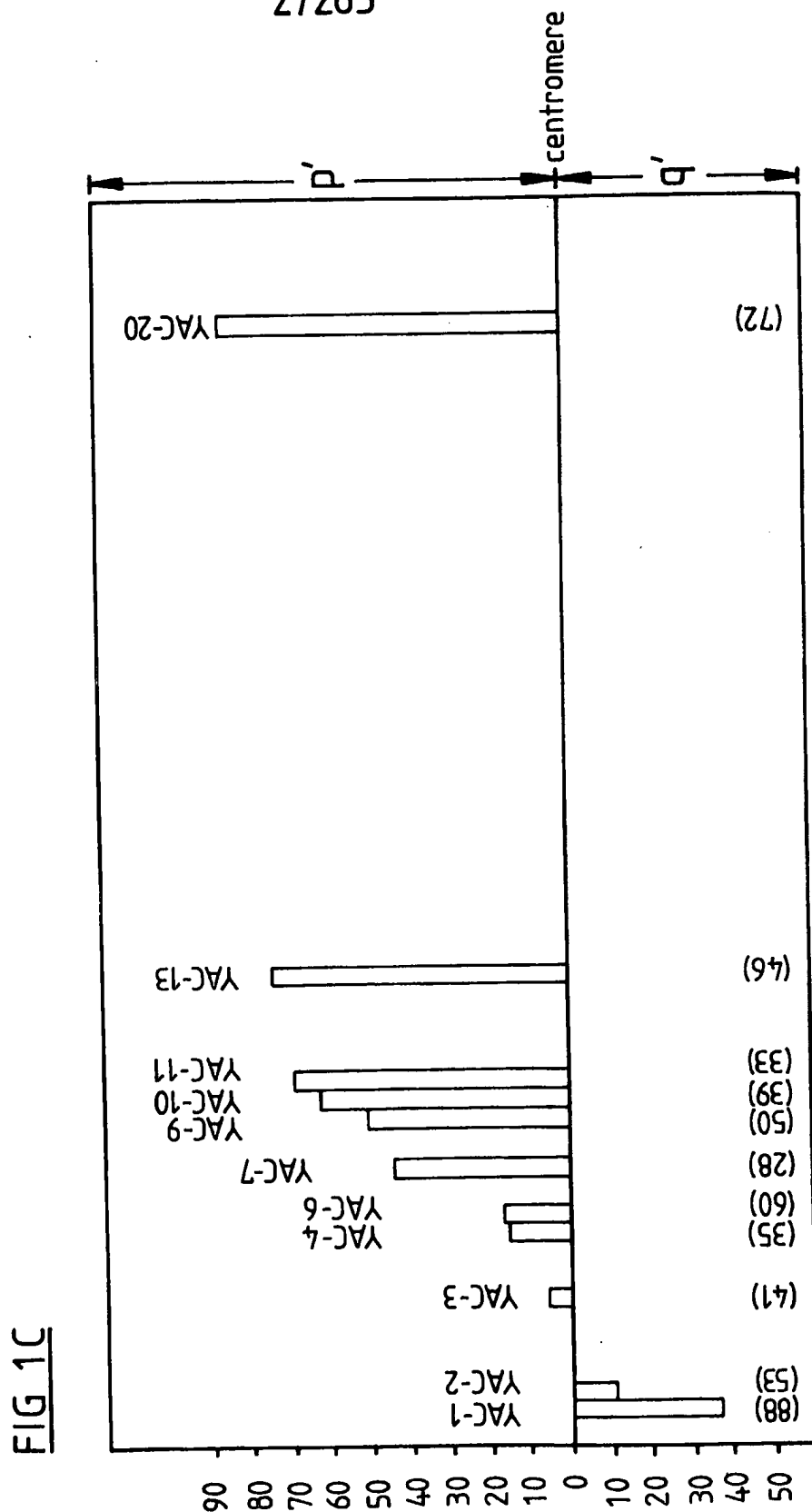


FIG 1C

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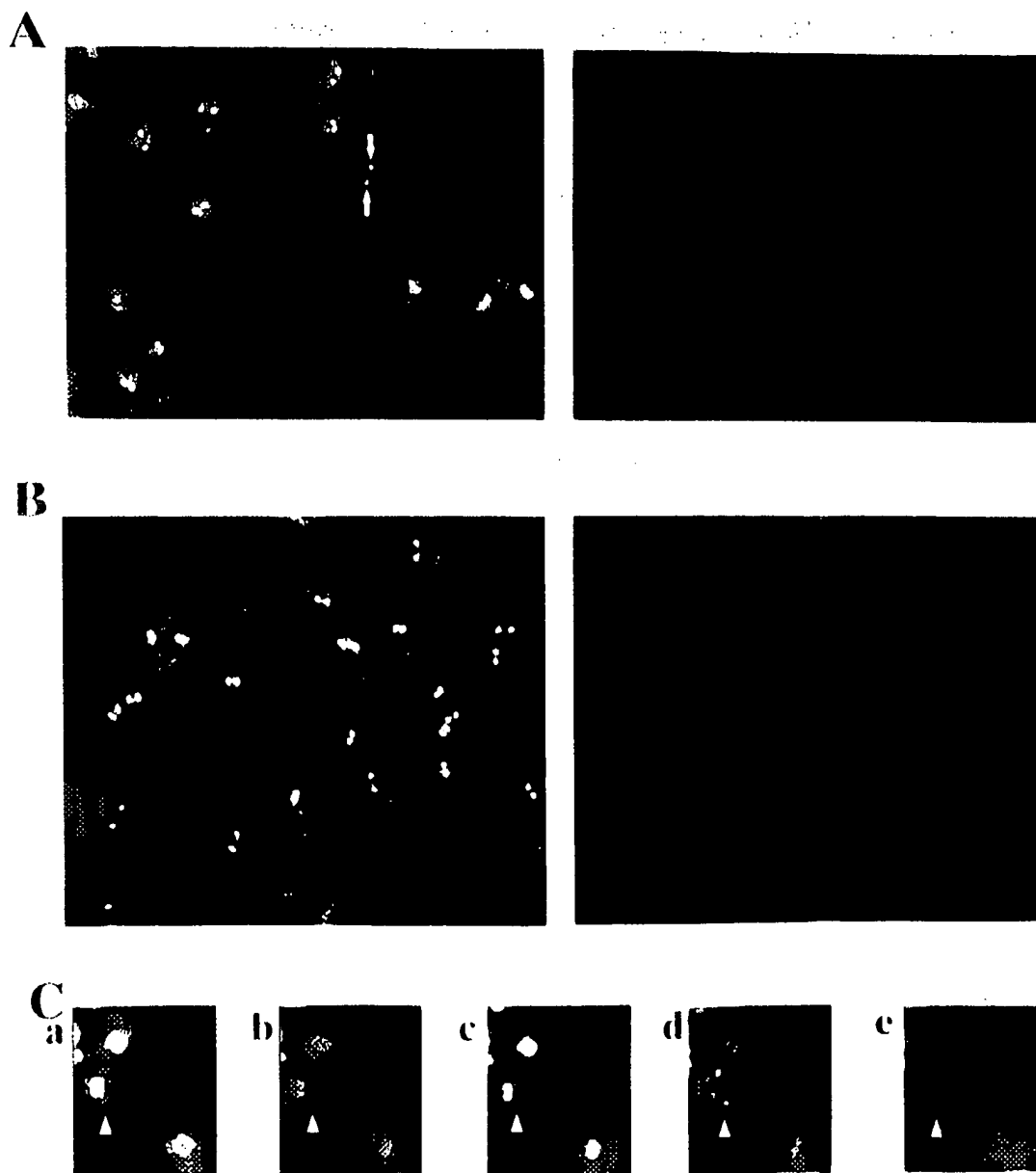
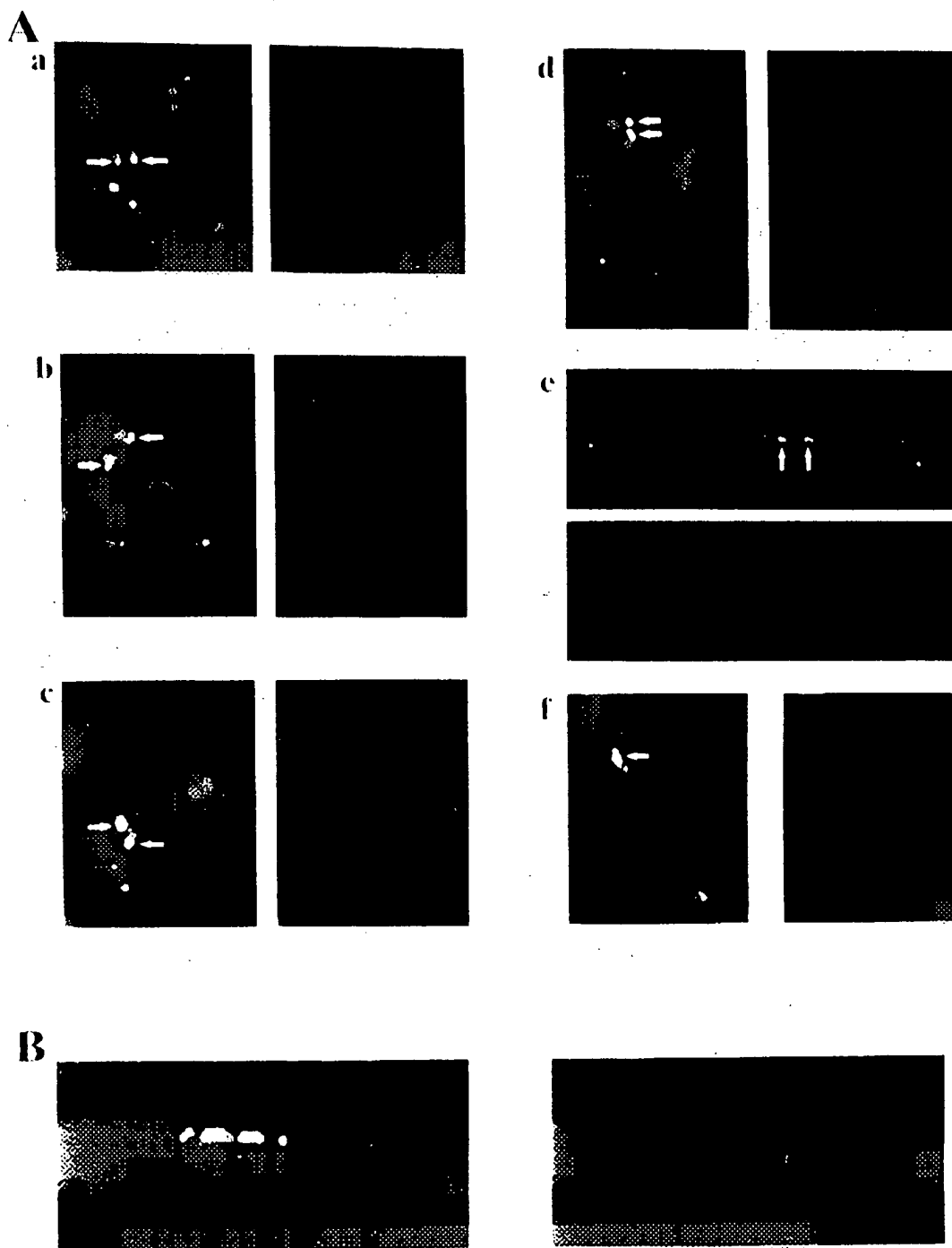


FIG 2

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FIG 3

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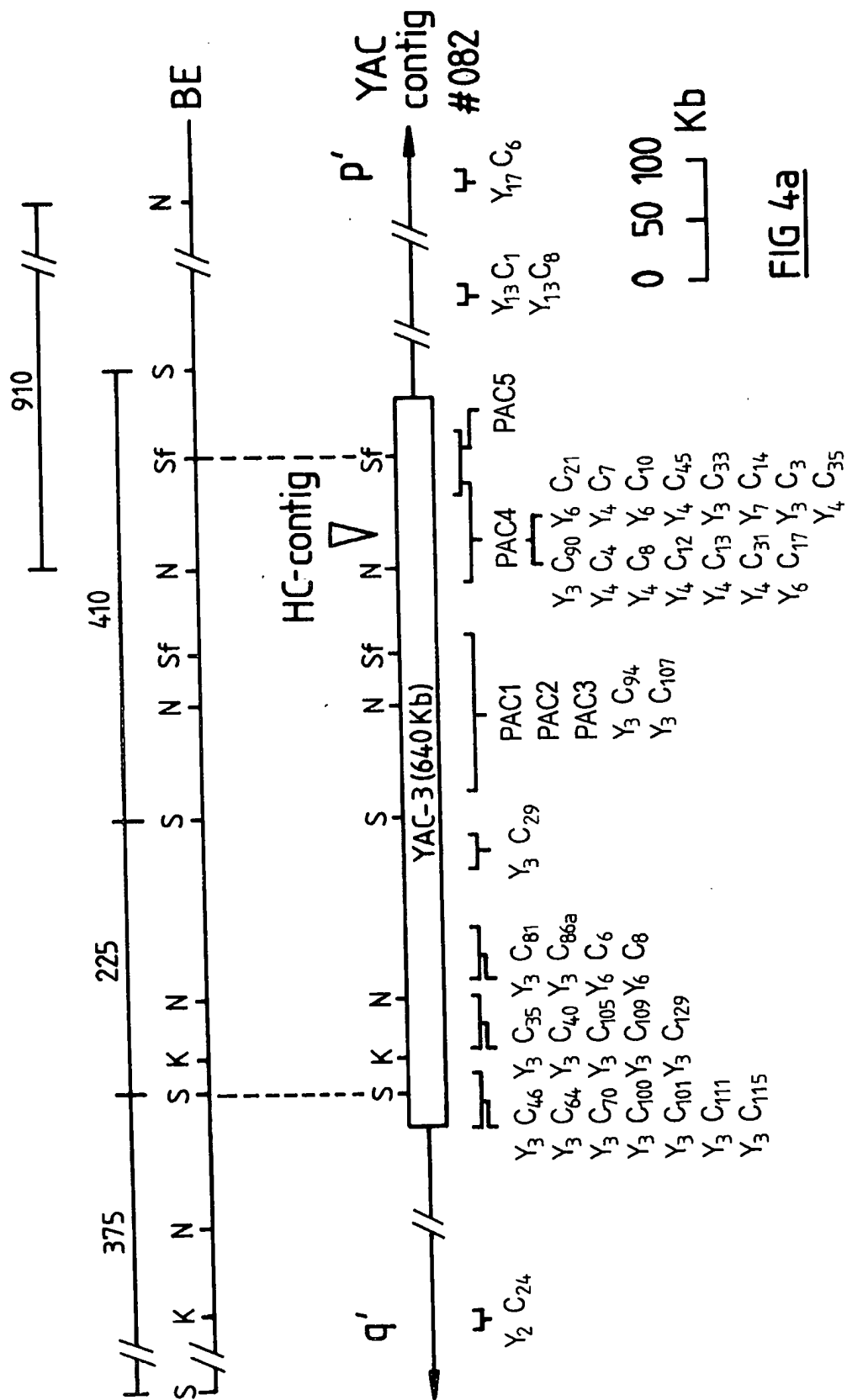


FIG 4E

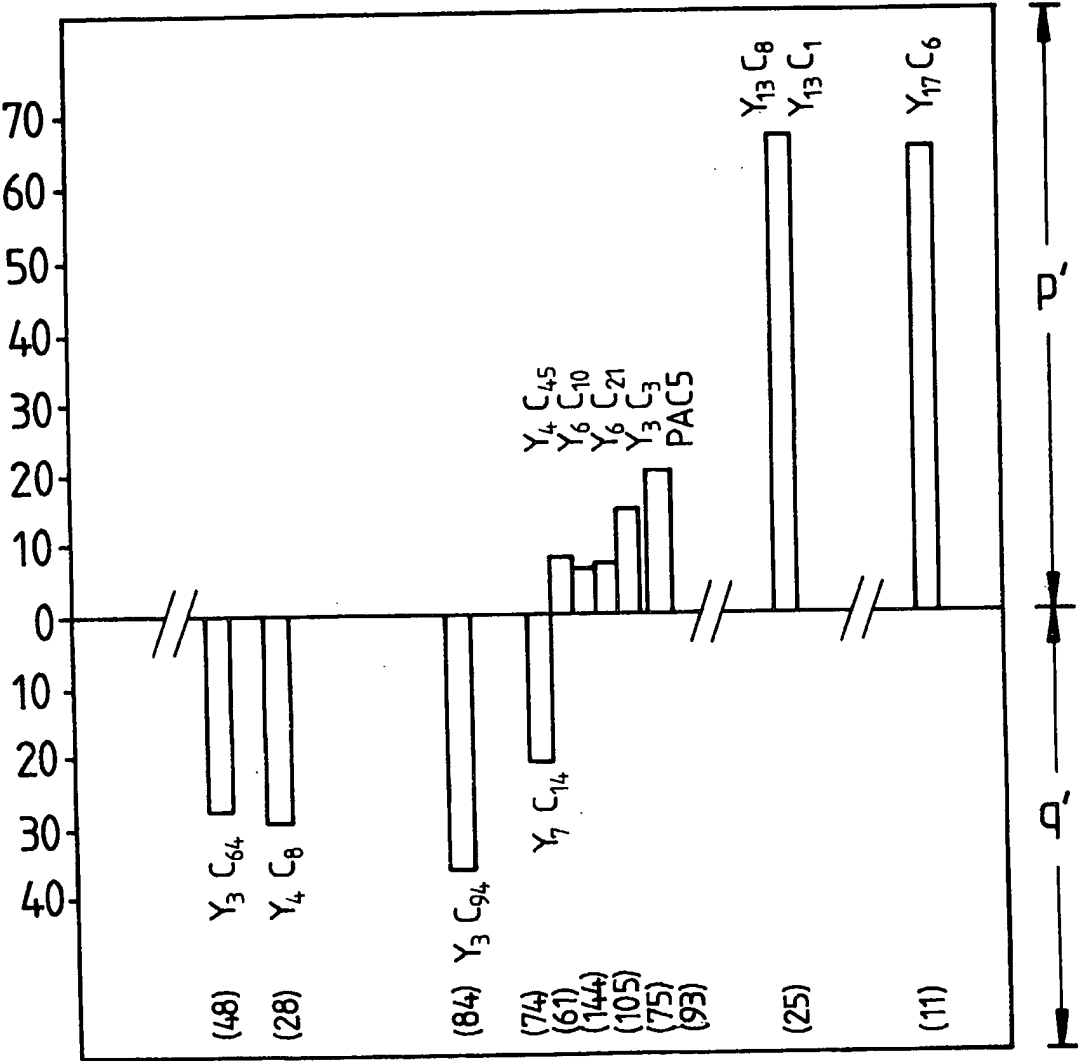
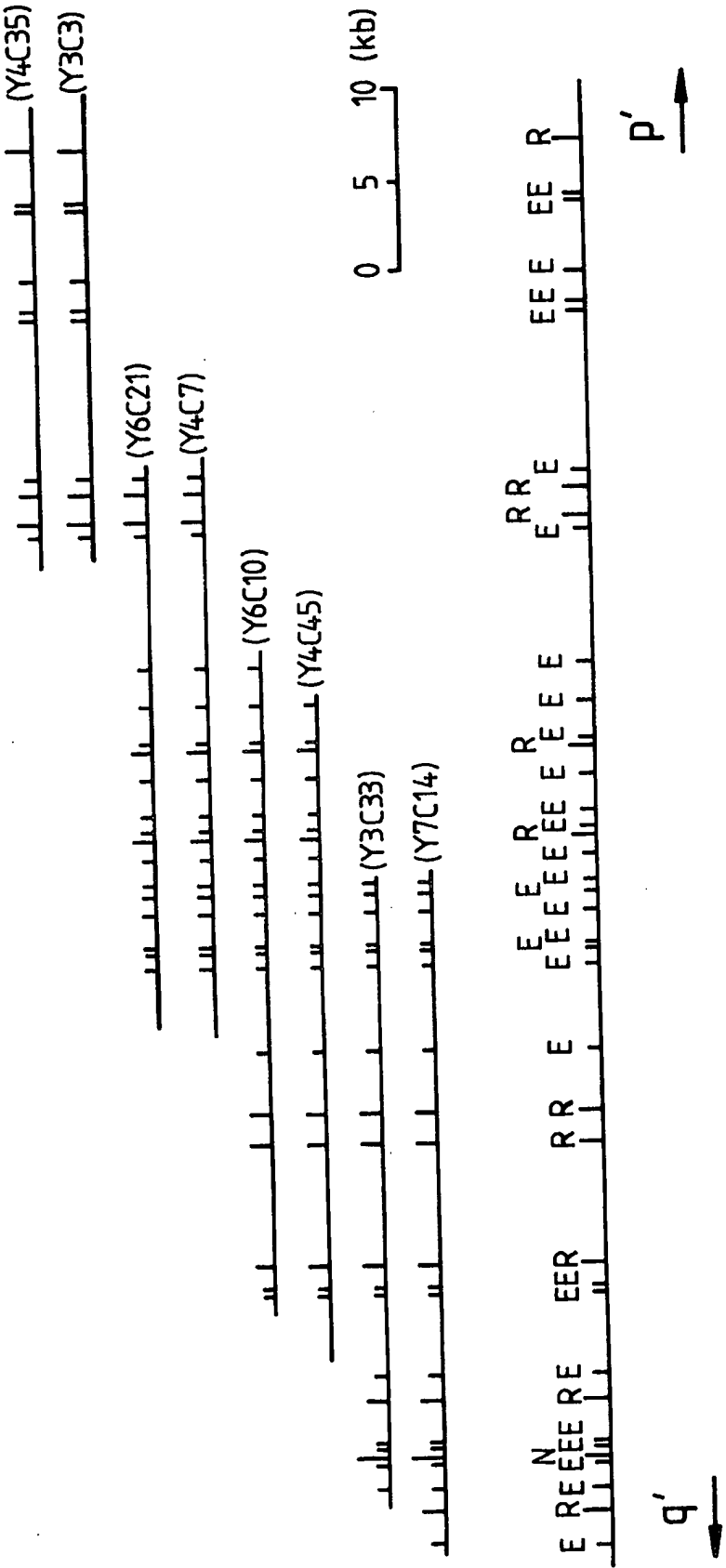


FIG 4b

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FIG 4c



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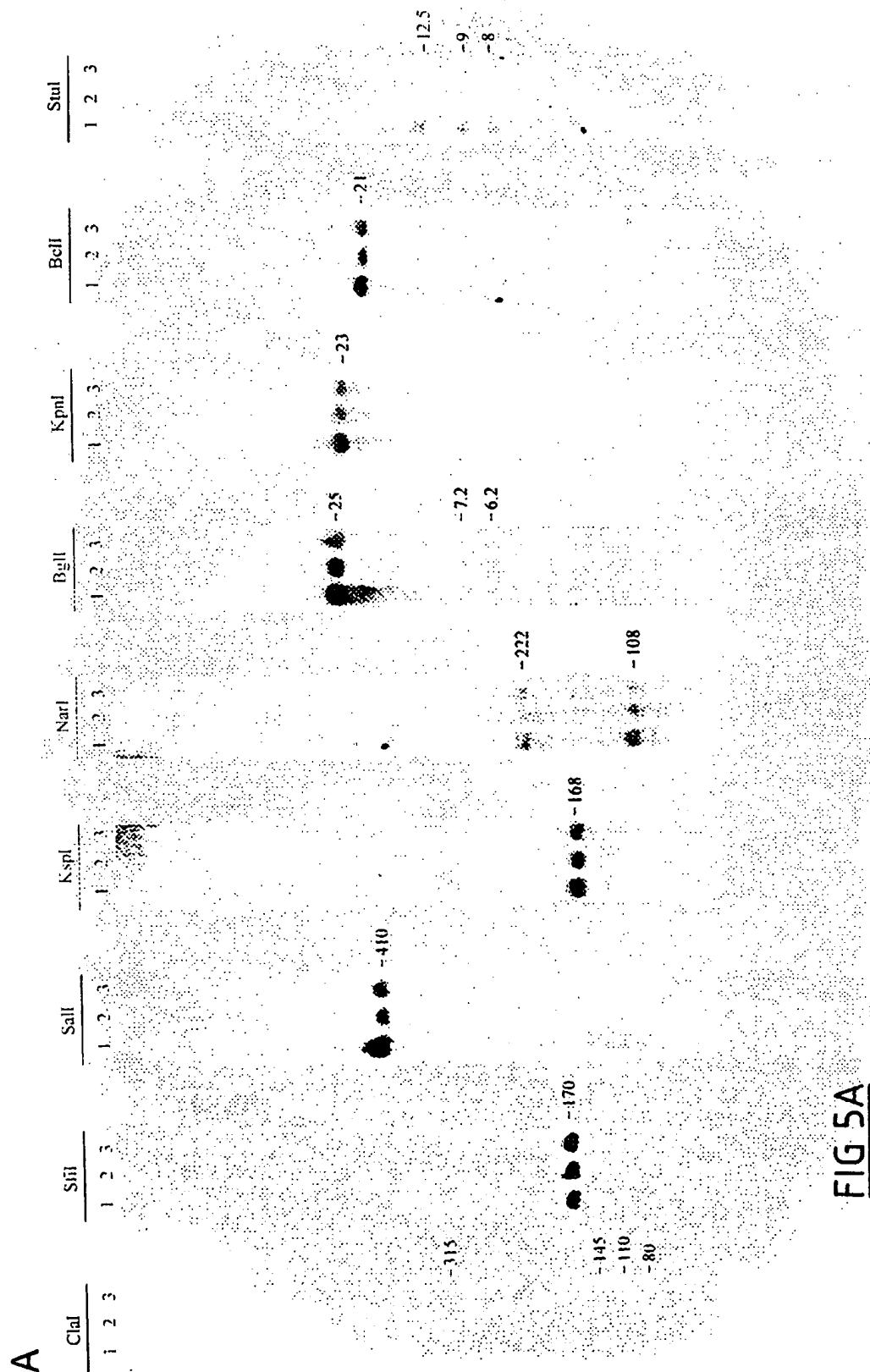


FIG 5A

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B

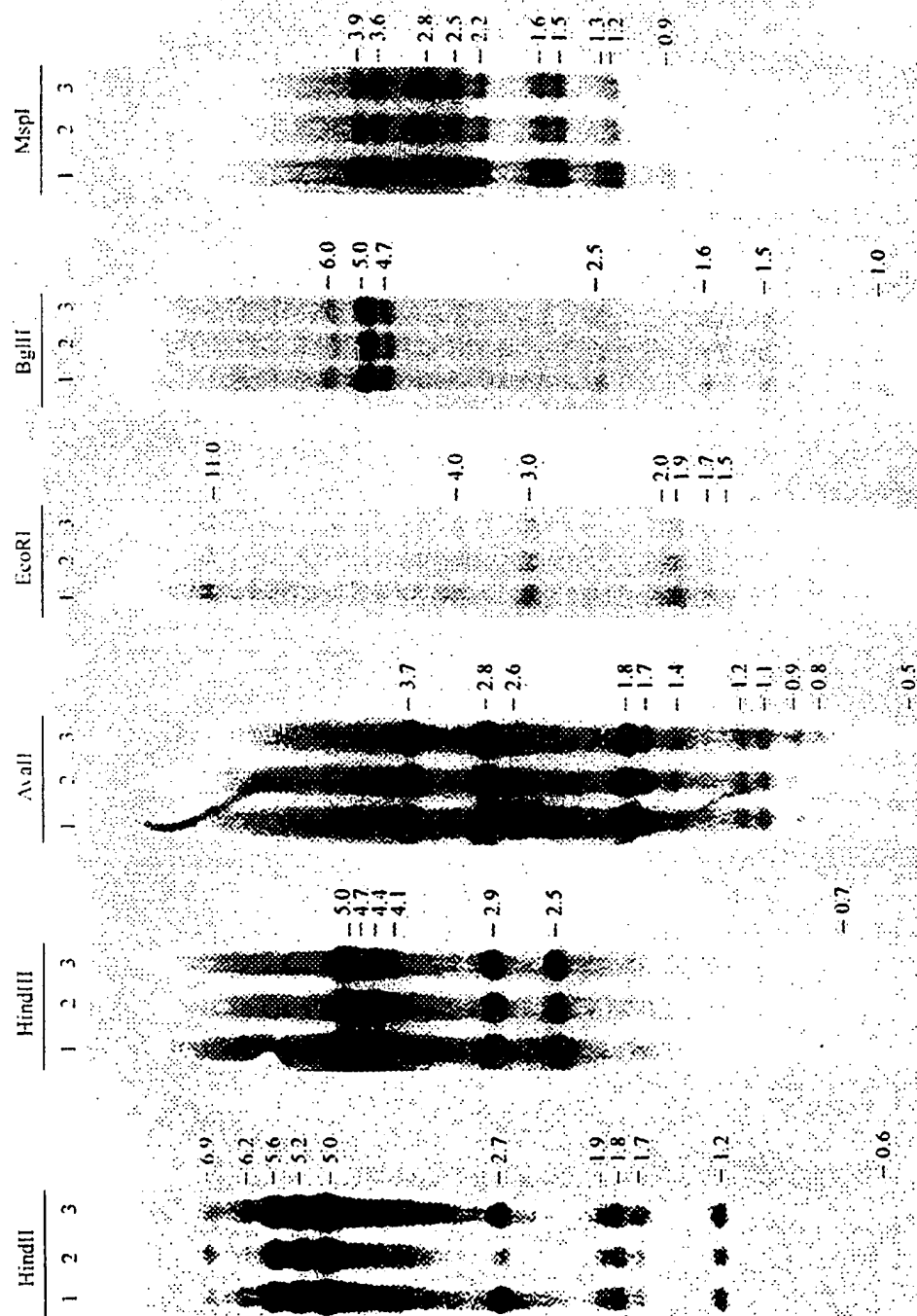


FIG 5B

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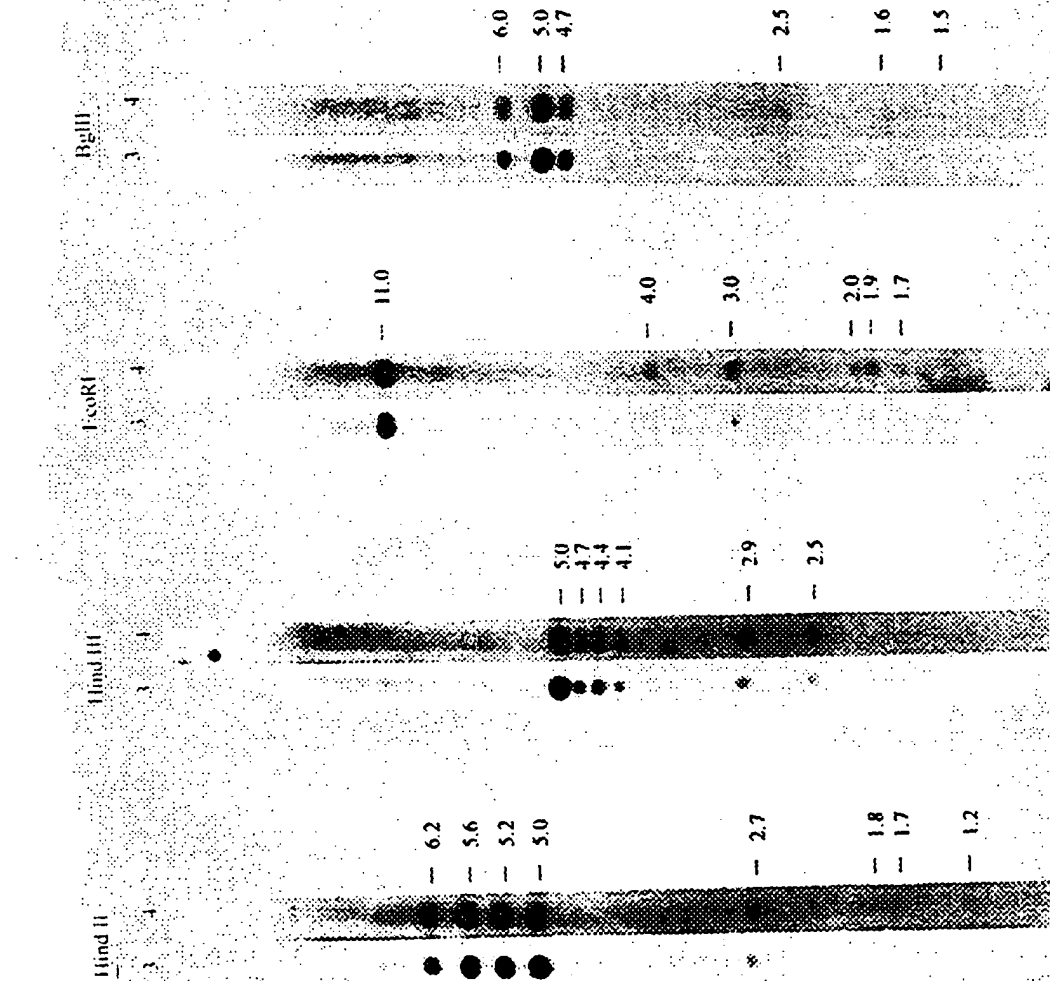


FIG 5C

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FIGURE 6 (1)

GAATTCCTT GCCTCAGCCT CCCAAGTAGC TGAGGTTACA GTGCCAGCC ACCACGTCCA
GCTAATTTTT GTATTTTAGT AGAGACGGGG TTTCACCGTG TTTGCCAGGC TGGTATCAAA
CTCCTGACCT CAAGTGATCT GCGTGCCCTCA GCGTCCCAA ATGCTAGGAT TACAGGTGTG
AGTCACCGCA CCCAGCCCTT CTTTCAGTTC TATCACCTCT TTTTGCTATA TTTGTATGAG
AGCTTTATTA TTAGGGGCAC ATACATTTAA AATTGTTATG TCTTATTGAT AGATTGATCT
GTCATTATGA ATGCTCTGTAT TCATTCCCTG ATAGTATTTC TTTTCTCTAAA TATTTTCTG
AATGTGCTG CTATTAACAT AGCCACTCTG GCTTTTAAA ATTAGTATTT TTATGGTATA
TATTTTCTCT TTTTCTCTCT TTTAAGTTTT AGATGTTATG TTTCTCTATA CTAAAGTGG
GTGTCTTATA GGCAGCATAT ATCTGGGTCT TGATGTATTA TTAAATCTGA TAATCTCAAC
CTTTTGTGTG GAGTGTTTAG GCCATTTACA TTAGTGTA TTATAGACAT GGTGTGATTT
GCTATACCAT CTTTTCATTT GTTTTATATG TGAGCCATCT TTTTCTCTCT CTTTCTCTCT

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FIGURE 6 (2)

CTTTGACCAT TTTCTTTAGT ACTGAATACT TTTTGTGTAT TTCAATTATAT CTATTGGCTT
TTTAGTTATA CCTCTTAAAA TTTTTTTTC TGTTTTATGT AGGATTATA ATACATCT
TTAACTTATC ACAGATTACC TTCAAATAGT ATTTACCAG CTCAAGTGTA ATGTAGAAAC
CTTACAAGAG TATATTTCA TTTCTGTCTC CTAATTTTA TGCTATGTCT ATAATACATT
AGGTTTGTG TTGTTTGTGTT TTACCTTTATT GCTGTTGGCT GGGTCAGCA AACATTTTCT
GTAAGGGCT AGATAGTACA GGCATACCTT GGAGATACTG TGGGTTTGGT TCCATACCAC
CACAATAATA CAAATATGCA AGAAGTGGAT ATCACAATAA AGTGAGTCAC ACAAGTCTTT
TGGCTTCCCA GTGCATATAA AAGTTTGTCT TATACTACAC TGTAGTCTGT TAAAGTGTGA
ATAGTGTTAT GTCTAAAAA ACACATACCT TAATTTTAA ATGCTTTATT ACTAAAAAT
GCTAACATC ATTGAGCAT TCAGTGAGTT GTAATCTTTT TGCTGGTGA AGGCTTTTC
TTATTGATGA CTGATCGGG GTCAGGTGCT GAAGCTTAGG GTGGCTGTGG CAGTTTCTTA

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FIGURE 6 (3)

AAACAACAGT GAAGATTGCA ATATCAGTTG ACTCTTCCCTT TCATGAAAGA TTTCTCTCTA
GTGTGTGATG CTTTTTGATA GCATTTTATG CACAGTAGAA CTTCTTTGAA AATTGGATCA
ATCCTCTCAA ACCCTGCTCT GCTTTAACAA CCTAAGTTAA TATAATATTC TGAATCCATT
GTTGTCATTT CAACAATTTT CACAGTGCTT TCACCAGGAG TAGATTCCAT CTCATTTCTT
GAGATGGAAT CTTTGCTCAT CCATAAGAAG AAATTCCCTCA TCTGTTC AAG TTTTATCATG
AGATTGCAGC AATACAGTCA TGTCTTCAGG CCTCACTTCA CTTTTAATTC CAGTTCTCTT
GCTGTTTCTA CCACATCTGT GGTTCCTTCC TCCATTGAAG TCTTGAACCT CTCCAAGTCA
TCCATGAGGG TTGGAATCGA CTTCTTCCAA ATTCCCTGTTA ATATTTATAT TTTGACCTCC
CATGAATCAT GAATGTTCTT AATGGCACCT GGAATGGTGA ATCCTTTCCA AAAGGTTTTC
AATTACTTA GTCCAGATCC ATCCATCCAG AGGATCCACT TTCAATGCCA GTTATAGCCT
TATGGAATGT ATTCTTCAA TAATAAGGCT TGAAAGTTGA AATTACTCCT TGATCCATTT

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FIGURE 6 (4)

TCTGCAAAAT AGATGTTGTG TTAGCAGGCA TGAAAGCAAC ATTAATCTTT TTGTACATGT
CCATCAGAGC TCTTGGGTGA CCAGGTATAT TGCCAGTGAG CAGTAATACT TTGAAAGGAA
TTATTTTCT TAGCAGTAGG TCTCAACAAT GGGCTTAAA TATTGGTCC ACCATTCTGT
AAACTGATGT GCTGTCACT AACTTTGTA GTTTCATTTA TAGAGCACAG GCAGAGTAGA
TG TAGCATAA TTCTTAAGG ACTTAGGATT TTCAGAAATGG TAAATGAACA TTGGCATCAA
TTTAAATCAC TAGCTGTATT AGCCCCCAAC AAGAGAGTCA GCCTATTTT TGAAGCTTGTG
AAGCCAAGCG TCGACTTCTC CTCCCCTGGTT ACAAAAGTCC TAAATGGCAT CTTCCTCCAA
TATAAGGCTG TTTTATCTAC ATTGAAAATC TGTTGTTTAG TGTAGCCACC TTCAATCAATG
ATACTATCTA GATCTCTTGG ATAACTTGTG CAGCTTCTAC ATCAGCATTT GCTACTTCAC
CTTGTA CTCT TATGTAATGG AGTGGCATCT TTCCCTCGTAC CTCATGAACC AACCTCTGCT
AGCTTCCAAC TTTTCTCTCTG TAGTTTCCCTC GCCTCTCTCA GCCTTCATAG ACTTGAGGAT

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FIGURE 6 (5)

AGTTAGAGAC TTGCTTTGGA TTAGATTTTG GCTTCAGGAA ATGTTGTGGC TGGTTTGATC
TTCTATCCAG ACCACTAAAA CTTTATCCAT ATCAGCAATA AGGCTGTTTT GCTTTCCTTAT
TATTTGTGTG TTCACTGGAG TAGCACTTTT AATTGCTTC AAGATATATT TCTTTGCATT
CACAACTTGG CTGACTGGTG CAAGAGGCCT AGCTTTCAGA CTATCTTGGC TTTTGACATG
CCTTCCCTCAC TAAGCTTAAT CATTCTAGC TTTTGATTTA AAATGAGAGA TGTAGGCCAG
GCACAGTGGC AGGCACAGTG GCATATGCCT GTAATCCAA CACATTAAGA GGCCAAGGTG
GGAGGATTGC TTGAACCCAG GAGTGGAGG TTGTAGAGAT CACACCACTG CATTCCGTCC
TGGATGACAG AGCAAGACCT TTCTCAAAAT AAAATGAGAG GTGTGCTTCT TCCTTTTGTT
TGAGCCCATTA GAAGCCATAG TATGATTTTT AATTGGCCTA ATTTCAATAC TGTGTGTCT
CAGAGAAATAG GGAGTCTGA AGAGAGGGAG AGAGGTGGG GAATGGCTGG TCAGTGGAGC
AGTCAGAACA CACATAACAC TAATAAATTG TTTGCTGTCT TATATGGATG TGGTTTGTGA

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FIGURE 6 (6)

TGCCCCCAA CAATTACAAT AGTTACAGCA AATATCACTG ATCACAGATC ACCATAACAG
ATATAAGAAT CATGGCAAAG TTTGAAATAT TCTTGAGAAAT TAGCAAAGTG TGACACAGAG
AAACAAAGTG AGCACATGCC GTTGGAAAAA ATTGGTGTG ATAGACTTGC TCCATCGCAA
GTTTGCCATA CGCCTTCAAT TTATAAAAAA CACAATATCT AGGAAAGTTCA ATAAAGTGAA
GTGCAATAAG ATGAAGTATG CCTGTAAATA TTTCAGGCTT TCCAGACCAT AGGGTTTCTG
TTGCAACTGC TCACCTCTGC CATATAGCA TGAAAGCAGC TATAGAAAAT ATACATAAAT
GAGGCCGTGA ATCCCAACAC TTTGGGAGCC CAAGGTGGAT GGATCACTTG AGGTCAGGAA
TTCGAGACCA GCTTGGCCAA CATGGCAAAA CCCCCTCTCT ACTAAAAATA CAAAAATGAG
CCAGGACTAC GCATGCCCTGT AGTCCCAGCT ACTTGGGAGG CTGAGGCAGG AGAATCTCTT
GAACCCGGGA AGGGAGGTT ACAGTGAGCC AAGATTGTGC CACTGCAC TC CAGCCTGGGC
AACAGAGTGA GACTGTCTCA CAAAAAAA AAAAGGAAA GAAAATACAC ATAAATGAAT

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FIGURE 6 (7)

GTATGTGGCT GTGTACCAGT ATATCCTCAT GCTCTAGCTT GCCAACCCCTT GCTTTACACT
GTCAGTTACC TTCTAAAGAG ATTAAAAATC ATAACAATAT CTATTACGTT TATTCACATC
CTAGTGTCAT TTCTTCCTTA TGTAGAATCA AATTTCATTC TGGTATCATA TTTCTTCTTT
CTAAATAATT TCCTTTAATA TTTTTTATAG CACAGTCTA ATAGCAATGC ATTATGCAAT
TCATTGCTAT TAGACCTGTG CTATAAAATA GCAATGAATT ATGTCAGTTT TTATTTGTCT
GAAAAAGTTT TTTGTTTTTG AAATATACTT TTGCTGGGTA TATAAATCCA TGTTCATATA
CTTCTCTTTT CTTCAGCACT TTAATGAAGT CACTCAGTTA TCTTCTGGCT TGTATAGTTT
CTCTGGCTGC CTTCAAGATT TTTTCATTGT CTTTAATTTT TAGCAGTTTG ATGTGTCTAG
GAGTGATTTT CTTTGTATTT ATCCTTTTGG GGGCTCTTA ATTTCTTTGA TCCTTTTTTT
CTTTTTTTTT TTTTTTTAAT CAGTTTGTGT CTGTCCTCTC AAGTGGGCTG AAAAAAAG
AAAAATAAAA TCATAGTTTA AAAAATAAT TTTGGAAAAT TTTCAGCTAT CATTCTCTCA

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FIGURE 6 (8)

AAATATTATC CTA CTCTATG CTC C C C C C C T C C C T C C C T C C C T C T C T G T G A C T C A A A T T A C A G G
T A T A T T T A A C C A T T T T A T T T G T T C A C G G C A C T T G G A T G C T C T G C T T T C T T A T T T T T G T C
T T T C A T T T T G G A T A T T T C T A C T G A C C T A T C T T C A A G T T C A C T G A T T C T T T T C T C A G T C A
T A T C T A G T G T G C T C A A C G C C T G T T G A A G A A A T C C T T T G T C T T T A A T A T C A T G T T T T T A T
T T C T A G C A T T T T C A T G T A A C T C T T T G T T C T G G T T C C A T C T C T A C T C A C T T T T T T T T T
T T T T T T T T T T T T T T T G A G A C A G A G T C T C G C T C T G T C A C C A G G C T G G A G T G A G T G G C
G C G A T C T C G G C T C A C T G C A A C T T C C C G T C C C C T G G G T T C A A G T G A T T C T C C T G C C T C A T C C
T C C C G A G T A G T T G G A A T T A C A G G T G C C C A C C A C C G T G G C T G G C T A A T T T T T G T A T T T T T
T A G T G G A A C A G G G T T T C A C C A T G T T G C C A G G C T G G T C T T G A A T T C C T G A C C T C A G G T G
A T C C A C C T G C C T C A G C C T C C C A A T T G C T G A A T T A C T G G C A T G A G G C A C T G C A C C C A G C
T C T G C T G A C A T T T T T T A T C T T T T G C T G C A T T T T G T C T A C C T T T T C A T G A A T C C T T A A

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FIGURE 6 (9)

CATAGTAGTC ATAGTTACTT TCAATTCCCTT GTCTGACAGT TCTGACATTC AAGCTAGGT
CTGTTAATAG CTTTGTGAGT CTGTTAACAG CTTTTTTTCA TTCTTGTCTG TGTGTTTTGT
ATTTCTTGAT TGTATGCCAA ATATTGCCCTG TAAATAAAC TTAGATAAGT CATACTTCTA
TCCAGAAATA GGCACATTTT TTGTGTCCAG TCATTAGTGT GGAGGGAGGT TGGGGCAGTC
TAGTCAGTGG CTGAACTAGG TTTGGATTG TTGATGCTAT ACTTAGAATG CACCAGACTT
CCATTCACTG CAAGAGTGGG CTGCTGCGCT TTGTGATTCA TGTGAGGCCT GAATTGTGGG
TTTTTTCCTTA GTGTGTCCCT CCATGCTCAG ATTTCAGCAA GTCCTCATAT CTGTGCCACA
GAAGGAATCT GACCCATGCT CTTTTTGACC TCCCCAAGTG ATCAACTGTT GCTTGTATA
GCTTGTATG GAGTAAGAGG GTGTTTTTTT AGTTTTTCATC CTCCAGCCTT GGTC TTGGGC
CCTGAGCTCC TAGACTCCAG GAGTGGATGG AATCCAGTGA TTTCTCAGTA ATTCAGCCCC
TTCTCCAGTA GTGGCAGATC TCTGCTTTGT ATCAGTGCAA GATCCTGGGC TGAGCTCATT

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FIGURE 6 (10)

TTCTGCCCTT CCTCGAGTGG CAGACAGCTC TTGCTTTTCAC CCTTCTACCA AAGGCAGTGC
ATCTTTTCTT GGGCCTCTCC CCATTGAACT TATGACTTTC ACATAAGAGA AGGGCTCATG
TATCAGAGAA TTCTGTGACT TTGTGCCACA TACAGAGTCT CTCAGTTCTC TTGCCCTGCC
CCAGTCTTTT TTGTGAGCAC CTAGTAGAGA CCCTGGAGA AGAGCAAGGA AGCGAGTATG
GACTTCTTTT GTGTCTGTCTG ATTGCTTTGT TTCTCAACTG CTACTCTTGG ACTTTAAGAA
TTCATTAAAA TTTCAGCTGT TTTCTTTTAT TCTTTTGTGTT TTTCTTTTTT TTTTTTTTTT
TTTTTTAGATG GAGTCTTGCT CTGTTGCCCA GGCTGGAGTG CAGTGGTGTG ATCTTGGCTT
GCTGCAACCT CCGCCTCCCG GGTCAAGCG ATTCTCCTGC CTCAGCCTCC CAAGTAGTTG
GGATTACAGG TGCCCACCAC CACACCTGGC TAATTTTGT ATTTTGTAGTA GACACAGGT
TTCACCATTT TGGTCAGGCT TGTCTCAAAC TCCTGACCTC ATGATCTGCC CGCCTCAGCC
TCCCAAAGTG CTGGGATTAC AGGCATGAGC CACCGGCCA GGCTCAGCT GTTCTCTTTT

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FIGURE 6 (11)

TACCTGCTGG GATGGCTAGT TTTCTGTGTC AACTTGA CTG GGCCATGGGA TGTCCAGATA
TGTAATTAAA CAGTATTCT GGGTGTTCT GTGAGGGTGT CTTCAGAAGA GATTGCAATT
TGAATTGGTG AACTAAGTAA AGCAGAGGGC CCTGTCTAGT AGGGGTAGGC ATCATCCAGT
CTGTTGAGGA CTTGAATAGA ACAAAGGCA GGGGAAGGTT GGAATTGCCC CCTCTCTGCT
TGAGCTGAGA CATCTATCCT GCCCTTGGCA CTCCTGGTTC TCAGGGGTTC AGACCTGGAT
TCCTGGTCTC CACCTTGCCC ATGGCAGACT GTGGGACTTC TCAGCCTCCT ATCTAATTAA
TAAATCTCTT CACACACACA CACACACACA CACACACACA CACACACACA CACACACACA
CCCTATGTAT CCTTCTGTTT CTCTGCAGAA CCATATCTAA TACACCTGCT TTTATGACGA
TTACCTATCG ATTCTGTATT CTGCCAAAAC TGAAAACAGT TCATTTTTC ATCTCTTCTC
AGAGAGGCTT GTCAGCCATT AGTTCTCTGA TGGGCTCAAG AAGTTATGCA GTTTTTTTTT
TCTCACTGTT AGGATGGAAT TGATATTCTG TTGAAACTTT CTATACCCTAA GTGGAAACTT

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FIGURE 6 (12)

GTTTGTGAGGT TATTTTCTCT ACTTACTTTT GCTGGAAATG GAACACTCTG TATCTAGTTA
AGACACATAA ACTGACTTGT GATACCATAA TGTGTGTGTG AATTTTATAT TCTTAGAAAA
TCATCTGTCA AGGTGTTAAC TAATGGCAAA GCATTTAATA AATCAGCATT CATGTATTCA
GGTGCTCTGA ATTATCTGAC TTTTAAATTC TTACTTTTATA AATGAGAAAA TTGGGGCATG
GAAAAGTTAA CTCTCCTAAC CCCGAATTAT TACATTATTA AGGACAGGAC TTAGAGGGCCA
GATATCTTAA GTCATTAAATA TTCTTTGGCT CACAGAAATG GCAGTATAAC CTAAGGTAA
TAACTAGGTG ATTTTCTTTT ATATCAATTA AATATGTCAG TTTTCAAATA TTCATAAGTA
CCTACTGTGC AGGGAAGAA CATGCCATAC AAAAGATGTA GTCCAGGCCT TTAAGAAACT
TTCATTTAAT GGAACCTCAA GAAGTGTA CA TATAAGGAGG GAAGTAGCAG TATGGTACAA
GATAATACAT ACATATCAGT GAATGATATT GCCAAAAAGT GCTATTGATA GAGAAATAAT
TCATTTCTGC AAACAGCTGC TGATCTCCTA CTGAAAAACAG AGGAGGGAGA ACAGGACGCC

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FIGURE 6 (13)

TCGTGGTCAG GATAGAAGAG AAAGACCTTG AGTTGAGCCT TGAACAGTAT TTAATATTCA
AAAGGTTAAG AGAGGAGAGC AATTGAGGAG GGGAGAAATAG TTCCAGCACA AATGATGGTG
TACAAGATGA ACACAGTCAG TAAAGAGCAG ACTGGTCTGG ATGGAGAGGA GGATTTGCAAT
CATTTGGGAT TACGTCATTT AGACCCTTGA AAGCCAGGAT TGAGTAAAGC CACAGTGAAG
CGACTGGCTC GTATGGAAGC TTTATTTTAA GAAGATTAAAT CTGGTAGTGA CATGTGCCAA
AAACTGAATA GGTAGAAATG AGATGCAGAG AGCCCAGTTA GAACTAAGTC TGGTGCAGTA
ATGCAGGATT GAGGCAATAA ACACCCAACT ACAGTATCAC CAGATAATGG ATGTTTGAAC
GGACGGTTTA AAGGAAAATT GATGGTATTT GGTAATTTAT TAGATAATCC AGGGCCATGG
AATGAGAGGG GAAAATGACT AACCATAGTC ATCAAATGGT TTTTCTTAAT GAATCTGAAT
TTTGGTGTAA GAGCAACATT TTCTTAGGCC TTGCCTAGTT GTACAGCTG ACTATGATAA
TGA CTGTAC CATGCTTGTT CCTCTTTTAG CAGCTGTGAG TCCCCCACC GCCAAACAAT

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FIGURE 6 (14)

GAGCCTCTTG AAAAGGACGA TGCCCTTTTCA CTTCTCTCCA AGTGCTTGGC AAATAGGAGG
CCTTTTGAAG TTACTTTATA GTTAGGGGTT CCCAGTGAGT ATTTGAAATA TTAAGTCATG
CCCGTGGTTG ACAGCATGGC CCTACTGCTC ATCATCAGCT ATTAACCTTA GGCAAGTTAA
TGAACTTTTC TAAGCCCCAG TCTACTCATT TATAAAGTGG GATTATTAAT AATGTCTACT
TCATAAAATT ATGAAGCCTG AGTTAGGTCA TTCAGATAGT GTTTAGTCTG ATTCTTCGAA
CCTAGTAAAC AGTCAGTAAA CAGAAGCAAA TGCCACATGC CTGATTTATA TCCAAGGGGA
GAAAGGTAAA AGTGAAATTT TCATGATTTA TGGATTCAAA TTATACATTT CAAAGATGCT
TTATAAGCTA TTGTTTGGT AAGAAGAATT GAGCTGAAAC AGAATTTTCT GACAGCAGTG
ATTATTAAAT GGTGAAATAG GCTATTGATG TCTTTAGAGG ATATAGATGT TCACCTTTTG
CATATAAGTG CACAAAAATT CACTAAGTAG ATATGTCGTCTGT CTACACAGAG AGAGAGAGCG
TGAGAGCATT AAAGTTAGTA AACATCCCCC TCGCTTTTTT TTTTTTTGAGA CAGGGTCTTA

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FIGURE 6 (15)

CTCTGTTGCC TAGGCTGGAG TGCAGTGGTG CAATCGTGGC TCACTGCAGT CTCAACATCC
TGGGCTCAAG CGATCCTCTC GCTCAGCCTC CTGAGTAGCT GAGGTGTGCA CCACCACACC
CGGCTAATTT TTAATTTTT TTATTGTAAA GGTGAGGTTT CACCATGTTG CCCAGGTCCTC
AAACTCCTGA GCTCAAGCAA TCTGCTCACT TCAGCCTCCA AAAATGCTGG GATTACAGGC
GTGAGCCACC ACGCCTGGCC AGTAAACCCC ATTCAATTAC ATCATCTTAC TTGTCCCTCC
AAAATCCTGC AAAGTAGGTA GGTTCCTGTCT TTATTTGTTA TTTAGGTGAA GAACTTGAAG
TGGTGTGAG GAATAGGTGT TTTGCCAAGA GTCACGCAGC TGGAGTGGCA GAGCTGTATA
CTCTTCTGAT TCCACCAACG CTGTTTACAT CACATCTGGA GAAAAGTGCT CTGAGGCACA
GATGTTTAGT GGGAGGGATG AGACACAGGC TGCAATGCCT AAAGATAATC GGGAATAAAA
GCAGAAAACA AGACGTTTGT TTCTGTATAA ATGAGACAGA AAATAAGGCG TTTGTGTGTTT
GGGATTGAGC ACTTGGAGAA GTGGGGAGCG ATTTGATTG GGTGAGACTG CTCCTGGAAT

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FIGURE 6 (16)

GCTGCATCTG GTTCTGGACT ACTCATTACT AGGCTTATAG AAAC TAGCTG GAGGAGGTTTC
AAAGAAAAGC TCCAAAATGA TTAGCGGGCT GACGGGATTG ATTTATAAGA AATATTAAAA
GAATTAAATG TGTATAGCTC AGCTAAGCAA AGATGAAAGA GACCAGCTAA ATGTATACAA
ATATCTGAAA CGTGCAAACT TTAAAAAGAG AGATTAAATTA TTTAACATGA TACACGGGGG
CACAAATATGC AGTCACAGGA TGAAAATTTC AGCTGAGTAT CTAGAAGAAT TCCCCGATAG
TGAATCTGTT AAGGCTGTCT GTAGTGTTGC CTTTCCCTGG AGAGGCAATA GAAATTTCAA
GTCTTACGAT TTTAAAAAGTT TCTTGGAAC TAGGTATTAG ATGATGTTAG AGAATTATTA
TTAATTGGT CAGGTATGAT AATGGTATTG TAGTTCTATA AGAAAAATTG TATTTTITAG
AGTTACATAC CCTGAAATAT AAGCATAGAA TATGATGTAG GAGATTGCT TTAAAAATACC
ACAGTAAGGA AAGAAAGGAA GGAGGAAGAA AAGAAAGGAA GGGGAAGAAA GGGAAAAAGA
GGCAAAGAAG GAAGAGAAGG TAAGAGAAAG AAAAAGAAATG AAGGAAGAAG GCTGGGCACT

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FIGURE 6 (17)

GTGGCTCATG CCTATAATCC CAGCATTTAG GAGCCAAGT TGGGAGGATC ACTTAATTAA
GCCCAGGAGT TCAAGGCTGC AGTGAGCTGT GATTGCGCCA CTGCACTCCA GCCTGGGTGG
CAGAGTGAAG CCTGTCTCT AAAAATAAATAAATAAGTTAA AAAGAAAGAA AAGGATAGAT
GAAGTATGGC AAGATGTTGG TAATGTTGAA CCTGAAGGAA GTTAATATGT GAGTTCACCTT
TCCCTCTCAG TCTTCTTTAT GTATGTTTGC CAACTTTTCAT AATAAACAAAT TTAAATTATA
TTTTCCCTGAT CAAAACCTTAG TAGCAGTATT AATCCCCTGGG CTTCCCTGACT AGAACAGCCT
CATTACCACA TGGGCAGAGT TCTGGCCGAC CAGGGACCAC GTAGTGGTTC ACCATCTTGC
TCTGGTAATG TGGTCTGGC TGAAGGGCCC TTTCTAAGGT TGTAGATAGA AATCCAGGAA
ACTTGTTAGA ACTGCAGACC TATCAGGGTA CCTGCAGGAG GTGAGTCTAC TAAGGTGAAA
AAGCAGAGG CAGAGGTCGT GATTAGCAGC TGACCGCCCC CTGCTTTTCT GTCCCTCATT
CGTGGAAAAT TGAGTGGAGC TCAATTTTGA GTGGAGCTCT AAGTAGCTCC ACTTGTAGAC

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FIGURE 6 (18)

ATTGAGTGGA GCTCTAAGTG TCTTCAGAAT AGCAAAACAC TAGTTTCTT TTTCTTTTCT
TTTTTTTTTT TTTTGGAGAC AGAGTCTTGG TCTGTCGCCC AGGCTGGAGT GCAATGGCAC
GATCTCCGCT CACTGAACTC TGCCCTCCCGG GTTCAAGCGA CTCTCCTGCC TCAGCCTCCC
GAGTAGCTGG GATTACAGGT GCCCACCACC ACGCCCAGCT AATTTTCCCTA TTTTTAGTAG
AGATGAGGTT TCACCGTGTT GGCCAGGCTG GTCTCAAACCT CCTGGCCCTCA AGTGATCCGC
CTGCCTTGGC CTCCC AAAAGT CCTGGGATTA CAGGTGTGAG CCACCACACC CAGCTGCAAA
ACCCATATTT TCTTGAATGG AGAAACACTT TCCCCCTTATT TATTGAGTTT GGAAGCAAG
AAGAGGGGTA ATTCATTAAG TGAAAATTTC CAAAATCCAG AAAACATCGA TAAAGCAGCA
GCTTAATTTT TTTAAGGAAG AATTTTTTTAA ACTATCTTCT TTTGAGCCTC TTTAGGAAGA
CCTCACGTCC TTGCCCTTGAA TGTTGAGAGT GGGAAATCCA GGGAGTTTTC GAATGCATGC
CTTATGCTG CTTTTTTTGT TGTTAGAGAA ATATAAATAT TTTATCTAGG TTTTGCTGAT

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FIGURE 6 (19)

GGCAGTCAAG CATGAACACA ACCCACTGTT TGAGAAGCTG TAATTCTGA ATTTCTGCAG
AGTGCACATC TAGGCCAGCA AATGGCAGTA AGAGTGAGGT GGATTAGCT CAGTGTAAAG
ATGAACTCCA GAACCATCGG CTC TGACTGA AAGTGAAGCG GCAGCCGCGT TGTGGAAAG
CTGGCTGGAG TCTCTCTCAT AAGCAGGCAT TCTTTTCTC CAGCCCGTCA CTGTGTTGGT
TTGGGCCCCAC GGTAAAGCCTC CTGGCCCTCTA GGCTGTAAACC CCCACCATCC TCCTCTGCCT
CGCCTCCAGA GTGATTGTTT TGAAGCACAA CTGGATGTCA TTCCCCCTTCC TGAACTCCCTA
GCACCTACAG GGAATCCATC CCTTGTGCCC CACATACCTC ACACGTAGAC ATTCCTAATG
AAGATTGAT TGAATTATTG TAAACTCAGT GCCTCCCACCT CTTCTAGTTG CCTCTCTGCC
TGCCTTTGTA CATTTATTTA TTTATTTATT TATTTATTTA TTTATGAGAC AGAGTCTTAC
TGTATCACCC AGGCTGGAGT TTAGTGGCAC CATCTCAGCT CACTGCAACT TACCTCCCAG
ATCAAGCAAT CCTCCCACCT CAGCCTCCCG AGGAGCTGGG ACCATAGGCA CGTGCCATAT

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FIGURE 6 (20)

GCCCCGGTTAA TTATATTGTAA TTTTGTAGA GATGGGGTTT CATCGTGTTG CCCAGGCTAG
TCTTGAACTC CTGGACTCAG GCGATTGCGC CGTCTCAGTC TCCCAAAGTG CTGGGATTAT
AGGCGTGAGC CACCATGCCC AGCCGGCTAGC ACTCATCTTA ATCGTATATT TACTTATCTG
GCTTTCCAC CAGACTGCGG GCTCTTCAAG AGTAAATGCC ATGTTTTCAC CTTTATTTC
CCAGTTTGTG GCACATTCTA GGCACTCGCC ATCATGAAAT AAACCTCTGG AGCTGTGATA
TTACAAACGT GGAAAGATGA CGAGCACTCA GCAACTTTCA GTGAGTAAAC AAAGGCTTTC
ATTCAGCATG ATTTATTGAC TGCCCAAATC TGGGCTGCTT CCTGCTGTG GTTCAAGGAG
AGCATAGTCT ACAGAACCCAG AGACCTGGCT ACTCTGGAAG TTAGACTTAA GCCCACCCCG
GTCCTTGAAT GGGGAAATAT TTCCCTTCAT TCCTGTGTTT TAGGGACAGA AAGATGAGTA
ATGCAGTGAT ACATGCTGGA AATGTTTATT CCACTACCCG AAGCTGCCCTC TCAACTTAAC
AATCCATGAA AGAAACAAGA TGGTATATAA CTTTTTCTAA TTTGTGATGC CTTTGTTTAT

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FIGURE 6 (21)

TTGTTTCCGG TTAAAAGAGG AGGTGGCATT GAATTGTTTG TTTGGTTTGG TTTCTTCTTC
AATAAGAAGC ATCTTAATAT AACTAGACTG GACATCTGTC CCATTTTCAA AAATTACAAG
TTTCGATCAT TGCTAAATTG TACAGATCCC AATCTGTCTG CTCTGCATAC ATTTGCATTT
ATAAAAGCAG AAGCAGACTA GCAGTCTTTC TAATGCAATC CCCCAAATGC ATGAAGTATT
AGATTGCTTC TCCCTATTGG TTCATGCATT GCTAAAAGGCT TAAAAGGATC ATTGATTTTA
ATTATTTAAT GTGTACAGCA GGCTGAGCTT CCTTCTTTT TTAAGGGAAG AACCTTCAGG
GGCATTGCTT TAGTTTTTTA ATGTTAAATC TCATTTTCT T TGAAAAATAA GAAGTTAAAG
CTGTATTAC ACAAGCTCTC AAAGTGCCAG ATTTTCATTG TGTTTTTAAA CCATCTAGGA
AATGTTTGAT TCTAATGAAA CATTACTGCT GAAAATTGGG CTGAAAATTGC TGGGCTGGAA
ATATTGTTAT AACTTCACAT GATTCCAGTG TTGTATTATT ATTTTTTCTT TTTCTTTTTT
TGACCCGATA TAGATGAAGC GAAGAGACAA GGAGCAATCC CATGTGTAAT AGAAAAAGGC

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FIGURE 6 (22)

AGCCTGAATT GTTGTGCTG TTTTGTGAAT TTAAGCTGGT TTTTCGATTAA ATTCAAGTAAA
TGGTCCAGGA CTATAAATGT TGAACATTTT TTACCGTG TG ATTTAAATTT TAGTCTTATT
GTTTTTTTT TTTTGTGATG TTTACATTTT CCCCATGGGA AGCAGCTATG TCATGTCGGC
ATGATTCATC ATGGTAACAT CTCGGGTTAT TTTGGTTTGT GTTATGTTCA GAAAGCGGAA
TGCCAAAAAT AAAGAGTGGT TTGTGATGTC TAGTGTGTCT TCCTTTAACA AATCAAAGGC
TTTTTATTAA TCCACTTAAT GGGACACTGC AGAAATTTAA AAAATGGAAG TCCCATCCAC
AGAAGGCAGG TACTATGATG TAAAAAGTTT AGTGGGGGA TTAATAGAGT GATCATATAA
TTTATGAGCT AAACCGGAGG CACTTTTTTT TTTGAGATCG AGTCTCACTG TTGCCTAGGC
TGGAGTGCAG TGACGTGATC ACAGCTCACT GCAACCTCCG CCTCCCGGGT TCAAGCGATT
CTCATGCCCTC AGCCTCCTGA GTAGCTGGGA CTATAGGCGC CCACCACCAT GCCCAGCTAA
TTTTTGTGTT TTTTGTAGAG ATGGGGTTTC ACCATGTTGG CCAGGCTTGT CTCAAACTCC

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FIGURE 6 (23)

TGACCTCAGG TGATCCGCCC ACCTCGACCT CCTAAACTGC TGGGATTACA GCGTAAGCC
ACCATGCCCTG GCCCAGAGAC ACTTTTGAGA GTGAAGAGGA AGCTGAGAAT AATTCACTGA
TCTACAAC TGACCATCCA GGGCAAGCCA GATGCCATTA CCACTAGCTA GAAAGCTTGC
CAAGGTCCTCA TTTACCTTGG TATATAGCAA ATTCTTCTTT TGAATTCTGG AAATCTTGGT
AAGTCATTGA GGTAGCTCTG TGCCAAGGAG CAATATGGTA GAATTCTAAT ATTTCAGGCA
GACAACACTT TCCTGCATTT GTAGCAGGTA AAGGGAGGTC AGGGCAGAAG ACAAACCAC
TGGGACTCGA CAAAGGGCAT AAACGCTCTAA TGCACCTGAT GTAGCTGATG GTAAATTGTT
ATCAGCTAAA GATCTTTCAT AATAAATAAA CTTATCATTT GTAGGAGGC ACAGAAATCG
TGGAAAGCTG GGATTCAGGT TGCCCTGTGGC TTTAATTCTG GAATCAGAAA TATTAGTCAA
GGATATCAGT CTATGAAGTA AGTTTTCAAT GTTATATGCC ACAAGATGCA GCTGTCCCTAT
TTTCACTTCC AGTAATTCTT TCTGAATTAA TACACCTTAA AAATAGCTGC AGCTTCTCAA

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FIGURE 6 (24)

ATCTGTGAGA ATCGTATGTG CTGCTTGCTA CACTTTCCTT TTCTCTGAAGG CTCTTTGAGG
TCTTTCAAGA ACTCAATTCA ATTCAGCAAC AATTAGGGG TCTAAGGTAT ACAGACGCTG
TGCAAGATGC TCCTGAGACA CAAAGAGGAG GTCAAGCCCC TGCCTTCAGG CACCTCTCTA
TAATATAGGA GGAGAAAGAG AAGAAACACT AATACACATA GGTAGGTGCC ATTAAAAGGG
TACATACATT AAAGCCAGGT GGTAGGTGTA AGAAGATTG TAAACATGAGA ATTTTCTGCA
TGTTTGAAAT ATCTTATAAT TTTTAAAAAT TAAAAATGGGA GATACATATA TATGTATTTA
TGTATGTATA TATGTATGTA CATATACACA CATATATACA TAAATATATA CATAAATATG
TATATATGTG TATATAGACA TAAATATGTA TATATGTGTA TATATACATA AATATGTATA
TATGTGTATA TAGACATAAA TATGTATATA TGTGTATATA GACATAAATA TGTATATATG
TGTATATAGA CATAAATATG TATATATGTG TATATAGACA TAAATATGTA TATATGTGTA
TATAGACATA AATATGTATA TATGTGTATA TAGACATAAA TATGTATATA TGTGTATATA

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FIGURE 6 (25)

GACATAAATA TGTATATATG TGTATATAGA CATAAATATG TATATATGTG TATATAGACA
TAAATATGTA TATATGTGTA TATAGACATA AATATGTATA TATGTGTATA TAGACATAAA
TATGTATATA TGTGTATATA GACATAAATA TGTATATATG TGTATATAGA CATAAATATG
TATATATGTT GTATATAGAC ATAAATATGT ATATATGTGT GTATATAATA ATGTGTGTCA
TATACACACA TATATACATA CATAAACATT CTGCATTATA CCATTCACTT TGTAAACCCAT
CTTCCCCTAAA AACTGTCTCA TAAAGAGTCT TCTTTTCCCT GTACCTATGC AATGGTAAGT
AGCAAAACAC ACATTCTTTT GGGTCCCCAT AACATTCCCT GTAGTTTGCC CTTAACAGTC
TTTGATGTGA AATTTACTGT TTCTGTCTTA ACCTTGCCCTG TCTCGCGTAC ATGGAGTTTT
GGCTCCTGGC TCCTAGTCTG CATCTTCACC CCATCCCCTTG CCCAAAGAAT CTGGTTATGT
GACCACTGCT CATCTTTTCT GCTGCCACAA CTCCAGTCCA AGCCACAAAC CTCTCTCTCC
TGGACTCCTG CGGGAGGTTT CTTTCTCTCC CTGCATGAGT CTATTCTCCG CACAACCTGGC

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FIGURE 6 (26)

ATAGGTAAGT GAGACTGCCG AAGAGGCAAG TTTGCAAGTC CAGAGGAAAT GAAGACTCTG
CTTGTGCACA TGCTGGGTTT GACGGGTGCT GGATATCCGA TGGATGGCCC TTAAGGTGAG
CTCAAGGCTT AAGGAGAGA TAGGGGCTGA TGATCTGAGA TTCAATCAGTG TGTGGCTGAT
GTTTAAACCC AGGGACACAG ATAAGAAGGT TATTCACAGG AGAGCGTAGA TAAAGAAGCT
AAATGGCTTC TGGGTCCCTTA GTCATTCAAA ATCGGACCTC TGAGGCAGGA GGAAAGCCCA
GAAAGAGTAG ATTCCTGGGA CTCACGGGAT AAAGACTTTC AAAAAGTGGG GGCTGGCCAG
TGCTGCTGAA GGAAGTAGCA GGACCGGAAC AGAAGGGTAA TCGTTGGACC TGGAGAACTT
GAATTTGAAT TTTAAGGTTG GTAACCTTAA AAAAGAGCAA TTTTAGATAC CTTTGTGAAAT
TATTTGCAAG ATTTGTTTGG TATAATGTGT ATTCCAGGCA AAGGACCAG AAAAGTAAAA
AATACTTACT GAACAGTTAC TGCATGCCCTG GCACTGTAAC ACCCTGTTTA ATTCTCACGG
CAACCCCTATA GAGTAGGTGT CATCATCCCC ATCTTACAGA TGAGGATATG AGGTGCAGCT

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FIGURE 6 (27)

AGATTAAAGCA GTTTCCTCA GGTACACCA ACTGGTTAAC GTAGAGCTAG GATTGAACC
CGGATGGGCT GATCCAGAG CTCATGCTTT AAATCGCTAG ACTGGTGCTC ACAGAAGACT
GGGACCGAAA AAAATTAAATA AAAAAAATAA GGAGCCCCCT GGGCTAGCAA ATTAGGAGTT
G TTCAGACAG ATGTGAAAAG GAAAGCAAGG CAGAGGGAAA GTCACGTGTAC AGAAGAGAGA
GACCCATGAC AGCAGAGACA GTGAGCTGGT AAAGTGGCTG GCGATCTAGC CCCTGAAAAT
ACCTCCAGAG AGGCAGGCTC ACGCCTGTAA TCCAGCACT TTGGGAGGCC GAGTGGGCA
GATCACCTGA GGTGAGGAGT TTGAGACCAG CCTGGCCAAT GGCGAAATCC CGTCTCTACT
AAAAATACAA AAATTAGCCG AGCATGGTGA CAGGCACCTG TAATCCCAGC TGTTCAGTTG
GCTGAGTCAG GAGAAATAGCC TGGATCCGGG AAGTGGAGGT TGTAGTAAGC CAAGATTGCG
CCACTGCATG CCAGCCTGGG CGACAGAGCA AGACTTTTCT TAAAACAAAC AAACAAAAAA
GAAAAAAGAA AAGGAAAGAA GAAAGAGACA AAGAAAGAAA GAGAGAAGGA AAGAAAGGAA

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FIGURE 6 (28)

GGAAGGAAGA GAAGGAAGGA AGGAAAGAAA GAAAGGAAA GAAAGAAAA GAAAGAAGAA
AGAAAGGAAA GAAAGAAAAG AAAAGAAAAG AAAGAAAAATA CCTCCAGAGA GCCAGGTCTC
TTAGGCCCTTC TGAGAAACTC ACATCCCCTTT TGATGAACAC AAATGCTTCA CACTCTCAAT
GTTATTGGTA ATCCAAGTTA TCAATATACC TAAATCACTT AGTACTGAAT CTGGCATATA
GTAATCACCT AATGAAGAGA TAAAGAGTCAT GGAGTATTCT GAAGCAATTA GAATCAATAG
ACTCAATATA CACATGGCAA CAAAGTTGGA TCTTAAAAAC CGACCTGAGT GAAAAAGGAA
AGGGAAGAT ACATAACACG GTACCATTTAT GTAAATTGAT AATATATGCT TACACAAATTT
GTAAGAACAC ATACAAATAG ATACATGTAT ATTAAATATA CTCGAACGGT TACCTATGGG
GTGGTGGCTG GAGTGGGGGT AAGTCCGTAA GCTGTAATGG AACCTAAACA AATACATGAA
ACGAGTAGGA ATCAGAAGGA GTAACAATAA AAATGTGCCA TGAAC TGAGG AGTGTAATTT
AATCAACTCA CTGCATCTGA GGTAAAAAT AGAAAGATGA TAATTGTTAT TCTTATTACT

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FIGURE 6 (29)

CGTAGGTCTT CCACTTGCCAC TCAGCTTTAC AATGTTGGAC TATCCTTCAG ATGGCACCCCT
CCTTGCACTT GCTCAGGCAG GAGAGCTTTT TCCCTCCAGCT TTCTAGGTGA TTTAATATAT
CAGGGAATAA GTATAAAAAA AGGCACGGTG CTCCCTGGGT AGCCTTTCTG GACTTCAGAG
CTAAATGCA AAGTCAGTTT TACACATGTG ATTTCACTCA TGAAATTAGG GCAAGGTAGA
AAACTGCGAC AGAAAAAATG TGATTTATTA TGGTGTTACT ATCCCTTACA AGCGGAGTGT
CAGCTGCCCTC TTTTGTGTCCA CTGATTTAAG GCAAGATGAA CTGAAAAGTGG CTATGATCAC
GTCCTCAAAA GCACACTCTG GCCCCTCGGC TGCAGGCGCC CTGCACATTC CCCAGCTGCG
TGTCCGGTGG TGACACAGTG CATAATTGTG GCGCCTTCCT GGTGCAAACT GTCTCACTTA
GCTCCGTCTT GCTGGCACAG CAGAAAGGAA GAAATCGAAA ATGTTTGAT TTCAAAGGTA
ACAAGAAGCT GGAAACAAC TACTGGCCGA GTCTGAGAGT TTCAGCGGAG ACTGGTGCAG
CCTTGTGTTT TTCCACTGAC AGCTGAAAAT GAGCCCAGCT TCAGTGAAGC TTGTTTCCCTT

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FIGURE 6 (30)

CCCTCCTCAA GGTACCCAC AATCTCAGT TCTCTCAGGA AAGCCAAAA ATGAATTGA
GGGTTAGGA TTGTGGTTCT TTTATCTATT ACAGGATTGA TAATATGTTC CTCCACCAGA
TGTTC TGCTT GTAACAATAC TCACTTCCTG AACTACTGC ATATGCAGGA GTGTTACTAC
CAAGGTAAAC ACAGAAATTGG CTGCCCCAATT CCAAATCCCT GAACTGAGTG AGAGAAATCA
GAATTATAAT AGGGGATTCA ACAGAGCTGG CTACGGATGT GCCAGTGGTC AGATACTTTG
CTCATCATAC GCAGGTGCTG CTGCTCTAGC AACTGCTCAC TGCTTCATTT CCTGCCTTGG
TCTTTAAATA CTGCTTTTCT CAGCTCAATT GGCTTTCTTC CCTCTGGCAG TCACGTTTCT
TTGGGTCAA CAGCAAATGA TTCTTTAGAA TCACCTGGTA CTCAAAGGAG CTACAAGACA
TTGGGCATCC ACTTCCACTC TCTTGAAAA ACAATTTTAT GGAAGCCAAG GTTGCCATAG
TGCCCTCTTGA GGTGTGTTGC TCAGCCAAGG CCCAAGCTTT GTGCTTCAA CATGAAATTA
GAGAGCTTCA GAACAAGATC CACATTTTCA ATGGCCTCAC CCAACTGGAT AAAAGAACAA

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FIGURE 6 (31)

TTGCCATATC TCAATGACCA CCTTTTTCAG GTGGGATGGT AGATGCTGGA ATGGGTCACA
GCATTGCCCA ACCAAACTTT GCAAAAAAGG CTGGAAGCTC TGA CTGGGA CCTAAATAT
GCAAAAGTTG ATAGGCTCTT CATGCAGAAT ATGAACCCCG TGTATGGATA TAGCTAAAGG
GTTGGCCCTT ATGTTTCTAT TCC TTCACAA ACC TGGTAGA ATAGATATGC TTGTTTCCCT
TTAAAAAATG TCAACAATG CATTATGAT GCTGTGTATA GTA ACTCACA GATCATGCTC
CATGAAAATG C TTCAGAAACC CAATATAAGG AGATTTTTTA GCCATGTGTG ACAAAGAGA
GGCCATTCA GTGTGAAAT TG TTCAGAGA AGTATTTGAT TATGTTTTCT CAGATCTTTT
TATTTTATT TTTTTTGAAA CAGAGTCTCA CTTTGTCAAC CAGGCTGGAG TACAGTGGCT
GTGGTCTCGG CTC ACTGCAA CCTCTGCCCTC CCAGGTTCAA GCGATTCCTC TGT CAGCTTC
CCGAATAGCT GGGATTACAG GCGCATGCAC CACCATGCCCT AATTTTGTG TTTT TAGTAG
AGACAGAGTT TCGCCATGTT GACCAGGCTT GCC TTGAACT CCTGACTTCA GGTGATCCAC

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FIGURE 6 (32)

CCACCTCAGC CTCCCAAAGC ACTGGGATTA CAGGCATGAG CCACCCGTGCC CAGCCTGTTTT
TCTCAGATCC TGTATTGTGTT TCTGAAGCCT TCATTTCTAT CTTCTTATTC ATTTTGGAAG
TAGTACACCT AAGTAAGGTT TTAAACAATC AAATATCTTT GGAAAATTCC CTGGTTCCCTT
TCTTATTCCCT ACAAAAATAT GTTCAGTATA GCTGATGTTA TGTTTCTTTC AAATTATTCA
TTTCTCTATC TCAGAAATTA TCTCATGCCCT AATTGTTATT GAATAGTCTT CACTTCTTGT
CATCCAGTTT CTGGTCTCTT ATTTCACTCT AAGTCTAAGT GGCTATTAGA ATAAAGAGCT
TGTAACAGAT TCTTTCTCCA ATATGTCCTTA TCTTTTGACT GCATGCCAGT GACAAACTGT
TAACTGTTTT GATTCTTCAT AACATTCCAC AGAACATGCT GACTCCTCTC TTCCCTGAAAG
CAATGCCCAA GCACAGCATT GTTAGATAGT ATGTACGCAA CAGGGACATG GGTGCATAGC
AAAAACTAGA AGGAAGGAGG ACCTTCCTTA GCAATGGGTG ATATGGTCCC TGGACTTAGA
CTCCAAAGG TCGTGAGGTG AAACACACAT CGTCCATACC CAGGAAGCAC ACAGGTGGGA

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FIGURE 6 (33)

TGGAAGAGCT GTGCCTAATG AACTTCATC CACGTGGAGG TGGAGGAGGC TGCAGCTGCA
AGAACTCAGA GCTGCCCTTAC CCAGACCAGG GACCAGGGAG GGCTTTCCTGG AGGAAACAGC
CTCTGAACTG CCAGCTGATA GAGGAGCTCT ACCTCAACTC TTCTGGTTCC CCAGGGCTGC
TTTTCCACGT CCATTTATTG GCACTGAAGT TTGAATACCT TCAGGGGCCC GAAAGCCTGC
CAGGTCCCTCT TCTCTGCAGA GCAATCACAC CAACCTGCAA AGGGCTAGGA AAGGGCTGTC
ATCATCTCCT ACTCAGAAAC TGGTTCACCTG GAAGGACTCA GGGGCCACTG AATACATCCT
GGCAGCTTTC ACAAGAAGGG CTTCTGACTC AAGGATGTTT CCATCTTTGC CAGGTCGCCCT
TTTCTCCTTC TCTTAGAGTT TGGAGGACGC AAATGTGCTG AGAAGTCAAC CTTTCCCTGCA
AGGTGAGACA CAAGGGCCTT TCCCAGCAGA AAGAAGAGAG CAAATGGAAG GTCCCTTCTTC
CTCCAGTAGA GGATGGACTC TGTCTGGCAG CCACCCAACA GGAAAAGCAC AATGCATGCC
TGCCTGCTTC CCTCCCTCCC TCCGTTTCTC CCTCCCTCCC TCCTTCCTCC CTCCATTCT

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FIGURE 6 (34)

CTTCCCTTCC CCTCCCTTCC CTTCCTTCC CCTCCCTTCC CCTTCCCTTC
TCCCTCTCCT TCCCTTCCCTC TTCCCTTCCCT TCCCTTCCCTTCCCT CTCCCTTCC
TTTCCCTTCC TCCCTCCCTT CCTCCCTTCT TTCCCTTCCCT TCTTTCCCTTC CTCATTTCCCT
CCCTTCCCTTC CTTCCTTCCCT TCCCTTCTTC CTACTTTCCCT ACCTTTAGGG CTCTGTGTCT
TTGGAGTCCA TTCTGATTAT GCTGTAATGT CTGCCCTTC CTCTTCTCTG TCAAAAAATG
AAAGACATGG AAGCCACTTG CCTTTTACTG AATTAAAAAT TAGTAAAAAGA GCTAAAAATT
AATGGTTAAA AATGTACGCA TAAATTATGC AGTATACTAA CCAATGAAAA GATACACTTC
TCTTAATTAA AAGCTGACAG GGAGGGAAC AAGAAAAAGAG AAACACAAAA CAATAATCTA
AATGACCTAT TAGTTGGAAG AACAACTCA GAGAAAATAG ATACTGTGTA TAGTCATGTG
TATGTCTATG GAATAACATT TGTAGAGAAA TCTGGACTGA TCCCTTCTGA GTAAAGAGAG
CTGTGGGTAC AATTAAAGGG AGATTGAAAG GAATCCAAA GCATAGCAGA TGCTGTGCCCT

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FIGURE 6 (35)

CACTGGAATG GTTGCCGATC TCCTCCAAC TATGAAGTGT TTGAGGCTCA ACTTAAATAT
AATTAAAGATA CAAAGACAGA ATGAGAGAAA GAGAGAAGGG AGCTCACTGG AAGAACACTC
AAGATTCCCTT ACTACTCAT TCTTAAATTT ACAATTGTTC TAGATGGAAA AGAAAAAAG
CTTCTCTGTT AAAAAAGGAG CTTGTGCTAT AGGAGGTTTA AAATATACTT CTGACCCATC
TCCAACATTC TAAATCCCTC CCAGAAAAGT ATGCCAATCC CAAGAAATAT TCAATCAAAT
TGCTGGAAAG AAAAATACAA AATATTAAAA TGTATTAGGA AGCGACAGTA ATTAAATCAG
AACTGGAGCA GGAATAGACC AGCAGATCAA TGAGACAGAC ATCAAGTCCC GGAATGTGGA
CTTGCAAATG CATTAAAGTAA TATGATATGC AATAAAGGTG GCACAGTGAA CCAATGGGAA
AAAAATTAAAT CTTATAATAA TTGATATTGC AATAATTGTC TAGTAATTGG GGAAGAAAT
AAGCTTATTC CTTATCTCAT TTCCTTTTTT CTTTTTGAGA CAGAGTCTCA CTCTGGTAGC
CCAGGCTGGA GTGCAGCGAT GCGATCTCTG CCCACTGCAA CCTTGCTCTC CCGGGCTCAG

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FIGURE 6 (36)

GCGATTCTCC CACCTCAGCC TCCCGAGCAG CTGAACTACA GGCGTGTGCC ACCACTCCCCG
GCAATTTTTT TTTCCATTTT TAGTAAAAAT GGGGTTTCAC CATGTGCCCT GGGCTGGTCT
TGAACTCCTG GGCTCAGGCA ATCCACCCGC CTTGGCCTCC CAAAGTGCTA GCATTACAGG
CATGAGCCAC CGCGCCTGGC AGCTCATTTT TTAGACTAAA TAAATTGGAG ATGGCTAAAA
GATTTCTATG TAGGCCAACT ATGTTTTTAA AAAGTTTTTT TTTTAAGGAT ATCTGCTGGA
ACCAATCATG CCACCAACCA AAGATGCAAG ACTATAAAAC ATACCCAGTT TTTCAAAGCA
TTTAAAAAAT ATTCTAAAAA TATTTTTTCT CCAGAAAATT TGCATTGATT CCCTGAAAGAA
GCATTAATAT GGGACCTGAC TTATAAAATG ATGAACTCAA TCTCCCCACT CAAGGTAGGA
GTCTCTCAGA TTTAAAAAAT AAGCATCCCTA GTCCTCTTGT CCCGTGAAAA GTTAACCCCTT
ACACCTGAAA CACCAGGAGA CTGGCGGTG TTTGCATAGG GGTACAAT AAAGTTGAGC
TACCTCTGAC ATCTATTAAAC ACCAAAATTA GTAAACTATG CATGTATGGA GACTTTTATG

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FIGURE 6 (37)

ATTGAACTTG TTTATTGAGT CAAGAGATAT AGTTACAAT GAAATTTGG GGCATATCAA
AATGACCTTG GCTTAGCTTA GCATTTGCTG ATGTTAACTA TTTTCTTCAT TGGGCTGATT
TTAGTTGCTT AGGAAAAATA CAAACACACA CACTTTAAAA TTATATTAAA ATCCCGTCCT
AAACCTCAGA GTCCAGAACC GCATCCTAAC ACTGGTCATG CATAATATGT TTAAATTTT
GTGCTTTAAA AACTACAAAT AAGGAATGTA TTAATAGTTC CACAATCAAT GGTCAAGTTAG
CCGAGGGAAG ATTAGCATAG TTAAAGACTT AAAATGGCTT TACAACATAT ATCAAAAGGA
CAAAATAAGG GGAACAGAGT CTAGAAATGA GGAAACTGGG ACACAGGCAA AAAAAA
TGAGAACTGG GACATGAATA ACGCAAGGA TAAGACTAAT ACACAAACA CCCCATAA
ATAGCCAGCA TTTTGCTGAGC TCTTACTGTG AGCCTGTTCT AAGCACTTCA CATATATTAA
CTCATTTTCAT CCTCAAGGAA CCATCTGAGG CAGGCACTGT TATCATCTCC ATTTTACAGA
TAAGGAATAG ACCCAGAGAG GCTGAGCAAC TGGGCCTATT CCACAGCTAC TATGGTGGAG

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FIGURE 6 (38)

ATGAGATTTA AATCTAATCA TTGGCTCCAG AGCCCATGCA CCCAATGGCT GCACTAAGTG
AATGCATGCG CTATCAACGT TGCCAAAAGT GGGCCACAGC TCGGATCTGC GTTTCCAGT
AGCCAAAGCA GAGAGTGTGA TCAGACCCTCA CTTTAATAAG CAAGTCTCAA GCCAGAGAGA
GGTGGTATCA GGCAGCAAAC AGGCTGCTAG TCGAAATCCC ACTTCTTCTC TGAGTGGTCC
ATACAGTTT ACTCTACTTG CTTACAGAAAT GAAAATAGCT GGAGTTCAGG TCGGCTTTCA
ATGCCCTGTT GTCAGGATTG GGCTTTTCAA GTTTATTTT TGTGTGTGTT TTTAATAGAC
TGTACTIONTT AGAAAATTTT TAGATTTACA GAAAGATTGA GAGGATAGTA CAGAGAGTTC
CCGTATACCT CACACCCAGT TTCTGCAATT ATTAACCTCT TACATTCTG CGGTACATTT
GTTACAATTA ATGAGCCAGG GCCGGCCGGG CACAGTGGTT CAGGCCCTA ATCCAGCAC
TTTGGGAGGC AGAGGCAAGC GAATCACTTG AGGTCAGGAG TTCGAGACTA GCCTGACCAA
CATGGTAAC CCTTCTGTGA CTAAAAATAC AAAAAATTAG CCAGGCATGG TGCTGGTTGC

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FIGURE 6 (39)

CTGTATTCCC AGATACTCAG GAGGCTGAGG CACAAGAATT GCTTGAACCA GGGAGGCGGA
GGTTGCAGTA AGCCGAGATC GTGCCACTGC ACTCCAGCCT GGGCAACAGA GCGAGACTCC
ATCAAAAAA AAAAAAAAAA AAAAAGAAGG AAGGAAGGAA GGAAAATTAA TGAGCCAATA
TTGAGACATT ATTATTACTA AAGTCCATGC TTTATGCAGA TTTTCTTAGT TTTTACCTGC
TGTCATTTTT CAGTTCCAGG AATGCATTCA GGATGCCATA CCACATTAG TTCTCATATC
TGCTTAGGCT CCTCTTGGCT AGACTGAGTT TTAATCTACT TTCTGCAGAG CCTGAGAACT
TTAGCATAAT TTCCCTTGGA ATTACAGCTC AATATTTCA AGCACTTATA CAAACAGCCT
AATGTTACGT TGGCCCATAA CAGTGTTTCA AGGTAATAAA CTTCCTTTGTT TTCTGTGCCG
ATTGAAAGAA CTGCTGCTTA GCCTCCTGCC AGATGATGAA CTGGGTACAC ACGAGCATTT
TTCCAGGTAA AGCATATTTC GTGCGACTTC TTAAGCTGCA GCCTTATATG CAATAATTGT
CCATTACAA GACTTATGTT CGAATTTCAG GCACTCTGTT TTCACTAACC ATATCCCTCA

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FIGURE 6 (40)

ACTTTGATAA G TACTGCTTT AATCAACTCA GAAAATTAA CTTGACTAAT TTTTTTTCAC
CATCAGTTTT TTTTCTGTTG ACTCTTTCTC CTTTTTCTGT TTGCCCCAGAA ACATGCTCAG
GATTCTCTCA GGCTTTAAAA AATGAAAAAA TGTTCCTGTC AATCTAGTTA CTCCTTGATT
CTCTTGTTCT GTTTATCGCT GGAATCTTG AAAGCTTGGT GTATTAGTCT TTTTTCATGC
TGCTGATAAA GATATACCTG AGACTGGATA ATTTATAAG AAAAAGAGGT TTAATGGACT
CACAGTTCCA CGTGGCTGAG GAAGCCTCAC AATCATGGTG GAAGGCAAAA GGCATGTCTT
ACATGGCAGC AGACAAGAGA GAATGAGAAC CAAGGGATTT CCCCTTATAA AACCATCAGA
TCTTG TGAGA CTTATTCACT ACCACAAGAA CAATATGGGG TAAACCGCCC CCATGATTCA
ATTATCTCCC ACCGGGGCCC TCCCACAACA CGTGGGAATT ATGGGAGCTA CAATTCAAGA
TGACATTTGG GTGGGGACAT GGCCAAACCA TATCACCTGG CCTATAGCAT TATTCCATT
TCTTCCCCAT CCTTTATTC CTCAAACCGG TACAACCAGA CCTCTTTTT TTTTTTCTA

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FIGURE 6 (41)

CCTGAAACTG CTCTTTTGAG GGTAGCTGAT AAGTCCAAA TACTGTCACC TTTTCTCAAT
TCCGTTCCCTT CTTATGCCCTT TGGAGCAATT GACTGTGTTG GTTGCCCCCT CTTTAAAGT
GTCCTCACT TGGTTTATG ACTAATGATG ATTTTCTTTT TCCTCTCTAA ACATTCCGCT
ATCTTTTAG CTCCCTTCC CCCCTCCATC CCTTAAATGT CCTGTGTTCC CAGAACTGTC
CTCACCTCTT TGACTTCTCT ATGCCCTGTC ATTCACATCAT GGGTCTTTAT TACATTATTG
CATCTGTGTC AATAACTCTG GTCTTTCTGT TAAGTTCCAG TCTCCCCATTT TCAAATGTCC
CCAGACATTT CCAATTGAGT ATCTCTCCAA TGTATTTAAC CTGCTAAATA TCTAACACAT
AATCTTTCCC ATCAAATCGT TTCCCTCTTAA GCTTTTCGTT ATTTCCCTATT AGACTCCCTGC
ACTTCTCCCA GGAGCCCAGA CTTAAACCT TGAATTCTC ACCATAACCT CTCCTTTGTC
TCCCATAATC AATTAGTAGC AAGTGTATC AATGATTACT TGACAATATC TTTTTCATTT
TCCCTCCCTG CTATGATCAT TCATCTAGCA AGAAGAGTTG GCCCTTTGTA TCTGTGGTTT

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FIGURE 6 (42)

CTGCATCCCT GGATTCAACC AACTGTAGAT GGAATAATTT TGAAGAAAA AGCGTCTATA
CTGAGTATGA AAAAATTTA TTTCTTGTC TTTATCCCTA AACAAATACAG TATAACAACCT
ACAGCATTTA CACTGTAGCG TATAGATCTT ATAATCTAGA AATGATTTC AGTACACCAT
TATATATAAG GGAATTGAGC ATCTGTGAAG TTTGGTATTT GTGGGGCATA CTGGGACCAA
TTCCCCCATG GATACAGAGG GACAACTATA TTTACTCAGT GCTTACTAAA TACCAGTTGG
CCAATGTGTT TTTCTTTTTC TGTTTTCCCTG TCTTTAGTTT GCCCCTTGCC AATTAATTCA
ATAGTGCTGC CAATGCCAGG TGTACCCTTCA GAATATTCTA TTCTAATTTT GTCATCTCCA
AGCTTAAAAA TATTTAATGG GCCAGGCGCA GTGGCTCACA CTTGTAATCC CAGCATTTTG
GGAGGCCAAG GGGGGTGTA TCACTTGAGG TCAGGAGTTC CAGACCAGCC TGGCCAACAT
GGCGAAACCC TGTCTCTACA AAAAAGTATA AAAGTTAACC AGGTGCTGGA GCATTTGCCCT
GTGGTCCCAG CTAATCAGGA GGCTGAGGCA GGAAATCAC TTTAATCTGG GAGTGGAGT

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FIGURE 6 (43)

TTGCCAGTGAG CCAAGATCTC TCCACTGCAC TCCAGCCTGG GTGACACAGC AAGACTCTAT
CTCAAAACAA CAATAACAAC AACAAACGAAA AACATTTAAT GGCTGCACCT TGCCGTGTGAA
AAATGCATTT CTTGGCCAGA TGTGGTGGCT CAAACCTGTA ATCCCAACAC TTTGGGAAGC
TAAGGCCAGG AGTTCGAGAC GAGCTGGGAT ATATAGGAAG ACACAATCTC TACAAAAAAA
AATCCACAAA ATTAGTCAGG CTTATTGTTC ATGCCTGTAG TCCCAGGTAC TCAGGAGGCT
GAGGCAGGAT TCCTCAAGCC CAGGAGTTCA AGGCTTCCGT GAGCTATGAT GGCACAACTG
CACTCCATCT TGGGTGACAG AGCAAGGTCC TATCTCTGGA GAAAAAAA AAAAGAAGGC
ATTCTTAGG AGAGTTCCTC TCTGTAGAGT CCTAAGGGTT CCATGGAACT CCTTAAAAGC
ATCAGAGTAT GTGAGTGCAA TGGGAGGAAG CATTAGCCA GAGCAGTTGT GCTCCCATTG
CATATTAATT TTTAAAAAAC AAAGCTATAA AAAAAAGTTG AAAACTACTA CGTTAGCATC
AGCCTGACAT TTAATGGCCT CGTAAATCAA ACCTTAATTG ACTTTTTAGC CAGTTATGCT

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FIGURE 6 (44)

ACTAGCCAAC TACAGACAAC ACACTTTTAA ACCAAATTAG ACTAATAGTT GTCATCAGTG
GAAATCAAGT TTGCCATTCT TCCATGCCCTT TGCTCACACC ATTACCTTTT CTGGAATGTC
CTGTACTCAT CTTCCTGTGT TGAACCTCTAT ACCCAACTTT AAAAACCTAG CTCAAAGTTC
AACACTTCCA TTCCATTTCA AAAAGAGCTT TCCCTCTTCCT TAAAGTTTAA GAACTCATTT
TCATGAATCT TTTTGGCATT TATTGCACAC ATGCTTGCTT TGTGTTATTT GTGTTCAGCC
TCATATGCC CCAAGGTGTT TTAGACTCCT TAACGGCAAA AATGATGCTC TAAACACCTT
TCTATCTTTC ATAGTGTCTT AGTCTGTTTG TGTGCTATA AAGGAATACC TGAGGCTGGG
GAATTTATTT AAAAAAGAGG TTTATTTGGC TCACAGTTCT GCAGCTATAT AAGAAGCATA
GTGTCAGCAT CTGCTTCAGG TGAGGGCTTC AGGAAGTTTC CACCCATGGT AGAAGGCAAA
GGGGAGCAGG CATCACATAT CAAGAGAGGA GGAAAAAAG GAAGGAAGAA AGGAGGGTGC
CATTCCTTT CAACAATCAG TTCTTGTTGG AACTAATGGG ACAAGAGGCT GGGCACGGTG

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64/285	75/285
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66/285	77/285
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FIGURE 6 (45)

GCTCATGCCCT GTAATCCCAG CCCTTTGGGA GACCAAGGTG GGTGGATCAC CTGAAGTCAG
AAGCCTGAGA CCAGCCTGGC CAATGTGGTG AACTCCGTC TCTACTAAAA ATACAAAAAT
TAGCTGGGCC TGGTGGCGTG TACCTGTAGT CCCAGATACT CAGGAGGCTG AGGTAGGATA
ATCACTTGAA CCCGGAAGAC AGAGGTTGCA GTGAGCTTGT GCCACTGCAC TCCAGCCGGG
GCAACAGAGT GAGACGGTCT CAAAAAATTT TAAAAACTTT AAAAAATAATA GAGCAAGAAA
GCACCAAGTT ATTCAGGAGG GATCCACCCC CAATGACTCA AATACCTCCC ACCAGGCCCTC
ACTTCCAACA CTGGGGATCA ATTTCCGTAT GAGATTGGA GGAGACAAAT ATCCAAACTA
TATCACATAG TAATGAACAT AGTACCTTAT CTATAGAAAG CAATGGCTAG ACAACTGTTG
AATGGCTAAC CAAATCTGCT TTCCCTATGGT CTCGCTCTAG AGGGGGTCAG TATGAGTTTC
TGTCAAAAGG AGAAAAAAA ATGTATAGTC AGTTTGTGTGT GTGTGTGTGT TCATGTAAAA
GAGATCAAGA GAAAAGAACA AGAGAAATCA TGAAAAGGAG GGGGAATATA AGAATAATAC

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FIGURE 6 (46)

ATAGAAAAA GCAAATTATC TTGTTTATCA GTAATACCCA AGGGGGTAGA AATGGTAAGT
AATAATCCTT CTTCACTTTG TCTGTAGTTC ACTTTTITGC ACCTTTATTT TGATGAATTC
ACATCGAAGA CATTAACCTCA TTAAGGCTTC CAATATTTT GGAGATAAGA AGGGCTGCTA
TGCTCTTTAT AGATGGAAAA CTTGGGTCAT TAATAACTCA AACAAAGACA TAACAAAGAA
ATGGAGCATA AACTGCCAGG TCCTGACTGT AGATTTGGAT TCCAGTTGG TGTCTTGTC
CCCTTTGTTA CTCTTCCTAA AGTTATGATC TTTTCTTGTC CATAGGAAAT TCATAGTGAT
TTCCCATCAC CCTTGGGATT ATCATAGCTC CTTTAAGGTC CCTCTATGC ACTCAATAAC
ATCAACAGTA AGTGTTCTTC GAGCACTTAC TGAGTGTATA TCATTGTGTT CTCACGCAGC
ACCCACAGAT CTCACCAAGA ACCTAGCTGA AGCCTGTAGA ATGAATAGGT AAGTACTGCC
ATGCCAATCT GGAGTACTCA AGCGATGCAA ATGATTCCCTT TAATTGTACT TTTGCAGGCT
TGTCAGTTTT GCTCATGGAG AAGTGGCTAC TGCATCCATG TTATATCTAT GTAATGTTGG

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FIGURE 6 (47)

ACTGCGAAGC ATCACTTGAC TTTTCCAAG CAGAAATTAC AGCTGATGAC AAGCTGCTGC
TGAGAAAATG GATATTTTC TGAATTCAGT TCTACGTGGA AACAGCTGAC TAGTTTCCAT
TGCTGTAAGA ATGGCTCTTT TGCTCTTGGT TGATTTTGAG TAAATGGCTTT ACTTCTGTAG
AAAGGAGATT TCATTTGAAG TCCACTCAGG GATTGGGTC AACAAACTGG AGTACAGGTT
TCAGAAAATA TCTCTTTAAT CCTCCAATAA TAAATTTTCT CATCTATAAT TCCTGGAACA
CTTCATCCCTT TGCAGCCGAG CATATAGATA GATTGTGTC TCACTGTGTT CTGATTGCCA
CTTTGACCTG CTTTTTCAAC TTAGGTACA AATAGAACAG AATCTCTCTG ATTTTCTCTCA
TTAATTGTTT GAATTCCCAC TTTTCCCTCAT TAGCAAGAAG TCCAGTATCT TCCTGAGAAC
TTCCCTTTTCT CAATCTAGGA ACTTACTTGG TCCATAAAGT AACAGTCTTA TTTTCTGACTA
TCAAGGAGAG AAATAACAGG AGCCATTATC ATCTTCATGG TGTCACCTTTT GAAAACTGGT
CCTCTGTAGA TCTTCAGATT CTTGCGTTAG TCCATTTCAGC TGCTATAACA AAATTGCATA

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FIGURE 6 (48)

GACAGCATGG CTTATAAATA ACAGAAATGT ATTTCTGACA GTTCTGAAGG CTAGAAAGTC
AAAGATTAAAG ACACTGGCTG ATTTGGTGTC TGGCGAAGGC CCATTTGCTC ATAGATGGAC
GATGACCTTT CACTCTGTCT GCACATGGCA GAAGGGCAAG AGAGCTCTCT GGGTCTTTTT
TATAAGGGCA CTAATCTCAT TTTTGAGGAC CCTGCCCCCA TGACTTAATC ACCTCCCAA
GGCACTGTCT CCCAATACCA TCACCTTGAG GGTAGGATT TCAACATATG ATTTTGGGG
GACAGAAACA CGCAGTCCAT CTCGCTTGTC CACTCCATGG TGGTATTCTT GCTGGATCAG
TTTCTCCTCTT GGGGTGCATT TGTGTTCCAT GTCTAACTG CAAGTTATAG CAGGCCCGAT
AGCAAAGTAT TCCAATGTTG GTATGCAGAG GCATTGAATA ATCAGAAATGA ACCCACGCCA
TAAACAACCTG GTAGAGCTGC AGAGAGTACC AGCTGATTAT GAGCCCTGGG TAACAGTGGT
TTTTTAGTTCC TATGTCCGTC AGCCCTTTTC TCCCATAGTA GCCCCACTGT GTTGAAGTGG
CTGAATCGAC AGAAGCTTC AGCTTGGGCC ACATGCTCAT GGAACCAATT CTCCTTATGA

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FIGURE 6 (49)

GCCGTACAAG AGCTGGGTTG CCATTCTGGA TACCCCTCTTT TTTCAAGAGA TTTTATTTC
AGGATATTTT TTCTTTTATC AACTACAGGG ATTATTTAGA ATCTTAGGGC AGTGGTGCCC
AACCTTTTGG GCCCCAGGGA CAGGTTTGT GGGAGACAGT TTTTCCATGG ACCAGTGTC
GGGGGCTGGG AGGCATGGTT TTGGGATGAG TCAAGTACAT TACGTTTGT GTATACTTTA
TTTCTATTAT TATTATATTG TAATATATAA TGAAATAATT ACACAACCTCA CCATAATGTA
GGAATCAGTG GGGAGCCCTA AGTTTGT TTTT CCTGCAACTA GACAGTCCCA TCTGGGGGCA
ATGGGAGATA GTGACAGATC ATCAAGCATT AGATTCTCAT AAGGAGTGCT CAGCCTAGAT
CCCCGGCATG TGCAGTTCAC AATAGGATT GCTCACCTAT GAGAACTCTAA TGCCACTGCT
GATCTGACAG GAGGTGGAGC TCGGGCAGTA ATGCGAGGGT TGGGGAGCAG CTGTCAATAT
AGATGAAGCT TTGCTCGCTC GCCTGCCACT CACCTCCTGC TGTGTGGTCC ACTTCCTAAC
AGGTCACAGA CTGGTACTGG TCCATGGCCA GGGAGTTGGG GACCCCTGTCT TAGGGAGTAG

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FIGURE 6 (50)

GGGTGGAGTT CCCTTCACTT CTAGAAGGCC CTGGATTAGT ATCCCAGAGC TGTCAATTACA
GAGTATCACA AACCAGGTGG CTAAAAACAG ACATGAATTC TCTCTTATTT TTGATGGCTT
GGAAGTCCAA AGTCAAGGTG CTGCCAGGC CATGCTCCCT CTGAAATGTG TAGGGAGAA
TCCTTCCTTC CTCCTTCTAG CTTCTGGTGG TTTGCTGGCA ATCACTGGCA TCGCTTGGCT
TGCAGCACTT CAACATCTGC CTTTACTGTC TCATAGTGTT CTCCCCCTCAT GTCTCCAGGT
CTCTCTGTCT CTCTTCTTTG TATAAGGAAA CTAGTCATAT TGGATTAAAG GCCAACCCCTA
CTCTAGTATG ACCTCATCTT AAGTCACAT GCAATGACTA TTCCAGATAA GGTCACATTC
TGAAGAAGCTG GGAGTTAGGA CTTCATATCT TTTGAAGGAA CACAGTTCAA CCAATAACAG
CCCCTGACT GTTTTACAAA TAGGTATTCC TCTCCTTCCC AAAGTTCTTC ATAGCAGAGA
CAACTTGTA CAAAAGGCAA AATACCTTAT TATGTAACCT TAACCTAGGA TCATAGATCC
CTACTGTCTG GTGCTTTTATA AGCACAGAAC CACCGGAAA TCATTATTAA GACAAGGAAA

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FIGURE 6 (51)

GGCCAAAGTGC AGTGGCTCAT GCCTGTAATC CCAGCACTTT GGGAAATTGA GGCAGTGGA
TCAACCTGAA GTCAAGAGTT TGAGACCAA CTGACCAGCA TGACAGAACC CCATCTCTAC
TAAAAATACA AAAATTAGTT GGGCATGGTG GCATGTGCCT GTAATCCCAG CTAATCAAAA
GACTGAGGCA GAAAAATCAC TTGAACCGAG GATGCCAAGA TAGCAGTGAG CCAATATCGT
GCCACTGCAC TCCAGTCTGG ATGATAGAGC AAGATCCGT CTCAAAAAAT TAATAAATAA
ATAAAAAGAC AAGGAAAGCC TTTTCCAAGG AGACCCTTCT GCTTTGCTAG TTCAGAGAAC
TTCTCTTTTG GAGAAAACAA ACACCCAGTC CATTAGCAGC AACGTCAGGG ATTGAATTCT
TAGGGCAGCA GGCTGGGCAC AGTGGCTCAT GCCTGTAATC CCAGTACTTT GGGAGGCTGA
GATGGGTGGA TCACTTGACA TCAGGTGTTC GAGACCAGCC TGGCCAAACAT GGTGAAAAC
CATCTCTACA AAAAATATGA AAAAAAAAAA AAAAAAAAAA GCTGGGTGTG TTGGCTTATG
CCTGTAGTCT CAGCTACCTG GGAGGCTGAA GCAGGAGAAT CACTTGAACC CGGGAGTTGG

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FIGURE 6 (52)

AGGTTGCAGT GAGCTGAGAT TGCCCTACTG TACTCCAACC TGGGTGACAG AGAGAGACTC
CATCTCAAAA AAATAAAGAA TTCTTCGGGC AGCAGTCTTT CCTCCACCCTC ATAGACCATG
GAGGTGAGCC AGCTCTGACA AACCATGAGA ACAATGGCAG AGACATACCT GTAACGTAAC
TGA CTGGGC AAAGACAAAG GTGAGGAAAA TGACAAGTTT GAGGAACTAT GAGACCAGGC
AGTGGGGAAC ACCACTAGCA GAAATGATGG AAGTTCTCAA GAATAACAAC AGAGAAAATAG
ACCATGGCCA GAGCTAGAA CCTCCAGGG AAAGGAGATG GGCTCCAGAG GCAGAAGAGG
ACGTTGAAGG GAAATGGGAG TGGGTGAAAT ATATAGACGA TGGGGACCAC CCAAGAGCAG
TCGCTATTGC AAAACTGAGG AGAAGGAGAG TCTGGAGGGG GTGGTGGAA GCTGGGTCTC
CTAAGGAGGT TTGACAAAA GCAGTCATGG AGCGGGCTTA GAAATCACAG TTGGGGACAG
GGTAAAGTTC CTCGGGATAT AGAGGATGAG ATTAGAAAGAG GTTCCAACTA GGTAGTGTG
GAGAAAAGCA CTATTGACCC AAAAAGGAAG GAGAAATGTGG GTGGAAGTGG CAGAGAAAAGA

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FIGURE 6 (53)

GGGGTTGAG CAGAGAGTGG TGAATTTTCT AATGCAGAGT TGTGGGAGGT GGAGTGCAGG
GAGCCAGGCT GGGTGGCTGT GCTGATGTGA TTAAGCACTT ACTGACTGCC AGGCAATGGG
CTAAGTACCT GAGATGCTTT GTCTGTTATC CCTCCCCGAAA CCCCTCTGAG CAGGTGCAGT
TATTATTCTC ACTTCACAGA TAAGGAAATT GAGGCACAGA GAATTGAGTA ACTTACCCAA
GGTGACATAG CTCATATATG GTAAAGCAGG CTTTGAACTC AGTCTAGCTC CCGAACCTAA
GCTTGTAAC TACTATGCTTT TCCCCAAAAA AGGGGGCTGG CACAAAAAGA GCTGAGGGGG
CTGGGCATGG TGGCTCATGC CTGTAATCCC AGCACTTCGG GAGACTGAGG CAGGTGGTTC
ACCAGAGTTC AGGAGTTCGA GACCAGCCCTG GTCAACATGG TGAAGCCCTG TCTCTACTAA
AAATACAAAA ATTAGCTGGG TGTGGTGGTG TGCACCTGTA GTCCCAGCTA CTTTGGGAGG
CTGAGGCAGG AGAATCGCTT GAACCCGAGA GCGGATGTT GTAGTGAGCC AAGATCATGC
CACTGGACTC CAGCCTGGGT GACAGAGTGA GACTCCATCC AAAAAAAGA AGAGCTGAGG

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FIGURE 6 (54)

TGATGGCCAC CATCAGCATC AGCCTGGAAG TTATAGCAGG ATGCTAAGTT TCTCTAAAGC
TGTCCTTCTT AGGACTTGAA AAAGATAACT TGGGTTTGTA TCCCATCTCT GCCATTAGTA
GTTTACTGGC TTTGGATAAA TTA CTTAGCC TTA CTGAACC AACTTTGGAT TTTTATAGAG
ATACTGTAAT GAAAGGAATA AGGTATCAGT CTTAGCAGAG CATCCAGAGT GTTCCTATTA
AAACCTAAAT CATATCCTGT CATTGCTGTG CCCCAAACCA TTCAATGGCT TCCCAACTCA
AAGTTAAAA CTCATCTTTC CAGTGGCCTG CAAGAGCCTA TGCTATCCGG TGTCTGACCT
CATCTGTTGT TCCTTTCTCC CTCCCCTTCT TGGCTCCAGA CGCACTCTGG TCTCCTTGCT
GTTCCCTTGAA TACACCAGGC ACACTCTCTT CGCCTGAAAC ACTTTACCCC AGATATCTTA
GCTTACTCTC TGCCCTCCCTC AATTCA TTGA TGAAATGTCT CAGTGAAGTC TTCTCTCTCT
CCTCTGTAAA AGTATACTCT CTGTTCCTCT TCTTTACTGT TCTAGCTACT ATTGCTGTGT
AACAAATCAC TCCCCAAATT TAATGAGTGA AAACATCAGC CATCATCTTA TTTCTCACGG

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FIGURE 6 (55)

TTTCTGAGG TCAGGAATTC TGGAAGGCT CAGCTGGGAG GTTCTGGCTC TATAATCTCT
TATGCAGTGA GAGTCAGATG CTGGCTAAAA CTGAAACAAA GCAGGGTTCT AGTAGCTGAG
GGCTGGCTGG GTCTCTCAGA TATAGTTCAG ATCTCCTCCA GGGGGTCTCT CCACGTGGGC
TAGTCTGAAC TTCTCTCACAG CATGGTGGCC TCAGGGCAGT GGA CTCTGCA TAGTGGCTGA
AGGCTTCGCA GCTGAGTATT CCAGCAAGCA AAGTGGGAGC TGTATTGCCCT CATATGACCC
AACCTTGGAA TCCACACAGC ATCACTTCCG TGTATTCTAC GGGTTGAAAA GTCACAAAAA
CCAACCAAGT TCAAGGAGAA GGAACAGAGA TCACATTTCT CAATTGGAGA AGGTCAAAG
TCACATTGTA ATCAGAGCCT ATGGGATACG AAGTATTGCG GTCAGGTATG AAAAATTGTA
TTTGCTGCAT CTGCTTTACT TTCTCCACAG CGTTCATGAT CTGCTTCTCA CATGATATTG
ACTTACGTCA TTTCTGCGTT TCCTGTCTTC CACACTAAAA TGTACGCCCTG TTTTGTTCAC
TGCTGTATCC CCAGAGCCTA GCACGGAGCC CAGCATGTAG TGGTATCCAA TAAATACTTG

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FIGURE 6 (56)

TTGCATGAAT GAATCTGTC TTTTAATCCT AGCTATAGGT TTCTAAGTTA AATATTACTA
TAATCATCTT ACAGACGAGG GAAATGAGGC TCAAGAAGAT TTGGTAACTT ATGCGGGATC
ACTCAGCCAC ATAATGGAAG AGACAGCATT GAAGTACACA TGCTTGCTCT GTCTGCTCTT
CCAAGCTGCT CATCACACAG CTGCACCTCT GAGGACTTCC CTCCCCAGTC CACCTCCACC
CTTACCCAGA GACACACATG GCCACAATCC ACTAGCAGAC CAAAATTCAA TTTTTCCTCCA
GTTGGTTGCA CTCAAGCTGA GAGCAAAGCA ATTGCACCTT AAATCCCCCT ACAGCAGATA
TTTCAGAGCA TGTTCCGGAAG AACCCATCAC ACTTGGCCTT TAGATCTTAT TTCTGGTTTG
TTACAAAAAC ACAATTAAAT GAAAGGTTAG GTAGCTTTTG AATGGCCAGC TCAAAGTTTT
GGCTTATTTT TGCCTTGCTG TCTTTATAGG CATTTTACCA ATATTATCA CTATTTCCTT
TAGGGAACCC TTAGATCTGT GATATTGAA ATAATAAAGC CTCTCCATTG GCCCTTTAAA
AGGTTTGTGG TAAAACCACA CCATTAAACAT TCACAGTTCC TTATTATGA GGCCGTGATTG

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FIGURE 6 (57)

CACTTATTTC CATAATTCTC ACTGTTTCTC CGATGAGGAT TTCACATAAT AGTGTTTGAA
GGCTAAAGAC TTCAAAGCAG ATTCTTTACT ATTTTATCT TGAAAAATAT TCAATATTG
TGTAATTAAA GTGAAGTCTT CCTAGAGAAA ATGACAACTC AAATAATCTT AAATGTACCT
CCAAGAAAAA AGCTGTCAA GTGACATTTA GTAATAGAGT CACATCTCT AAGGCCTTG
CTTCTCCTTC TGATTCTTAT CATCTTTGAA GGTATGTCA TGGGCTGACT TCAAATCAAC
TTTTAAATTT ATTATGGCCT TCTTTAAATG TGAGTCTCTGA AGGTGAGGGG CTTTATCTTT
CTTTTGCTCC AGATTTTTTT TACCGCGTCA TTACCAAGCA TCTTAAACA AAACCTAAAA
ACAAAAATCT TCCTTGACCT GGTTTTCCC ACTAGCTAAC ATCCTATTTT TATCTTTCCC
CTTTGCACTA AAGTTTTTA AACGGATCTT TATACCCCTCT GTCTCCATTT TCTCATCTGC
TAACTTATAT GGCAAAGATT ACCACTGCCCT TTCAACATAA TTGGCCAATC TACAGAAAGT
TTTCAAGTTC TCTTTTAAAT TGACCACCTC CTGCCCTACCT CCCACCTTT GACATCTTGC

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FIGURE 6 (58)

TTCTCACTTG GCACCTTACC CAGTGTCAA GATCCCTCC TTTAGGATGT CTTCAGAGCA
GCTACACAGT TGGTACTATA ATTTATACAT CCTTGTACAC AGGGCTTGCT GGGATATTGA
TGGAGAGAAG GAGGAAACTG GAAGTAGTTC AGGCCAGAGC TAGGGAAATT GACCCATCTC
CAGGTCTCAG GTCTGCAAGG GGAGCTCACA GCTTAACACA TGGAGTCTAG AAAC TTGTGC
TGGACCTTGA CCAACACCAG CCCATGGAGT CCAATACAGT GCTCAATAGG GATTTC CAGG
AAATTGCTAT ATTTATTCAA AGAGAACTTA CCAAGTGTCA GCTACGTGTT GGGCATTTGTG
CTAGGCACAG GGACCACAAA GATAAGACAT TGTAGCTTTC CTTAAGTTGC TCACTGAGTA
AATAGAGAGA CAGAAAGGTA AACAGGTAAG TGCAAAAATA CATACAATTC AGCAATAGTG
TTCATAGTGG CTATGGAGAG AACGCTCACT AACTTTGTTT AAACAGTTGT TC TTTCAAGG
ATTTGACATG GATTTGATTG GAAAAGCATG ATACCATTTT TTGCAATTAA ACACAGGAAT
ACATAAATAA AATGCATCAG TATTTT TAC AAATAGCTAC TAAGAGCTAC TAGAAAACCT

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FIGURE 6 (59)

GGGAATTCTT AAAACCTTAC CATGCTACTT GCTCTAAAAT ATTTATTTT ATGTTATTTT
GTACATTTCT TTACCTACAC AAACACCACT GTTTTCTTCA TTTCTTAGTC TATTAAACC
TCACACCCTT TCAGCATCTC TTAATTATT ACTACCATCT GTTAGTTCTC CTGTCCTGAA
TGAAACAAA ATGGCAGAAT GTAAAACGAG GGCGAACAGA TTTTGTGACAG GAAGTATTC
GAGGTAGAAG GAAATAGTCA AGACACATAT GATAAACGAA AACAAATAA ACTTTATACA
TAACAACCTA TAGACACATT TAAAAAGTTT AAGATCTCAA GAGCTATGTC TGAATAGATA
GGAGTAAAA CTCATTAAG TAATTAGGAA AATAACAAGA ACAGTGAATT TCTTAATGAA
TGGCATGTAA TCAAAACTGT ACTATCGTC TAATTCATAA TCTTGAAATGT TTTTATTTTA
TTTATTTATT TTTTATTTT TTGAGACAGA GTCTTGCTCT GTCACCCAGG CTAGAGTACA
GTGGCGTGAT CTCAGCTCAC TGCAACCTCC ACCTCCCAGG TTCAAGCGAT TCTGCTGCCCT
CAGCCTCCTG AGTAGCTGGG ATTACAGAGG CCGCCACTG CACCCGGCTA ATTTCTGTAT

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FIGURE 6 (60)

TTTTAGTAGA GATGGGGTTT CACCATCTTG GCCAGGCTGG TCTTGAACTC CTGACCTCAT
GATCCACCAG CCTTGGCCCTC CCAAAGTGCT GGGATTACAG GCGTGAGCCA CCACGCCCTGG
TCGAATGTCT TTATTATTG AAGAGACAAC ATGGGCCCTTA AATCTGTCTT CTATTGACA
GACTTTGATG GAGTCAAATC CCAATGCTGC CACTTACTGA ACGGCCTTAA ATGACTTAGT
CTCTCTCAGC TGCTTTCTG CATATGTAAG GTGGAATAAT GATGGCTTTC AAGGAGGAAT
AAACCTATGA AAAGTGTTGA GGATAGTGTT TGATATGAAA TAAAGGATTTC AACAAAGTAGT
AGCTGCTATT GAAGATTTAA GAGTTATTTA TTACAACCTAT TTAATAAAAT TTTAAAAAAT
AATACACTTA AATTATTAAA GAGCTTTGAA ATGGGCCCAGG CGCAGTAGCT CCGCCCTGTA
ATCCCAACAC TTTGGGAGGC CAAGGTGGGC GGATCACCTG AGGTCAGGAG TTTAAGACCA
GCCTGGCCAA CATGGTGAAA CCCGTCTCT ACTAAAAACG CAAAAATTAG CCAGGTGTGG
TGGCATGCAC CTGTAGTCCC AACTACTCAG GAGGTGAGG GAGGAGAATT GCTTGAACCT

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FIGURE 6 (61)

AGGAGGTGGA GGTTCAGTA ACCCGAGATG TCACTGCACT CCAGCCTGGC AACAGAGCAA
GACTCCATAA AGACAACAAA AGCTTTGAAA TTGTGTAAAT GAGTTGTACC TATCTTCATT
TAAGAAATTC ATCTTTGTTT ATTTATTTTT ACTTGACATG AGAGCTTCCA GCAATTTTAA
ATTAAGCCCT CACAGATTTT ATGTCACCTGG CTATGTGATA AACAAATTAT TTGCTAAAAAT
AATATCTTG CTTCTTTTTT AAGGAATTGT CTCCCTAGAA ACGGTTTGT CCAAACAATA
CACTGACTTT ACACAAAATC AGATCTGATT GGCAACAGTT GCAGATGTTT TCAAAAGATT
TTCATTTGAG AAGGGGCCCA TTTGGGTTAT TTAGATTCTA AGAACTGAAA CTGCTTTGTT
CTGTTTCTT GGCCTCTGGG AGAGGAGGAG ACATGAATTC AGTTAGCACC TTGGTATTTT
CTTTATCCTT CATTCAATA CAGAAGATGC TTCATATGCA CAGTGGTGTC AGGTCACATC
AAAAGAAAGA GAAACAGTTT CTTGGTTTTT AATTTTCAAC CGGAAAGGAA AGGCACCCAT
TTTGTTCCGC TCTAATTAGC CAGTGCATGA CTTAGAGAGC AGGCAGATGC TTTGAAGGCG

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FIGURE 6 (62)

TGGTAACACA GGCTTTCATT AATCTCCACG CAGGACTTGC ACTTCTACTA TGCCTAGGCT
GAAGAAAATG GCTCAGGAAG ATGAACAATC TCACAGAGCC CTAACATACT GAAGCCAGGT
GTTATAAAGC ACAAGTCAAG AGGGTGAGAA ACTAACGTTTCTC TTGAAATCTC CCACTTCTTT
CTACGTCAGA AGAGCCAAGC TGATTATTTT AGTTGGAATT TAGAAATTTT TAAAAATTAT
TCTAAAGTCA TGAACAAGCC TAATTATAAA GATAGTTGCT GTGAAGGTGC TGAAATAAAT
CGATTTTACC AACCCCTCT TCTGGAGGAA GCCATAATGG AATCCTGTAC AATGTTCACT
CTACCAACGA ACTCTTGTTT TTCTAATGAG GAAACAGAGG CCCACAGTAT TAAACTATCT
TAACCAATAC AAAATGACTA GTGCTCTGGT CCTTTTATTA AGCACTAAAA TTTTGATCCA
ATAATAAATC TGTCCATTAG AAGGAGTTT CCTAATGTAC TGGTTCTAAC TTGTTCCCTT
CAAGGGCCA GTGTCCCGTA CACATAGCTA AATGGGACTT CTCTTCACT ACCATTACCC
AGAGGGCAGA ACCTAAAATG CTGTGAATGA CATCTGCTG TTCACATCTC AGCAGCA

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FIGURE 6 (63)

GTGTTGCATT TGAGCTTCTG CAGGGCCACC CAGGACCTAT ATCTGCTCAG ATGTTTAACT
CATCTAATTC AGTGAACACT TCATTCTAGT TAACTGAACA TCTACTTTGT ACAAGGCACT
ACAGCGGTC AGAGATGAAT AAAATCATGA GATTCCTACTG TCTCCTATAA ACCATCACTT
TGGGAAATTT TAGAAATGTG GGTAAGCTCC AGGGCTTCCT GCAGCGTAGA AGTCACAAAC
TCAAATGCCT GCAGAGGCC AGCTGACAAC ATAAGTAAAT GATTCTGGCT GGGCGGAAAA
CAATTACGGG TGGGTGGGTT TCCAGCTGGG GAGTGCACGC CTGTGTTAAA GGACAGCTGC
TACTCATTTT CAGCCAACTG TGTTCCTCATG TAGAACTGCG GCCCAGTGTA GCCAGTACCG
AAGATTCTC AGAAAAAGCC GGAGATCTCA ATGTTAGTGT AAAATCTCTC AAATTTCCTAA
GAGGATTATA TGGGGCAAAG GTTCTCAGAT CAGTTTGCGAG TCTCTTACTT AGCCCATGTG
CAGAGCAGTC GTAGAGGGTA GCATGCAGTG TCCTACATAA TAATTCTTTT TTATTTTATT
TTATGCCCTC CTCCCTTCCCTG TCTCTCTTTA ACCTTTCTTC TTCCCTCAGG CTGGCTTCTT

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FIGURE 6 (64)

CCCTCAGCCT CGTCCGACCC CAGCCTGGGT TCAATGAACA TTCGGTAAAG GAACACGGAA
TGTCAGCGC ATTAGAGACA ACCTTGAGAC ACATTCCTCT TCGGGTAAGC ACTTCACTGT
AGATTTTAA TTTTAAACAA GACAATGTTT ACGACTTGCT TCTTTCAGGG AAGAGCGATA
TCAATTTAG TGAACACTTC AAGGCTGAGA TACGCTAGGA GAGTCGTGTG GTGTGTCACA
GCAAAGAATT CCACTTTGAA GCGAGTGGGA AAAAAAGCAT CAAATGCCAC ATGTAAC TCA
CCGCCCTGAAG GGTACATTG GTATGAAACC TGGGTTTAA AAGGACCGA ATAGACTAGC
CATTAAAGA CCTGCGTACA ACCTCTCTCT CTCTCTTTGA GAGATAATGT ATCTGGACAA
TAAACATGAA CAGAGTGGAG TCTATCCTGT TTAAACAATT GCCTACTGTA CAGGCACCAG
GAGCTGAAGG GTCAGAATAT TAGCAGTGGG AGCTTGATTA GAGTTGATGA GAGATGGGTA
GTAGGAGGAA AGAGTGAGAT AGAGGAAGAG GACATGGGGG TTACCCATAA GTGGAGAGTA
GAAAAGTAGA ATCAGCTGGC CATCAAAGG CGTGGGACTG AGGAACAGTA TGGCATGTAT

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FIGURE 6 (65)

TAAATATACT AAGCGCTGAC ATTGGAGGAG AACTAGGAAG TTAAATGAAA TCAATAGGGG
ATGATGGAGA ATAGTAGGT GTGCAGGGAT TAGGGTTATG ATAGAAATAC ATGTGAATAC
ATGCAGTATT GTCCTGAAA ATGGTTAACA GTTGGTTCTC CTGGGGGGTG AGGGGAAGCC
CTGATTGTGA ATATTGCCT ATTTCTGTGG TGCAAATACT CCCACCATGA CCAGTTTCAA
GCTATGAATG TTGAAGTCAC AGAAAGCAGG TTGGGAGGAG ATGCCGACAT TTGTTCCCCG
GCAAGGTGGA AGGTAAGGAA GGTGAAATCA ACAAGGTCAA AGAAAACCTCA AGATTTCGAG
GTGCCCTCAGG TCTGAGGGGC AATGAAGTCT AGGAATGGCT GTGCTGAGGT AGCTGAAATA
GAAGTGACTG CAGAGGTCAT GAAGCTGAAG AGGTGAAAAC AGAAATTAGA AAGCAAACC
CCCACCGCCC AACCCCCACC CCTGCAGCCA GTTTCTGAGG GTGACAATAG AGGAAAGGGT
GGAGATGGAG TTCAGGTCCA GAAGCCATAG AAGCGAGTGT GACATTGTGC TCAAGGTCAG
CACATGTCAG TGTGGGGTGT CACATGCTGT TGTGAACCAT CATTATCAC CAATTATGGA

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FIGURE 6 (66)

AGACCTCCTA TGGGCATCTT GCCATATGCA TTATAAAGAT GTGTAAGAAG ACATTTCCCT
CCTCTTGGTG AGGAGAATTA GGGCTGTACA CAGATACTGT AGAGTGCCAT GTGCCCTGGTA
CAGATAAGGT GTGTTAGAGG TTAAGAAGATG AGGCTCTTAA TATTAATGAT AGATCCCCACT
TACCTGAGTC TGACTTACAA TGTGCCCTAGC ATTAAGTGTT TTACCTGTCAT TCCCTTTGAC
GTTCAGAACA ACCCATTTTA CAGATAGGGA AATTGGGTCA GAAAGTTTCA GTAAC TTATC
CAAGGTCAAC ACAATTGGCA AGTGCCAGAG CTGAGCCAGG AACTGAGGTC CTTCTAACAC
CAAACAGCTT GTCTCCCCAA TCACTGTGCT ATTTTCCCTCC CCCAGAAGAT AATACTCTGA
TGGAATGAA GGATAGTGT AATAGAGATT CGGTGTTCCCT TTTT TTTTAAA AAAATTCAGC
TTGCATATTC CTAAGAGTC AATTCATGTT TAAAAAAAAT TTCCCTTTGTG CTTGCATGTG
ACATGTATTT TTAGGATCTG CTGTTAGCAA GTGTATTTT GTGTGATTGA GTGGGAGAGT
GGGAAAAGTT TTGCAGAGCT GTTGAAGCCA GAATGCAGGG GGGCTGCCA GCAGAGACTG

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FIGURE 6 (67)

TAAAATCTCT GCCATCTCAG GTCTTGGAAC AAGCACAAAG AGATGTGTTC TCGATTATT
ATTCTATGTA CATCCCCAGA TGAATGACTA GTTAAAGGTA TTGTTAAAGC ATTTTAAATG
ACCCACTTCC AGCAGCGAAC AAAATCACTT GCTGTGCCAA GCCAACTGGC ATTTCTGAGA
TGATAAAACC ACAAAGTGAG GAAAACGTTA AAAC TGCTAA AGCAAAAATG ATACACAATA
ATGGAGAAGG AGAAAAATTG AGCTTTATTG TCTGCCCTAGG CAGATGGCTG ACCACTAGGT
GGGCCTCGGC GTCACGTCCA GGGTAATTGG TTGCTGGGGT GTTCTCTGGC AGGAAGATTC
ACGCTTCAGC TCGGTCCACA AGATCCTGGC TCATTCTTTC CTAGATTCCA TTTTCTGCCT
CCTCTCCATG ACTGGGTCTG ATGGTTGATC CAAACGGGCA ATTGAAATCA GAAGTTACC
TTTACCCTTAA AATGCTTTTC TGGAAATAAA AGGACATGAA AAGTAACTAA GGACCGGATT
TCCTAGCCGT CTTTCTCTCC TGCATGCGCA ATTTATCCCC AGATATAAAA TTGCCTGCTT
TGATAATTAT ACCCTCTAAA TGAGGGGCAA GTGGCTAATT ATGCCACAT GTGGCCGATT

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FIGURE 6 (68)

GCAC TCCCA TTAGCCAATT ATGTGCTCAA TTATTGTGC ACATGAATAA TTGCACTCAT
GGAAAATAGC GCCCTCCTTT CAAATCCTCG TGCTTGGAGT GGCTGATGGA GTAATTGTCA
CACTGGAAAT GCACTTGGTG GGGAGGGAAA GAGTATCAGA TACCAGGAAA CGCATAAGTG
ACCAGAGCTC GCAGATGTTT ACTGCCACAA ATGGCCCTAG GAGCCAGAGA GAGCGGGAAG
GACCACAGGA TGGAACGGGC CAGCCTGTGA GTTAGGAAGC CTGCTTCTGA AGTTGCCCTGG
GCAGCTCATG TGCGGTGACC TTGGGCAAGT CATTAACCTT CCTTCAGGTC TAACTGGTTC
TGCATACACA ATGAGGATGG TAATAACGCC CAATTCCCAT CACTATCGTG GGATGGATCA
GACTATTAA AAGGATTTAC AATCTGCTTG GGTA AAAAGCT TTACATAAAT ATGAGGCATT
ATCATGTCGC TTGGTACATC TCCAATTATG AAGGAAGGGT AATGACCCCTC CACAGCAATG
CAGGACTCCT GGTTTGAGG GAGGAAAAGT TTGAGAAAGGA CAGGAAGCTT GTTGCCCCAG
CACTGATGTT TCTACTGAGG TACCAGAAA TGT CATGTGG TCATACAGAA TTCATTATTT

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FIGURE 6 (69)

CATTCAACAA ACATCTGTCA ATTGTTACAC TGTCCCTGAGA ATTTGGAAAA ATGATGAAAG
ACTCAGTCCT GCCTTAGGAG GTCACCTGGCA CATGGCCCCG GCCCCCTGTT TTGGGCCCTTT
TACTCTGACC TGTGCTGATT TGCAAAATAGT GGGAAATTTT ATCTCAAGTC TATGAAATCT
GGCATGCATT TTCACGGTTT GATTGCCAGG TACATTTCGAT GGCAATGAGT CTTATAATGT
TTGGTTACCT TCATTTACCT AAGAACTGTG GTTGTTGCTG TGGTTGTTGT TTTTGTGTGT
TTTGAGACGG AGTCTTGCTC TGTCAATCCAG GCTGGAGTGC AGTGGCATGA TCTCCGGTCA
CTGCAAACTC CACCTCCCAG GTTCAAGCGA TTCTCATGCC TCAGCCCCCT CAGTAGCTGG
ATTACAGGCG CGCACCACCA TGCCCCGGCTA ATTTTGTAT TTTTGTTCG GGACACAGAT
TTCACATGTT GGCCAGGCTG GTCTCGAACT CCTGATCTCT GGTGATCCGC CTGCCCTCGC
CTCCCAAAGT GCTGTGATTA CAGGCGTGAG CCACTGTGCC CAGCCAGAAC TGTGTTTTA
ATGACAATGC TAAAAAGTGG TATATGTCAC AGTGTCGGGT GGGGCTAAGA GGCACATTGC

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FIGURE 6 (70)

TGCAGTGATC CATCATTCAT TTCCACCAT TCTCGCCTGG ATTAGCGCAG CAGCTCCCAG
AGAGGCACCT CACTTTGACC TTCTTCCTCA AAGACATTCT CTGTGACCTG CCTGGCCCTT
ATTACCTCTC TAGCTTTGCC ACTTCCCTAT GTCTCCATCT CCCCTCTCAC ACGTAGTAGA
AAGAGACTCT ACCTCATGGA GTAAGGAGAG GCTTCACAGA GGCAGGATTG CTATTAGTCT
TCAAAGATGA GGTATTTGCT AAATGAATGA GACAAAGGGA TTGGGGCCAC ATTACAGGGA
AATTGAGGTA TGTAATAGCC TGGTGCAGGT TAAGAGTGTG GACTCTGAAA CCAGACTCAG
CCTGGAATTG AATCCTGGCT GTGTGATGTT GGGCCAGTGA CTTAACCTCT CTGTGCTTTT
ATTCACCTCT CTATAAAATG GGGATTATAA TAAACCTACC TTATAAGGTT ATTATAACAG
TCAGTAAATA TAAAAATAGA AGTTTTTGGA TGATGACTAT CACATCAGTA AACACTTGTT
TGCCATTATT TTTATTACTT GACTAAAAAT ATACCAGAAA GACCATCCAA GAAAAACCTT
TAAGCTGCTA GTGCAGAAAG ATTCCCCCTTG TGTTTGTGTG CTGGGGGGTC AGTGGTGCCCT

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FIGURE 6 (71)

GTGGCCCACT GGAGAGGAGA CAGCTATGGC TGGAGTGATT CTCAAACTTC AGAATGTCTA
AAATCATCAC ATGGACAACT TATTAAGGAA AGCAAATGCC TGGGCTCCAT CCTCAGAGAG
TCTCATTCAC TGGGTCAGGA TAGAGCCAG GAATCTTTAC CTTAAAGAAC CATCCACCT
CCCACCTCAT ATGATCCTTA TGCAGGTGAT CTGGGGCCCA CACTTTGAGA AATAGACTCA
GGTCAAAGTG GCTCTAACTG CATCTCATTT CTTACCCTGGC ATATCTAATA GTAGAGAAGA
AGACAAATGCT AAGATTTTGG TTGGAGATCT TTTGCTGGGA TTGCTGCTTC ATTCAATCAC
TCATTTATTT ATTTATTTAT TTATTTTGAA ACAGAGTCTC ACTTTGTCAC CCAGGCTGGA
GGGCAGTGGC ACAATCTGAG CTCACCTGCAG CCTCAGGCTC CTGGGTCAA TCGATTCTCT
TGCCTCAGCC TCCCAGAGTAG CTGGGATTAC AGTCATGCAC CACCACGCC AACTAATTCT
TGTAATTTTA GTAGTGACAG CGTTTCACCA TGTTAGCTAG ACTGGTCTCG AACTCCTGAC
ATCAGGTAAT CTGCCTGCCT CGGCCTCTCA AAATTAGTAG CTGCAATTAC ACGTGTGAGC

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FIGURE 6 (72)

TGCCGTGCCCT GGCCTGCTGT TTCTTTTAGT TGGGCCCTCTT CTGTAATAGA GTGTGAGAAT
TCTGACTTGC TGCAACAGTC TGCTTTGAAG CAGGCGTG TG TTTACACTGG TCAGATGTGG
AATTGTGGG CACACTTAGC AGCTTCCTTC TCTAATTTT CTGTATTTTC AGGAGAACAA
TTTTTAAAAA TTTAATAAAA ATGCCTTAAA AATTAAACATT ATTATAAGAT GAATCCCCATT
TTTCTAATCT TGTAATTA AAACAATCAT AAGCATATGA GCACCTGCAC TTAGGGAATC
AAGGTGGCA AAGCTAAACA CTTCCAGCTC TAGGTGATTC GCGGCAATAC AAATGGAGCT
GGACTTTGGC CACAGTGCAA AAATATTGAT CTGTTGTTAG ATGCTCTGAA GTTTCAGAA
AGAATTGGTT CTGCCCTGCTG TGCTTCAGTG CTTAAGGGAA GTGGTTCCCTC AAAATGTTAG
TTTTTAAAGC CAGCTTTCTT AAATAGGAAG ATTCTAATAG TAGCAAAAAT ATAAACTGCT
TCTAGGTTTA AAAAGGACCC AGCACACAAT GGTATCACA CACCTTTCTC CTCAGGTGAT
GAGTGGATGA GTGGCCCTGGT GTATTTCATA ACATCTCCCA GGTCCAAATG CTAAAGCAAT

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FIGURE 6 (73)

TGCTGAAAAG ATACCATGTG TACCGGAACC TTGCAGAGGT ATTTTGTGG CATAAAAAGA
AATATTGATC ATCTATAGTA AAAATGGTTC TACTTTAATA CTA CTAGAGAA AAGATTTTCT
TTTCCCAGAT CTACATCCTG AATCTTCATG AAGACAAGAT CCCCTAACT TCCACTAACA
CCATAATGTG TGCTGTCCCTT TGTAATGTAG TCCACAGATC TCATAAACTG TCAGAAATAG
CAGAGATTGT AAGGTCATCC ACTTCCCCCTG TAAGGCCTGC GTCCCTCACT TACATCCCTA
ATAACGTCCCT CTAACCTCTG CTGGAGGGCA GATTAGCTG CCAGCTGGGA AGAGCTCTGC
CCTAGTCAAC ATTTTATCT GTGGCTTTCA GATGAGAAAC CTGGATGCTT ATCTGAAAAA
AGCTCCTCAG GCTGGAGGGA GGGATTGGCT CTAACAAGAT GCAATGTGAT AAGAATAAAA
GCGAAGCCAA ACTCTAGGCC CAAAGGCTCT AGCAACACAC TTTTGAGAAC CTTGGAGACG
AGTTTGGCT GATGCGAGCT TCTCCGCCCTG CTAAGTAGC CCATTCCATT TGGACGGCTC
TAGAGGCTGG CATGTTCTTC TCCACGTTGT GTTAATGTAC TCCAGTTTCT TCCTGCCCATG

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FIGURE 6 (74)

AACTGGCATG CCTGGCTCC TCCTACCTTC CCCACTTTAA GTCTTCCCTC CCTCCTTCTG
ACCTTCCCAT TCCAGCCACA CTGGCCTTT GTCTGGTCCT AACAAACCAT GCCTTTCCCTG
CCTCCAAGCC CTACACCTGC TATCCATCCC TCTGTCTGAG AGACACTCCC ACCCCCTTAC
AAAGCCCTGT TCTCATCCTT CCAGTTCAGA TGTCTTCTCA GCTTGCCCTCA ACTGACCTCT
TTCAGCTATT CTCACCTTT GTA CTCTGT CATTTCCCTC CTGGCAGTCA CCATAATTTA
TCTTTATTG AATCAATTTC TTAGTTGTAT TATTAGTTA TTTGCACACT CTGTCTCTCT
GTGCCCTTCT TATCACTGC AGGCTTTCTT ATGTAAGTAA TTTATTACT TAAATTTTA
AAAATAATT CAACTTTTGG CCGGGCACAG TGGCTCACGC CTGTAATCCC AGCACTTTGG
GAGGCCGAGG TGGTAGATC AGCTGAGGTC AGGAGTTCTGA GACCAGCCTG GCCAACATGG
TGAAATCCCA TCTCTATTTA AAATACAAAA ACTAGCCGGG CGTGGTGGTA TGCACCTGTA
ATCCCAGCTA CTCGGGAGGT TGAGGGAGGA GAATCACTTG AACCGGGGAG GTGGAGGTTG

FIGURE 6 (75)

CAGTGAGCTG AGATCACGCC ATTGCACTCC AGCCTGGGGC ACGAGAGTGA GACTTCATCT
CAAAAAACA AAAACAAAA AACCCCTGCT TTTCAGAGGG GCTGAACATA TTTACATTCT
CACCAATAGT GTATAAGCAT TCCCCTTTCT CTACAGCCTC ACTAGCATT ACTTTTTTAA
AAACTTTTT AATAATAGCC ATTCTGACTG GTATGAGATG GTATCTCCTT GTGGTTTTCA
CTTGCAATTC TCTGATGATT AGTGATATTG AGCATTGTTT TATGTTTGT GGCTGTTCTG
ATGTCTTCTT TTGAGAAAGTG TCTTTTCATA TATCTGCCC ATTTTGTGA TGGAGTTGTT
TTGTGCTTGT TGAATTAAAGT TCCTTATAGA TTCTAGATAT TAGACTTTTG TTGGATGCAT
AGTTTGTA TATTTCTCC CATCCTATAG TTCTGTTTAC TCTGTTGATA GTTCCCTGTTT
TGTTATGTTT TGTTTTTTTG CTGTACAGAA GCTGTTTAAAT CTAATTGGTC CCACTTGTCA
ATTTTGTTT TTGTTGCAAT GGCTTTTGAA TTTTAATAAT AAATTCTTTC CTAAGGCTGA
TGCCAGAAC AGCATTTTCT AGGTTTTTCT CTAGGATTCT TATAGTTCAA AGTCTTATAT

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FIGURE 6 (76)

TTAAGCTTTT AATCCACCTC AAGTTAATTT TTATATATAG TGAAATGCAG GGGTCCTGTT
TCATTCTTTT GCATGTGGCC AGCCAGCAAT CCCAGAACCA TTTATTGAAT AAGGAATCTT
TTCCCTCATG CTTATTTTGT CAACTTTGTC AAAGATCGGA TGA CTGTAGG AGTGTGGCTT
TTTCTGGGTT ATCTACTCTG TTACATTTGT CTATGTGTCT GTTTTGTAT CAGTATCATG
CTGTTTGT TACTATGGTC TCATAACATA GTTTAAAGTT GGATAATGTT ATGCCCTCTGC
TTTGCTGTTT TTGCTTAAGA TTGCTTTGGC TATTGAGGCT CTTTTTTCAC TTCATATGAA
TTTTAGAATA GTTTTTTCTA ATTCCTTGAA AAATGACCCTT GGCAGTTGA TAGGAATAGC
ATTGAATCTA TAGATTGCTT TGGGCAGTAT GCTATTTTAA TGATATTGAT TCTTCCATC
CATGAGCATG GAATATTTT CCATTTGTTT GTGTCATCTA CTATTTCCCT TAGCAATGTT
TTTTAGTTTT CCTGTAGAG ATCCTCCTAG GTATTTCAAT TTTTATGTGA CTATTTTAAA
TGGGATTGCA TTCTTCATGT GGCTCTCAGC TTGAATGTATA TTGGTGTATA GAAATGCTAC

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FIGURE 6 (77)

AGAGTTTGT ACACTGATTC TGTATCCCTGA AACCTTACTG AAGTCATTTA TCAGTTCCTAG
GAGCCTTTGG CAAAGTCTGT AGTGTTTCT AGGTATAGAA TCATATCATT AGCAAAAGAAA
GATAGTTTGA CTTCTTCTTT TCCATATTGA ATGCCTTTTA TTTCCTTTCCC TTGTCTGATT
GCTCTCCAG TACTACGTTG AATAGGAGTG CTGAGAGTGA GCATCCTTGT CTGTGCCAC
CTCTCAGGG AAATGGTTCC AGCTTTTGCC CATCAATAT GATGTGGCC ATGGGTTTGT
CACAGATGGC TCTTATTATT TTGAGGTGTA TTCCCTTTGAT GCCTAGTTTG TCAAAGGCCT
TTATCATGAA GGGATGTTGG ATTTTATTGA AAGCTTTTTC TGGGTCTTAT TTGGTGAATT
GCATTTATTG AATTGTGCAT GTTGAGCCAA ACTTCCATCC CAGGGATTAA ACCTACTTAA
TCATGGTGTT AACTTTTTGA TGTGCTGCTG GATTGGTTT GCTAAATTTT TTTTTTTTTT
TAAGATGGAG TCTCGCTCTG TCGCGCAGGC TGGAGTGCAG TGGTGTGATC TTGGCTCACT
GCAAGCTCCA CCTCCCGAGT TCATGCCATT CTCCTGCCCTC AGCCTCCCGA GTAGCTGGGA

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FIGURE 6 (78)

CTACAGGCAC CCGCTACCAT ACCCAGCTAA TTTTGTGTA TT TAGTAGA GACAGGATTT
CACCATGTTA GCCAGGATGG TCTTGATCTC CTGACCTCGT GATCTGCCCTG CCTCAGCCCTC
CCAAAGTGGC TAGTATTTTT TTAATTACTA TTTTTTCTCA CCTTGCTGC CATCTTATGA
TTTTCTAGTA TTTTGTGAA GATTTTGCA TCTATTTTCA TCAGGGATAT TGGCCGTGAA
TTTTCTTTTT TCAATTCATC TTTACCCACAT TTTTGTATCA GGTTCATACT GGCTTCATAG
AATGAGTTCA GGAATGGTCC CTCCTCCTCG AATTTTCTCT GTAGAAATTAG TACCAGCTCT
TTGTGTGTCT GGGAGAAAGTT GTATGCCAAT AATTAAATG CAGTTAATAT TTACTGGACA
ATTTCCTCCA GATAATTGTA TATGATTTTT GTCCACCCT GAGTTGATAC ATGTATTTTA
ATTGTATCAT GGTATGAAA GAGCAAGAGT TATTGGTCA CCTAGTCTTG CCTATAGATG
TTGCCCTAATG ATTCAAAGTA GATATTTTGG GAGCCTTAAC AGTGCCCGTG GACTAGGCAG
TTTTGTTTTT TTTTTTTTTT GAGGACAGA GTCTCGTTAT GCTGCCGAGG GCTGGAGTGC

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FIGURE 6 (79)

AGGGGCATGA TGTAGGATCA ATGCAACATC CGCCTCGTGG GTTCAGAGCA ATTATACTGC
ATCAGCCCTCC CCAGTAGCTG GGA CTACACAGG CTCACGCCAC CACGCCCTGGC TAAATTTTGT
ATTTT TAGTA GAGATGGGGT TTCACCATAT TGGCCAGGCT GGTGTTGAAC TCGTGGCCCTC
ATGATCCACC CGCCTCGGCT CCCAATGTGC TGGGCTTACA GGCGTGAGCC ACCGCACCCG
GAGATTAGGC AATTTTATAT TCCCAAATAT CCAACTCTTC TGACCCCGCTT TCTCAGCCCTG
GGTGTATCAG GCACAAGGCC TGTT CAGATT ATGTGGTCTC TGAAGATATG GCTCTCCAGG
GTTGACAATG TGGATAAGGA TTCACCTGGT TTAGGATTTA CACATTCGCC TTGAATGTCT
GTTGCACCAA GTAGACAGTC CATCCCAACT TGGCCATT TG CAGAGCTG TAAGGAGACA
AGGAGGTGGG CAGCCGCTGC TGTGAACTGC TTGGACAAAG ACTGCCAAAT AGCTATCAGA
CAGTGTAAAC AACAGCTGAT TTAGGTTTGA AGGGGGCAGT CTCTTGGGCC ACTTACTATG
CTGCATCATC CTCTTTGGAA AATGCTCTTC AGGTAAC TGC CTAACAGACT GAGAAAAATAA

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FIGURE 6 (80)

AATGCTCACA GAGAAAAAG ACCCGGAAAG TCTGACTTCT CAGAGCTCAG TGTTTAGGTG
CAGAACTGGA TTGTGAAAGG ATTTTAAAT TTTTATATTT CATTCAGGG AACATTCAAT
TATTCCATCC TTCTCCACTC CCACCTGTCT GTCGTTGTCT TTGTCTCTGT CTCCCCACCT
CTCTCTCTAG ACACACACAC GCACACACAC ACACACACAC ACACACACAC ACACACACAC
ACACACACAC ACACACACAC ACACACACAC CCTATTTCAT TGCCAACAGT AATAGAGTTG
CTTCTTTACT TCTTGAGAG AAAAGCCTCA ATCTGAGGAA GCTGTGCTGA CTAGCCTTGC
TCTTAATCAT GGAGACAATG CTTTATGCCT TTATCTTTGC ACAGCTGAAA GCCATGGCAG
AAGCAGTCCT CTAAACGAAA TAAAATAGAA AGGTTCCCTGC TAAGCCCCTGG CAAATGCAGC
CTTCTATCCC TCCCCCAACA CTCACAGCTT CTGAGCAAGA TGTGTCTGCC TTCCAGGAGC
TGGGTGATGG GCAATAATGA GCAGAGCCAC GTGAAGGAAA GATGGGTGAA GAAATGTGTG
TGGAGTCATG CTGGCTGCAC TGACCATGAA ACAAGGATC TACCCCTCTA GTAAC TGCCC

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FIGURE 6 (81)

TACTCCTTTG GTAACGTTC TGAATATATA ACTTGCCAGA AGTTCAGAAG GACCTAGTGC
AGGTATTAGA GGAATTCGT AAGATTGAGC CATTATTCC TGCACAGATA CATAATAATG
GACACGGCC ATGGTGGCCA GCATTCTTGC TCTTGACAAT GGTGAAGGGA AGGTTGTAG
GTCATGGCTA TGCTCTCAGA ATTATAATGG AAAGAAACAG CTCCTGAGTG TTTACTATGA
GCCAAGGGCT GTGCTAAACA CTTTACCATA TGATGACATC TTTTCTCAC AGGTATCAAA
AAACAATAGG ACATACCGGA TAGCTACAAT CTTTGGGCC CTGCAAAACAC AATAATGTGT
ATTCTCTCT TCAAATCCTA CATATTGCTA CAAACTGTAT CCTGAGGCA TATTCATTGT
AAAATAAAA CATATAAAGT ACTACTTTTG TTTTGTGAGA TGGAGTCTCG CTCTGTCACC
CAGACTGGAG TGCAATAGCA TGATCGTGGC TCACTGCAAC CCCCTGCTCC TGGGCTCAAG
TGATTCTCCT GACTCAGCCT CTCAAGTAGC TGGATTACA GGCGCACGCC CCCATGCCCTG
GCTAATTTTT GACTTTTTAA TAGAGACCAG GTTTCACCAT GTTGGCCAGG CTGGTCTCAA

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FIGURE 6 (82)

ACTCCTGACC TCAAGTGATC CACCTGCCTC GGCCTTCCAA AGTGCTGGCA TTACAGCTGT
GAGCCACTGC ACCCGGCCCA TATAAAGTAC TACTAATGTA ACAGGGTGCT AGTCCAGACA
GTGACCCACAC GTGGTGTTCA TTGAAGGCTG GACTAACAC TCCAGCCTCT CCGCCATCAC
AGAGTGATGA CTGCCTTCCC TGAAGCAAAG CTTCCTGGTC AAGGAAAGGC CAGTAAGTGA
CTGCTCTTTG TTGTATACAT GTTAGATGAT CAGGCCTCAA GAAAAGTATA AAGAGATCTT
TGTGCTCTCT GGGACTCAAA AAGCTGCACT CTTTGGGGGA AGGATAGCCA GGTAAAAGTG
GCCCAGGTAA AGAGGGCCCTG GTACACCTGG TTCTGCAAGA TGGTAGACAC AAAAATGAGA
GCTACATTTG GAGCTTATGT GCCCCTAACT CTGTACATAA CCTGCAAGAT CTAATTACTA
ACAACTGGAA TCTTGGAAC ACCTGTAGTA CATCCTTGGC TAAGGTTAGC CCCAACAGAG
AGGGCTCTCC TCTTACAGAG AACCATTACA TTTGTGCCTT CATCCTAGAG TAGAAAAGGC
ATGATCAGAC TACTAAAAAG ACATCAGGAA AGGCCTGTG ACATCTGAGG GAAGTGGTTG

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FIGURE 6 (83)

CCCTCTCTGG GATGTTGGTT CGGGAAGAGG GGCATGGAGG AGTGCCCTGCT TTAGATGGTC
ATTCAGGAAC CCAGGCTGAT AGTGAGAGGT GAAGCCAGTT GGGCTTCTGG GCTAGGGGGG
ACTTGGAGAA CTTTGTGTGTC TAGCTAAAGG ATTGTAAATG CACCAATCAG CACTCTGTAA
AATGGACCAA TCAGCAGGAT GTGGGCAGGG CCAATAAAGG GAATAAAAGC TGGCCACCAG
AGCCAGCAGT GGCAAACTGC TCAGGTCGCC TTCCACGCTG TGGAAAGCTTT GTTCTTTTGC
TCTTCACAAT AAATCTTGCT GCTGCTCACT CTTTGGGTCT GCACATATCTT TATGAGCTGT
AACACTCACC GTGAGGGTCT GTGGCTTCAT TCCTGAAGTC AGTGAGAGCCA CAAACCCACT
GGGAGGAACA AACAACTCTG GACACGCCAA CTTTAAGAGC TGTAACATTC ACTGCGAAGG
TCTGCGGCTT CACCTCTGAA GTCAGCGAGA CTATGAACCC ACTGGAAGGA AGAAACTCCA
GACACATCTG AACATCTGAA GGAAGAAACT CCAGACACAC CATCTTTAAG AGCTGTAACA
CTCACTGCAA GGGTCTGCGG CTTCATTTCTT GAAGTCAGCA AGACCAAGAA CCCACTGGAA

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FIGURE 6 (84)

GGAACAATT CCGGACACAT TTTGGTGACC CAGATGGGAC TATCACCAAG TGGTGAGTAC
CATCAACCCC TTTCACTTGT TATTCTGTCC TATTTTTCCT TAGAATTCGG GGGCTAAATA
TTGGGCACCT GTCAGCCAGT TAAAAGCGAC TAGCATGGCT GCCAGACTTA AGAAACTAAA
GACACGGGTG TCAGACTTTC TGGGAAAGGG CTCTCTAATA ACCCCCAACT CTTTGGAGTT
GGGAGCGTTG GTTTGCCCTGG AACCAGCTTC CACATTTCCT GTACTTCTGG GCTGAGACGA
GGGTCAACAT AGAGGAAAGC CATTGAGCTC TGGGGTCCCG ACAGCAAGTT GGTGACCCCT
GTGGCCATGA TCACAACTCT CGAAGTCATG TTGCCCAAGC GAGACTCACC CATCTATCCT
ATCTATCCTG ACTCTTGCTT CCTGGGTCCT AATGCCCTGA AGACAAAAC TCCTCTTGTC
TCTGTCTCC AAGGCTAGTC CCACTTCTAA AAACCACTCC CTGTCTCTGG TGCTTTTCTA
GTTTCTCCTA TAAGAATGAT TTCTAGTATA AACTCCAGGA CTCATTCTC TTCTTTAGGC
ACCCGGGCTC ACCAATCAGA AAGCCATAAT TTTTGCCCAA AGCCCCATCT TAGGGGGAC

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FIGURE 6 (85)

TATCTGGAAT TTTAGGATCC CTCCTCAGAC AAGCAGGCCT AACAAAAGCT ATTCCCTGAAG
CTAGGATATG GGGAGCCTCA GAAATGATAT CCTTCCTATT CAAAGTGAGGA CAAAAGGCAT
CACTCTTCCA ATTCTGGAGA TCCCTTCCCT CCCTCAGGGT ATGGCCCTCC ACTTCACCTT
TGGGGCATAA CGTCTTTATA GGACACGGGT AAAGTCCCAA TACTAACAGG AGAATGTTTA
GGACTCTAAC AGGTTTTCAG GAATGTGTCG GTAAGGGCCA CTAAATCCGA TTTTTCCTCGG
TCCCTCTTGT GGTCTAGGAG GACAGGTAAG GGTGCAGGTT TTCAATAATG TGTGTGTAAG
GGCCACTAAA TCTGACATTC CTTGGTCCTC CTTGTGGTCT AGGAGGAAAA CTAGTGTTTC
TGCTGCTGCA TCAGTGAGCG CAACTATTCC AATCAACAGG GTCCAGGGAC CATGTGGGT
TCTTGCGCAA GAGGTGTTTC TGCTGCTGCA TTGGTGGGCT CAACTATTCC AATCAGCAGG
GTCCAGTGAC CTTTGCGGGT TCTTGGGTCG GGGGTGGGG GGAACAAACA GACCAAACT
GGGGCAGTT TTGTCTTTCA GATGGAAAC ACTCAGGCAC CAACAGGCTC ACCCTGAAA

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FIGURE 6 (86)

TGTATCCTAA GCCATTGGGA CTAATTTGAC CCGCAAACCC TGAAAAAGAG TGGCTCATTT
TATTCTGCAC TATGGCCTGG TCCCAATATT CTCTCTCTGA TGGGAAAAA TGGCCACCTG
AAGGAAGTAT AAATTACAAT ACTATCCTGC AGCTTGACCT TTTCTGTAA GAGGAAAGCA
AATGGAGTGA AATACCTTAT GTCCAAACTT TCTTTTCATT AAAGGAAAT CCACAACAT
GCAAAACTTA CAATTCACAT CCCACAAGAA GAACTCTCAC TTACCCCCCAT ATCCTAGCTT
CCCTATAGCT CCCCTTCCTA TTAATGATAA GCCTCCTCTA TCTCCCCACC CAGAAGGAAA
CAAGCAAAGA AATCTCCAAA GGACCACAAA AACCCCTGGG CTATCGGTTA TGTCCCCCTC
AAGCTGTAGC GGGGAGGGG AATTGGCCC AACCCAGGTA CATGTCCCCT TCTCCCCCTC
TGATTTAAG CAGATCAAG CAGACCAGG GAAGCTTCA GATGATCCTG ATAGGTATAC
AGATGTCTA CAGGTCTAG GGCAAACTT CAATCTCACT TGGAGAGATG TCATGCTATT
GTTAGATCAA ACCCTGGCCT TTAATTTAAA GAATGTGGCT TTAGCCACAG CCCGAGAGTT

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FIGURE 6 (87)

TGGAGATACC TGGTATCTTA GTCAGTAAA TGATAGAATG ACAGCTGGGG AAAGGGACAA
AGTCTCTCCC GGTACGCAAG CCATCCCCTAG TGTGGATCCC CACTGGGACC TAGACTCAGA
TCATTGGGAC TGGAGTCGCA AACATCTGTGTT GACCTGTGTGTT CTAGAAAGAC TAAAGGAGAAAT
TAGGAAAGAG CCTATGAATT ATTCAATGAT GTCCACCATA ACTCAGGAAA AGGAAGAAAG
TCTTGCCCTTC CTTGAGTGGC TACAGGAGCC TTAAGAAAAT ACACTCCCCCT GTCACCCCAAC
TCACTCAAGG GTTAATTGAT TCTAAAAGAT ATGTTTATTA CTCAATCAGC TGCAGATATC
AGGAGAAAGC TCCCAAAGC AAGCCCTTGG CCTTGAACAA AATTGGAGG CATTAATTA
CCTGGCAACC TTGGTGTCTCT ATAATAGGG CCAAGAGGAG CAGGCCAAA TGGAAAAGCG
AGATAAGAGA AAGCCACAG CCTTAGTCAT GGCCCTCAGA CAAACAAACC TTGGTGGTTC
AGAGAGGACA GAAAATGGAG CAGGCCAATC ACCCAGTAGG GCTTGTGTGTC AGTGTGGTTT
GCAAGGACAG TTTAAAAAAG ATTGTCCCTAT GAGAAACAAG CTGCCCCCTC ACCCATGTCC

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FIGURE 6 (88)

ACTATCGCTG AAGCAATCAC TGGAAGCCAC ACTGCCCCAA AGGACAAAGA TTATCTGGGC
CAGAAAGCCC CAAGCAGATG ATCCAACCAC AGGACTGAGG TGCTCAGGGT TAGCGCCAGC
TCATGTGATC ACCTCACTGA GCCCTGGGTA CATTAAACCA TTGAGGGCCA GGAAATTGAC
TTCTACTGGA CACTGGTGCG GCTTTCTCAG TGTTAACCTC CTGTCTCTGGA CAGCTGTCCT
CAAGGTCTGT TACCATCCGA GGAATCCTGG GACAGCCTAT ATCCAGGTAT TTCTCCCACC
TCCTCAGTTG TAACTGGGAG ACTTTGCTAC AGATAGTAAG TATGCTTACC TAATCCTACA
TGCCCATGCT GCGATATGGA AAGAAAGGGA ATTCCTAACT TCTGGGTGAA CCCCCATTAA
ATATCACAAAG GAAACTATGG AGTTATTGCA CACAGTGCAA AAACCCAAGG AGGTGGCCGGT
CTTACATTGC CGAAGCCATC AAAAGGGGAA GGAGAGGGGA GAACTGCAGC ATAAGTGGCT
GGCAGAGGCA GGGAAAGACA AGCAGAAAGG AAAGAGAGAA AGAGCAGAAA GTGAGAGAGA
AAGAGAGATA GGAAGTGATA GCAAAGAGGG AGTCAGAAAG AAAAGAGAGA GGAGAGAGAG

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FIGURE 6 (89)

AGGGGAAAG ACAGAGAGAG ACAGAGGAAG AGACAGAGAG ACAGAAAGAG AGAAGCAAAG
AGAGGAAGAG ACAAGAAGG AGTCAAAGAG AGGGAAGAG AAGTAGTAAA GAAAAAACAG
TGTACCCCTAT TCCTTTAAAA GCCAGGTAA ATTTAAAACC TATAATTGAT AATTGAAGGC
CTTTTCTGTT AACCCATATA TACTCCCAAT ACCACCTTGT TGTCAGTGT TAAACAAGGG
TTATTAGCCC AAAAGCCACT GAGGCCACTG ACAACCCGTA GCCTTCTTAT CCAAATCCT
TAACACAGCA GGTTCCTCTAA CAGGGATCTA ATCTTAGGTC GACCAGACTG GAGAACTGCC
TTCAGGACAG GATGATAGAT GGTTCCTCCC AGGTGATTAA GGAAAAAGAC ACAATGGGTA
TTCAGTAAGT GATAAGGAAA CTCCTATAGA AGCAGAGTTA GGAAAATTGC GAAATAAGTG
GTCTGCTCAA ACGTTGAAGC TGTTTGCTGT TTGCACTCAG CTAAACCTTA AAGTACTTAC
AGAATCAGGA AGGAGCCATC TATACCAATT CTAAGTTAAT ATGGACTGAA CGAGGTTTTA
TTAATAGCAA AGAAAATTAA AATCTCAAC TTACGAGGTT TTCAAGTAAA GTAAAGTTTG

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FIGURE 6 (90)

GTAAAAGTTA ACAGCGTAAC ATGTATTATC CTAGTACCAC ACATTCTCTC AAAGGATTTG
CTCAGACAGT TTGCAAAAAA GAACGAAATC TGTCTTACT CTACAATCCC AAATAGACTT
TTGGCAGCAG TGACTCTCCA AAACCGCTGA GGCCTAGACT CTCATGTTGA GAAAGGAAGA
TTCTGCACTT CTAGGGGTA GAGTGTGTGTT TTTATACTAA CCAGTCAGGG ATAGTATGAG
ATACCAACCA GTGTTTACAG GAAAAGGCTT CTGAAATCAG ACAATGCCCTT TCAAAACCTT
ATACCAACCT CTGGAGTTGG GCGACATGGC TTCTCCCCCTT TCTAGGTCCCT GTGACAGCCA
TCTTGCTAAT AGTCGCATT TGGCCCTGTA TTTTAAACCT CTTGGTCAA TTTGTTTCCT
CTAGGATCGA GGCCATCAAG CTACAGATGA TCTTACAAAT GTAACCCCAA ATGAGCTCAA
CTAACAACTT CTGCTGAGGA CCCCTGGACC GACCCGCTGG CCTTTTCAAT GGCCCTAAAGA
GCTCCCCCTCT GGAGGACACT ACCACTGCAG GGCCCCCTTCT TCACCCCTAT CCAGCAGGAA
GTAGCTACAG CGGTCATCGC CAAATCCCAA CAGCAGCTGG GGTGTCCCTGT TTGGAGGGGG

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FIGURE 6 (91)

GATTGAGAGG TGAAGCCAGC TGGGCTTCTG GGTGAGGTGG GGACTTGGAG AACTTTTGTG
TCTAGCTAAA GGATTGTAAA TGCACCAATC AGCACTCTGT GTCTAGCTAA AGGATTGTAA
ATGCACCAAT CAGCACTCTG TAAAATGGAC CAATCAGCAG GATGTGGCGG GGTCAAATA
AGGGAGTAAA AACTGGCCAC CCGAGCCAGC AGTGGCAACC CACTCGGGTC CCCTTCCACA
CTGTGGAAGC TTTGTTCTTT TGCTCTTCAC AATAAATCTT GCTGCTGCTC ATTCTTTGTG
TCCACACTAC CTTTATGAGC TGTAACACTC ACTGCGAGGG TCTGTGGCTT CATTCCTGAA
GTCAACAGAC CACGAACCCA CTGGAAGGAA CAAAGAACTC CCGATGTGCT GCCTTTAAGA
GCTGTAACAC TCACTGCGAA GCTCTGCAGC TTCACTCCTG AAGTCAGTGA GACCACAAAC
CCACCAGAAG GAAGAAACTC TGGACACACC TGAATATCTG AAGGAACAAA CTCCAGACAC
ACCATCTTTC AGAGCTGTAA CACTCACCCG AAGGGTCTGT GGCTTCATTC TTGAAGTCAG
CAAGACCAAG AACCCACCGG AAGGAACAAA TTCCAGACAC AGTAGGAAAT CTGTATTTT

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FIGURE 6 (92)

GATCTGTGGC TTCCAGGGTT ACTCCAGTCA TTGAAGTCTC CATTGCAGCC TTAAGGAAAC
AGAGAAATGGT TTGGAGGAGC ACATGTGGGA ATTGTTATGG ACCAGGCTTG AGATGCACAT
AGGGCATTTC TGATCAAACC TAGCTGGAAG CAGGGCCAGG AAATATAATC TAAGGAAGAC
AGTTTTTGTG GACAGTAGTA GTCCTTGCAT CTGAGACATG TAGATTATCA AGCAATTAAT
TAGAAAAAAT ATAGCCAGGT GCGATGGCTC ATGCCGTGTA TCCCAGCACT TTGGGAGGCC
AAGGGGTGTG GATCACGAGG TCAGGCGGTC GAGACCAGCC TGGCCAAACAT GGTGAAACCC
CGTCTCTACT AAAAAATACAA AAATTAGCCT GGTGTGGTGG CACGCATCTG TAATCCCAGT
ACTCAGGAGG CTGAGGCAGG GGAATCTCTT GAACTTGGGA GGCAGAGGTT GCAGTGAGCC
AAGATCACAC CACAGCACTC CATCCTGGGT GACAGAGCGA GACTCTGTCT CAAAAA
AAAAAAAAA GGAAAGGAAA ATATAATCAA GAATATTGAC AGGTAACATT TATTCAACAC
TTACTATGCA CCAGGCAATA CACTAAGTGT TTACATGGA TTAACATATT TAATCTTAAC

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FIGURE 6 (93)

AATAGCCCTA TGAAGTCAGT GCTGTTATTA TCTCCACTTT ATAGATAAGG AAACTGAAGT
ACAGAAAGGT CAAGTAGAGA AATGGCCATG CTTGCATTCT CAGTTTTTGA AGCAACTGTT
ACAGGAATCT GGTGTGAGAA ATGCTCTAAC AAGATGTGAG TCAGGGGTTG GGAGGTACTG
AGTCTGAGTT GGCAGTTGG GGATGGAAGG ATGGATGAAG AACAGCTTGA CAGAGAAGCT
GACACTTGGC AACTCTGTGG GACCTTGAAG GGTAGAGGG ACTTCACCAA AGAAACTGGT
GGTCAGGGAT ACGGAGGGT CACGGCAAGG AGGAAAGGA AACTGTACCA CAGCAGAGAG
TCTGAAGCTA CTACAGTGTA GTTCAGCGTA TAAAGAATAA TTATTTTAAAG GTAAACTTAT
AACCTCATGC AAATATAAAA TGAACACGTG TCAAAGATCT TATTTAATTT ATTAATTAAT
GAGGGAACCT GTAAGATGTT ACAGCCAGTT CAAAGGATAA TTCAAATAAA TCCATGCACA
TATGTAGGCA ATAAGGAATG CTGAAATGAA TTAAAAAGTA GATGTAAACT GATTATCCA
CAGAGAAATA ATCAGTTGCA TTTCACATAA CAAAATTCAG TTGCTTTTCT ACAGAAGGAA

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FIGURE 6 (94)

TTGTTTGCAT CATTACCAAT TTTTCTACAA CTAACAGAAT TATAAAATAA CTCAAAACACA
ATGAAAGGCA GATATAACCC ACAATGGTAT GATAGATACA ATATCCACAT CCAGGATGTT
TTTTTCTCAT TTCAAAAGTCT TTCACAAGTT TTCCTGATAA GGGAGTGTC AATAACTGT
ATGGCAGGCA ATAAGACTGG ATGGATGGTT GGGGCCAGGT TTTAAGGGT AATAAATGCC
ATGTAAGGT ATGTGCATAC TGTGCAACAT GTCGGGAAT CTCAAATTAT TGGTAGAGTA
TGTAAGAAC ACTTGTGGAG CTTGTTAATA AATTCAAATT CCCAGACCCA ACTCCTCAAG
GGTCTAATAC AGTAGGTTTG GAGTAAAGCC TGAAAAATCTG CAATTGTGCA AAAAAAAAA
CCCAGGTGAT TCTGATACAC TTTGAGAAGC ACTGGTGGAA CTAATAGTCA CTGAACGTTT
TTGAGCAGGG GAGAAACCTG AGGACGTCTA TGTTGCAGCA GTGAAACTT GATTAGAAGT
AGGAGAAGAT GCATGGTCTT AAAAGAATGC AAAATGATGG CTAATATTG AGTGCTTATG
ATGGGCCAGG GGCTGTGCTA GGC GCGTGGC ACACATTCAA TACGATGGAA GCCTGTACCA

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FIGURE 6 (95)

GTCAGTATTA GTGGGGTATC TTAAAGAGTG ACCAGAATTA AGGGGGGTTT TCACCAAAGC
CTGAGGACTG AGCCTCCTCA TCCTAAATTC AGACACAATG CTGTACCCTAT GCATTTGCCT
CCAGGCTGTT CCTGGGCCCTC CAGGGACTGG CCCAGGCTCC TGATAAATAG GGAATCCCAA
CAACATAAAG CCTGGATTTT GGAACCTCCT GAATGTACT CAGGCTTTCT AGTAACTGTG
GAGATCTGAA TAATAACACA ATTCTAAGTT CCCCTACTCA TAAAGCTGCT CATCATTTAG
ATGGGGTAAA GCACCTGAAA TACAATGAGC ATCACTATTT TCATTCATCC ATGAAATGAA
CATTCCGGGG AGATCAGTAA GTTGATGTAT CACCCTTGAA CAGGGCAAAA TGAATACTCA
CCAGGAATAT GTGGTATTTT AAAAAGAAGG CAAAGGGAAG AATAGTGGGG ATGGGGCAAA
AACTTTAAAT AGATTCCCC AATCATATAT GGCAATTGAA GATAATTAAA TTATCATTTT
AATTGAGTAA GTACTCATAG AGCCCTCACT ATTTGAAAAT GAACTGCCCTC CTAATTGTTA
TTGTGCAAAT GTGATACATT AAACCTAAGC TATTTTAATA AAACATCCAT TTTCGGAAGC

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FIGURE 6 (96)

TGTAGTAGGT TCTCCCAGGT CAGATTGGAT AAGCCATAAA GAACAAATGC CAACTCCTAT
TTTTTCTATGG TGCTGGGAAA TAAGAGAGAA ATGTGTAATT CAAAGCAATC ATTTAATTTT
ATCCAATAGC TTGATTCTCC TCTCTCTTCT AGCCTTTTAG CTAAGCTGTT ACCAAGTAAC
CACACTAGTT GGCTTGAGTC TTACCACTGT TTCCCTGACC CCACAGTGA GAGACTGCAT
CTGTTAAAGA GCAGTTATGT AACCATGGCT ATGCTGAGCT GGGATTCCCA AGGCTTAGGT
TCTTTCTGTG AATGACCCTC ACCAAGACAC CTGAGGTCTG TGTGGAACCA CAGGCTTGTC
ATCTCTAAGG CAGAGTTGAT AATTCCATCT GTTCTTGAG CCCACACTGA GAAAAAGATT
ACATGACTGC AGTTATTGTA ATGCCCTCATG GAAAGACGTC TTATAAATAT TATAATTAAT
GTTATCATTA AGTAATGCTT CAATGCAGAT CTTCCAAGTA TAAATATCAG CTGAGTAAGA
AGTCAATCTT CCCTGAAGCA AAATTGAAAT TTGTAAATGC GATTCTGGG AGCTTATTTT
GTAATACATG ATTCCAGAGT GTCCATAACA CACACAATTG TCTTTTTCCT CCTACATGGG

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FIGURE 6 (97)

CTATTTACAA CAAAATTGGA CTTATAATGT TTATTTCAG GGATGACTAG AACTTTAATA
ACAAACCTTG GGCCAGGCAT AGTGGCTCAT GCCTATAATC ACAGCACTTC GGGAGGCTGA
GGCTGGTTAG ATTACTTGAG GCCAGGAGTT TGAGAACAGC CTGGCCAACA TGGCAAAACC
CTGTCCTAC TAAAAATACA AAAATTAGCC GGGTGTGGTG GCGCATGCCA GTAATCCCAG
TTACTAGGTA GGCTGAGGTA CGACAATCGC TGAACCTGG GAGGCGGAGG TTGCAGTGAG
CTGAGATTGC ACTACTGCAC TCCAGCCTGG GTGACACAGAGA AAGACTCTGT CTCAAAAAAA
AAAAAAAAT AATAATAATA ATAATAAACC CTGATGAAAG GTTTCATAAA TGTTTTCATC
TAATGGTTTT CTTGACAATT AAATTTTCTA TATAATGTCA GTTCATAAAA AACTGAGAA
CGACCACATG TCATATCGAC TGCTTAAAG AAAATACGTA TATTACAAA CATATACACA
ATACTGTCTT TTGTCGGTT AGTTAGAGG TTAGATAAAC TGCAGTATGT TGTAGTGGAC
AGATCATAGA ACTAGGAGTC AGGATGTCTG GATTCCTAGG AAGCAATGAA TAGGTTGCAC

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FIGURE 6 (98)

GGTGCAGCTC AAGGTATTTC AAAGTGTGGT GCCCAGACCA GCATCATGAG TATCCTCAGG
GAGCTTGTTA GAACTGCAGA TCCTTTAACT CATTGAATCA GAATCCCTAG GTGTGGGGCC
CTGAAATCTG TATTTAGCA GGCTCTCTGG GATTGTGATG TGCCTTAGAG TTTGACAACC
ACTGGGTAGC TGATCCCTGAC TTAGACTTAT CAGGCATGTG ATCTTGAACA AGTCACATAA
TCTCACTGAG TTCAGTTTTC TTATGTTTAA AATAGGCCCA ATAATATCTA TTTCACATGG
ATTGCTTTGA GGATTAGGCA AGAGATCTGT AACAGACACT GTAGAACAGT GTCTCTGGTC
TACAGCTGAC CTTCCATAAA TGGTAGTTGC CTTGATTCTC TGCTCTGCCA CATAATAGCT
GGTTAACTAT GAGCAAGTAA TTTAGTTCTT CTCAGTTTAG TTTCTTCCCC TGTAAAAGAA
GGAAAATAAC TGTTATACTC CATTCTCTGAA TTGCTATAAA AGTCATTTAA TTATGGGCAT
TGAAGCTCTT TGTTCACTGT ATAAGGACTG TACATCTAAG GGATTAAATGA GACCAGGCTT
ATGATTTTAA GCATGGAGTA AATAGTAACA CTGACTCTGT TCTATGAACC ACATGGAAAC

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FIGURE 6 (99)

TCTAAAGAAT ATGCACATTT GAAACACAGG TATCATCTGG GGAAGGTGAT CTGCTCACCC
AAACCAGTTC ATGAACATCA ATCTCCAGTG GCGTGCTGGA GCTAGCTGTA CCAGCTCATG
AGGGCCAATT GTTTCATTTT TAGGAAATTTT GTTTGCTGGT TAAAAAATAGT CATTATTTAA
AATTAAATTA TGTAAACAAT AATATTAGAT AAAATAAGTT AAAATAAAAA CAAAGGAACT
AATTATCCCC AAACCTCTCC CCACCTAATT ATTTTACTAT CTGTGCCCTG GGATTATTTA
CATTGATTTT ATCCATATGG TGACAATACT ATTCATATAT AAATGGTG TG CTTCTCTTCA
TAACTCTACA TAGCCTGATG TCAGGCTAGT AGCTTGAAAT TGGCCACAGT GGGAGTGTA
GCATTGTAC CATGAGGCTT GGCCAAGGCT ACAATCCAG ACTTTTGTTT TTCCCTCCTG
GAGAGCTGTC TGTTAAAAAT TTACCAACAC ACCACTGGTC TTACCTTTGT TAATTTACCA
CAGTCCAGGT TCTGACCCTAG ACTTAGAAAC CTGGATTGT CAGCAAGCTG AGGATAGAGC
CATTATTCT AAGAAGGACT CACATTACCC AAGTGCAAAG CCTGATATAT ACCTTCAGAA

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FIGURE 6 (100)

TATCAATTTA TTAATTTACA GTGAAGAAAG CCACCCCAGG GCATTCCCCA GGGGAAGGCA
AAAAGAGCTA GTTGCCACATT TTGAATGTTT GATGACATTA GGGTAAGGTG ACACAGAATA
TCCATTCCCA CAACTGAGAT ACCTGCTGCC TTAAGGAAGG GACAGGCAAG TCCTTGGGCA
GGACCTTAGA TTGTCACGTG CCATCTTGCT GTAGGACTCT CCTTCCAGG CATGACGATG
GCCAACTCTG TCCTCCTACC CTA CTGATGG GATTATCTTT TCTTGACACA TGGCAATGCC
TCCAATCAGA GGCTGGTAGC TATTTTTAAT CTTCAGGGCA GTATTTTCA AAGGGAAGTT
CATGGACCAT ATGCATCTGT ATCATTTAGA TGTATATTAA AAATGCTTAG TCTTCCCCAG
TTATACTAGA TCAGAATCTC TGTGGTGGG GCCCACGAAT CGGTATTTTC AACAAATCAC
TAGGTAATTT CTGTATATAC TATAGTGTGA AGACCACTGC TTGAAGGTTT CTTTGCATAT
CTCCACTAAA TATAAAAAAT ATTGACTTCT AGATTAACT CCCAAAGCAC TTGCATTTT
AAGTTCTGG GGGCATTATA TTGTGGTACC CCTATACCAC TCACACTCTA GTCAGGAGGT

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FIGURE 6 (101)

ATATTATGGA CTGAATGTTT GTGTCCCTCC AAAACTCATA TGTTGAAAGTC TTAGCTTCCA
ATGTGATAGT ATTAGGAGAT GGTGCCCTTCT GGAGGTAAAA TCAAGCCCTC ATGAATGGGA
TTAGTGCCCTT TAGAAAGAGA GCTCGTCACT GTCCTTCCAT CAATTGAAGA TGCAGTGAGA
AGCTGGTAGT CTTGCATCTG GAAGAGGGCC CTCACACAAC CTGATCATGC TGGCACCTGG
TCTCAGACTT TCTGCCCTCCA GAACTATGAG ATGATAAATT TCTGTGTGTC ATACCCACC
CAGGCTACAA TATTAGGTTG CTGCAAAGTA TTTGTGATTT TTGCCCTTTAC TTTTTCAGGGC
AAAAACTGCA ATTACTTTTG TGCCAAACCTA ATATTTTGT ATAGCAGCCC GAACTAAGGC
AAGGAGACT ACATCAGACA GTGTAGCTAT GTAAGTACAA ATGTATCCCT GTTGAAGGAA
AACTAAGTTC TAACCCCTGAC TTCAGGCCAG TAGCCACCTT TTCAATCTCT TTCATGAAGG
GACCATTATC ATTATCACTG GTGGCAAAA TAGAGCACGA GAATGGAATT TGCTTTTCTG
TGAAATCTCA GTGTATACAG ATGAAGAGCA AGGTTTGCT TTCACTCTTA AGAAGCAAAA

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FIGURE 6 (102)

GTGAGTACGG ACTGGCACAT TATCAGAGAA AGAATCATTC TAGCTCGGTG GGTCTTAACC
AGGAGTGAAT TTGACTCCAG GGAACAGTTG GCAATGTCTG GAGACGTTTT TATTGTGTAT
AGCTGGGGA TGAGTGGTG GGTGCTACT GGCATCTAGT GGGTGGAGAC CAGAGATGCT
GTTAAACATC CCGCAAAGCA CAGGACAGTC CCCGACAACA AAGAAATTATC TGGCCCCAAA
TATCAATAGT GCCAAAGTTG AGAAACCCTCA TTCTAGCTTC CTTTTCCTT CTACGTTCTA
ATCAACTGTT GTTCTTTCAG CATTAGGATT CATCCAGCAG TCTCTTTCCC CAGCAATTG
TTGAAATTTT TTTAAAAATG GACTCATTTT AGTGTACAA GAAAAAATA CATCACAGG
AAAGGATGGG TCATTTTGTT TAATGATGTT TTGCCTTTCA CATAGCAAAA GCTTAATAAA
GTATTTTAA ATAAAATGGT GAATAGATCA AAACATTAAT TTCACATGTG TTTTAATAAA
TAACAGGAAG ATGGCTATAT TATATAAATT GTTCTTGAT ATGTCTTGAG TGGATCATCA
AACACAAACG TATCTACATG CCTTTTCTTG TGAATAGATC TAATAATAAC GCTCTTCTAA

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FIGURE 6 (103)

AAACAAATTA AATGATATT ATTTGCTGAG AATGTAATGC TTGTGTGAAT AGAAGCCAGC
CCTGAATCCA AGCCCCCAGA TCTATTTAAA GAATTGAAG AATGTCAGAA AAGCACGTGG
CTTCAAGGTT AATGTGTAAG ACTCACAGAA ACTTGAAAAA TCACTATGAC TAAAAAGAAA
GTATGAGCTC CCTGCATGCC TGTAAATTGG AATGACAGCC AAAACCAGTT AATTATAAAA
ACAGCTAATT TAACAGGTTT TCAAATTGT TCTTTTCTCC AAGTAGCATA TAGTCAATAA
TCCTTAAAGA GAAAGCAAAG AAGGGGAAGC ACTGAACCAA ATTTGCTTTT TTGTACCTGC
TCAGCTCAA TGCAGAGTTC TCTACCTGGA AATTGACTGC TTCCATAGTT TGATAGCCAC
AGAGAGATGG GAACAGAAGG AGAGGTATAA TCCCAGACTT GATTCAGCTA TAGAGAAATGA
CAATAGTGC AGAGGCCTTC CAACCAGAGC GACTCCATCT TGAATACGGG CTGGGTAAAA
CAGGGCTGAG ACCTACTGGG CTGCATTCCC AGGAGGCTAA GCATTCTAAG TCACAGGATG
AGACAGGAGG TCAGCACAAG ACCTTGCTGA TAAACAGGT TGTAATAAAG AAGCCAGCCA

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FIGURE 6 (104)

AAACCCACCA AAACCAAGAT GGCCATGAGA GTTATCTGTG GTTGGTCTCA CTGCTCATTG
TATGCTAATT ATAATGTATT AGCATGTAA AAGACACTCC CACCAGTGCT ATGACAGTTT
ACAGGTACAT TGGCAACTTC CGGAAGTTAC CCTCTATGGT CTAAAAAGGG GAGGAACCCCT
CACCTCCCAG AATTGCCAC CCCTTTCCTG GAAAACTGT GAATAATTCA CCCTTGTTCA
GCATATAATC AAGAAGTAAC TGTAAGTATC CTAGGCCAG AAGCTCAGGC CACTGCTCTG
AATGTGGAAT AGCCATTCTT TTATCCTTTA CTTTCTTAAT AAACCTTGCTT TCACCTTTACT
GTATGGACCC CTGTGAATTC TTTCTTGCAA GAGATCCAAA AACTCTCTCT TGGGGTCTGG
ATCAGGACCT CTCCCAGTA ACAATAGTAG TAAGGGGTCG GGGAAACTGG ACAAAGGAGT
TTAAGAAGCC TTAGATAAAG GGTCCCTCATC ATTGTCATAA CATAAAATCA TGGACTCCCTA
GAATTTTATA GCTGATAGGA TTAGAAATTT CAAAATTCAA TTTTCATTAAAT TTTCATCTGC
GAAAACAGAT GGCCAGAGAG GCCAAACAAT TTGTTAAGGA GCACTGAGGC GATGGAACAC

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FIGURE 6 (105)

CACACTGGAC CGCAAACCTC CTAGCAGAGT ATACAAGGCC TTTGATCTCC TCAGTCAGAA
TGAAGTAGAG CTTTCCAGGG GTACCCCTTTC TGAAGTTTA GCATGTTTGC CAGTCTGACT
AATTTGAAG TTGCTTAAAT ATCTGTCATT TCCACTGTAT CATAATCTCC TCATTCATCT
TCAATCTCCA ATGCCTTGAA CTCAGTAAAT GTTAGTTGAA CAAAAGTAAA TTGAACCCAG
AATTTCTGAT CATAATCTGG AGCACTTTAA AATTGTCAGC TTACTGGGAA ACGGGATAAC
ATGTGATTG TCTTTGATTT TTTTTTTTCTC ATATGCTTTT TCCACCTATA GATGCTACAC
GAATGTTTTT AAAATCTGAT ATAAAAATTA AAATTAATAA ATTAATAAAA GAAAAATTGA
TACAATGCTA CATTTAGAGT GTTGATTA GATTCCTTAA GTGTATCATG GTGATCTCTA
CATCACGTGG TGATCAAAT GCTTTGGGTT TTAACACATA ACTGACAAAG GCTTGGGAC
ATGTAAGATC CCAAATACAT TTTTATGAT TTTTTTTTCT TGTGTTGCTCT CTTTAAATA
ACTTTTTTTT GTTATAAGAA TAATTCATGT TCAGTGGAGA AACCATAGAA AATAGTGACA

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FIGURE 6 (106)

AGTGAAGGAA TAAATTTAAA ATGACCCATA ATTGTACCAT ACATTCTGAT TTTTAAACG
CTGAACAAAT TAGCCTTGGG TAAGTACCAG GAATAGAGTG CAGCATTGAA AGTTAAAGTT
TGGGGAAGGA TAGCTGACTT AAGAAATTAT CTAGTTAGAC ATTTTTTGGG TGGGGTAATT
TTGCAGATGA CATTAGTGAG AGAAAGGACT TGCCACTCTC ACACAGCTAG TAGGGGTGTG
GGAGGATATT GGAACCAAGT TTCAAGTCTT CAGTGAAGAA TCAAGGAGA AGTCTAAAA
CCTAACAAATA TCCCTCTGGA TGGACATTTA TTTTATTACT ACAATAAGCC ACACGGTGAG
TCATAAGGAG CATTTCATTG TTCTAATATG TCTCTACTGT ATTTAGAATC TGATAAAGCC
CTATTAGAAAT TCATCTCTTT AAGAATAAAA GAAGCTGAGG AACTAAAGAG AGGGTTGGAA
TAATCCACTA ATTATATCCG TTAAGCTTCA GTTACGCTAA TAAGGAATAT CACATGACTG
TGGTGTGTGC TTGTTCTGAA CAGTAAAGTA CATGAGGAAA GATAAGATTC AGGGCTGAAA
TGTCCTTCAG CATATGTAGG TAGTGGTGAT GAAAGTCATT AAAAGAAAAA TTGATTGAGG

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FIGURE 6 (107)

TATTTTAGTA AACAAAAGAA CTCACCACTT ACCCATCAGG AAGTGATATG TTAATGCAGT
GCTGTCAGC CTTCTGGAAG AAAAGGTTTC TTTCATGCTTC TCTCTTTAGC CTAATTCCTTA
TCCTGTCACT TTTTCAGGCA AATTAAAAA AAAAAAAGAT TGA AAAACGAT GCTCCCTATTT
TATTTGCTTC AAAAGAAACA GGCTGTTGCA TTGTGCTTGG AACAGTTTAC TCTTGGCCCTT
GATGTAAGTG TGA AAGGAAG CCCATGTAAT TGACTAGGCA GTATCTGAAG AAGCAGGAAA
TACAGTGTTA AGAAAATGAA CAGGCATGAA AACCATGGCT ATTTGATAAA AGTAAATAAT
TTCTGCAGTT CACATGTTCT CAGCATATTT TCTTTGATAC TGACTTGCTT AATATGACAA
TAGCAGAACC ATGGTAGCTT GTAGGCATTA CTTTTCCTTTT AATTCTTTT ACATTTTGAA
TTTACCAGCA CTCACATTTG TATTACTTTT GGGTTATACT GAGGATCTAT AACTTATAGA
TCAAAATACCT GACATATATA TGCATTCTCT GAAGTCTTAG GGCAGAACTA GAACATTCTT
GTGAACATCA GTATAAGATA TTAAAATGGA AGTTTGCCT AAGACTGAAG ACAATAAAAA

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FIGURE 6 (108)

TATCATAGTC TGAATGAAT GCCAGCACAC CATAcAGGAT TTAAATATCT ATACATATAT
ATGTGTGTGT ATTATATATA TTAAATATAT ATCTGTGTGG GATAGGAAGA GTAGGGGGA
AATCAGTTTT ACAATTATTA AGTATTTCAC CCTTGACAAG AGTATATATA TTGAAATCA
GTTGGAGAGT ATTTTCAAAG ATAAATGTTA GTGTGCTATG AATGAATCCA CCCCTACCAC
CACTGAGGCA GGTAGGAGA GGCTGTGCT CCTCAAGCAT AGTTGGAAAA GGACCTCAAC
AAGACCACTT CAAGAGTCTA ATGTGTGGAG ACTGTTGCTT AGGGAGACCT TATGGTCTAG
CTTCTGACTC ACAGCTAAGT CAGGGAGACA GGTGGCTGC TCTGATCGTG GAGTCCAAAA
GATGGCCTGC ACTGAAAAGC CTCATGAGTG TTGACTTAGG GCTAGTCTAA GAGTCCCCTG
GAAGAAGAAA CACTCAGTAG GAGAGAAGCT GGAGGTACCT TCAGTGCTGA ATTGAACTA
GATTCATTCC CCCGTGGAGC AAATTACATA GGAAAGATGC CCAGTGATGG AGAGTGGGG
TGCTCTAAC AATTACCCAC CCACTGCCCC CACCCTAAGA AAAAGAAAAT CACATACAAC

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FIGURE 6 (109)

CAGTCAGCTG TAAACATATG CCGAGCCCTAG TAAACTCAGA TACTAAGTTA CCAGGGTACC
TGGCAAGTAA GAACATTCCT GATTCCTTC CTCCTTCTC TTTGCCCTCC AACCTTAGTG
GCTAGCAAGA TGGGAGAGG AGGAGAAAGCT GTAAGTGGG AAAAAAGAGC AGCTTTCTCT
CCTTTTCAGC TGCTGGATTC TCCCTCATCA TAGGCCTGAG CTGGGGAATC AGGAAGAAGG
ATTCTTTTAA AACTGAAGT AACGTATATCA TTTAATTTTA AAACATTTTA AATTTTGACA
ATGTTGAGAT TAGATATACT AATTATTAAA CTAAGATTAT GTTTTGCAGC TTGAAGTGAT
AAGAAAAACT CTTATCTAAG AGCATCCAGG AAAGTCGGG GTTTCCTGAA CATCCTTTTA
AATCCTTTGG AAGTCAGCTT TCAGAGAGGA TTAAAGTGT AGACTGGGCC TTCAGAAACT
TGGTTAATGT AGGGGTTTCC TATGCAGACT TGGGGACTAT ACCTTGTGTG GAAGAGAGAA
AATAAGATTA TCTTACATTT TTCCCATTCC TTTTTCAAAA AGAAAGCTCA GCTAGCATGA
AAGTTAAATT CAAAACGTAA TGGGTATTAT TTGCATATTC AAATCTAGTG CATATCATGT

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FIGURE 6 (110)

AAGTACTGAA TTATGGTATT CATATTTC AATGACAAGC TGGATTTTTT TTTCTTTTCGA
ATTTCACAAA TTAATTTTCC TTGGAACCTT TTGGTTTGGG CTTTAAGAGT TTAGGCTTTC
ATCACAAAGA GAGGACAGCC TTGAAGATTA AAGTG GTGG CTCCTCTCAA GATGTTCTTA
GTCCAGCAAA GGATTCTATG CATATTGGG CTTCCTTCTG TCTCATAACC TGTATTTCTT
GATATTCTAT TTATATTCTG TAAGATTTTT TTTTAAAGG AAAAATTCCT CCATGGTTGA
AGGACATGTC AAAAATAGAG GATACAGTTT TATATCAAAG GAAGTTTCAT GATATGACTG
TAGAAGCTCA TTGACTTAA GACACATCAT TTCCCTCATGG AAGTGTTAAA CAGATCTGTA
CAATAAGGT GGCAATCTTT GTGTAAAACA GTTTTTTTTC TCCTGCTCTA AAGAAAGTGT
ATATTTCAA ATGTGAATGT CAGCAGTCAG AAAATAGTAT TTTTTTAACT TCGTTTTTCAA
AGTCCTCAA AACCTGTACC TAATCATGAA TTTTTTTTCC CACAGATTGT TTCTTCTTCT
CCCTCCCAGA AACTTTGAAG TTTTCTACA TGACACCAGG ACCATGTCT TTTTTTAAAT

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FIGURE 6 (111)

ACACAGAAAT GAAAGAAAAA AAGTGTGTG TATCGTTAAC CAAATATATG AAATCTTTAA
GCTGTATTTT TATTTTAAAC TTTGTTTTGC AAAGAGGCCA TTCCCTTTGG TTAAATAATT
TGTTATTCAC AGTTTCCTTG TCCTCATATT ATCAAGGGGA AAATTGTAGA AATTTTAAAG
GAAGCTCTAG GCAATGTTTT CATCCCTGAA TCTTTGGAGA GTTATAAAAA CAAACAGATT
ACTGAACCTG TAAGAGAAAC AATCGTGAAG TCATTACATC TAAGCATAAG CAAAATCTCC
TCTTGGATCA TTAAGTTATA GAAGAAAAGA AAGCCTGCAC TTTGAAATTT AGATAAAGCT
TGGTAACTTG TAAGTCAAAC ACGTAAATTT TTACAATTCA GGAATATCGA TAGCAGTTGA
GTTTAATAGA CTTCACACAT TCCAAATTTA AAGCTTCCTT CTCTGTGCTA ATAGAGATAC
AATAGCAGTA GCGGTTTAAAG AAGAATGAAT CAACAATTTA AAACATAAAT GTGTTTTTTA
TTCATCTCCC TTATTCACAT ATATTTGTTT TGTTTTGAGA AGGAGTTCTG CTCTGTCGCC
CAGGCAGGAG TGCTGTGGCA CGATCTCAGC TCACCGCAAC CTCTGCCCTC CGGGTTCAAG

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FIGURE 6 (112)

CGATTCTCTT GCCTCAGCCT CCTGAGTAGC TCGGATTACA GCGGTGCGCC AGCAACCCCG
GCTAATTTT GTATTTTAG TAGAGACAGG GTTTCACCAC GTTGGACATC TTGGTCTCGA
ACCCCTGATC TCAAGTGATC AGCCCGCCTC GGCTCCTCCAA AGTGCTGGGA TTACAGGCGT
GAGCCATCAC TTCTGGCCCT TATTCGCATA CAATTAAAA ATCATCACAG AAGTTTGAA
AGAAGGAAG GGCAGAAAAT TACCTACTTT TCCCTCTCCC AGCGATCTCC TTCAAATCTG
TGCCTTTTCC TCAGGCCCCAG GCCTCAATT ACTGAGCAGT CACACCTCAC AGAGGGAGGT
CTGGGCAATC CACTCTTGGT CACAGGAAAG CCATTGACCC TCCCACCTCC TCTCCTCCAC
CTTGTTCTCA ACTCTTGACT TTGGGCTTTG TTTCTGTTC AATCCTAGAA CTGGTTTCTT
TTATCAGGTT AAGTGATTAG TTCTCTTTCC CTCTAGTTGC TCTCACTCCC TGAATCTTGC
CTTCTGTAAC AACTGGAGAC AACTCTTTCA AAACCAGCTC CAAGCCCCAG ACTTCTCTCT
GGGCTTTAGT TCGTAAGGCA GGTGCCCTAC TGAGTGAGCC TAGATCAGAC AGAAACATAG

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FIGURE 6 (113)

CTGTTGGCAA GGATTAGGT GAATTTCCTT CCATTGTTTT TCTAATACCT TTTTTTTTTT
TTTGTAATA TAACCATGCA CCTACACACA TATTGAATA TCCTGCCCTTT TTATTTAAAA
TGACATGATA GGTCCGGGAG TGGTGGCTCA TGCCTGTAAT CCCAGCACTT TGGGAGGCCG
AGGTGGGCAG ATCACCTGAG GTCAGGAGTT CGAGACCAGC CTGGCCAACA TGGTGAAACT
CCATCTCTAC TAAAAATCAA AAATTAGCCG GGCATGGTGG CAGGCTCCCA GCTACTCAGG
AGGCTGAGAT GTGAAAATCG CTTGAACCCG GGAGGTAGAG GTTGCAGTGA GCTGAGATCT
TGCCATTGCA TTCCAGCCTG GGCAATAAGA GCGAAACTCC ATCTCAAAA AAAAATAAAA
AAAAAGACAG GATAAACATT CTAGATAGTC TCTATAATGG TCATGATTAA GACAATAAAA
TAGTCTGAAA TTGTCAATAT ATATTAATAA TAATTTATTT GGCCATTCTG CCAAGTAGCA
GACACCTGTC ATTCTGCCCC CTCAGCACCT CTCTTTCTTT TAGGGAAATG CTACCCACTC
TTTGCAATGG TTCTGGATGG AACTGTTGAT CACAGTGTTT TCACTCCCCA TTTTGCCCTCA

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FIGURE 6 (114)

CCAGAGGTAG ACAGAAGACC CAAGCCAGGC CAGTTACACA CAATCTTCAG ATAATTACCG
TATTGATCAC AGTATCACCC CACTCAAGGC TTGGTTGGAG ATGAGCAGAA GAGACTAAAG
CTGGGTCATT TTAATTAAACA CCTGTACCCC AAAGAAAGAC TGTCAATGAG GCTTTTATAC
CGACACTCCT GGTTCCTCATT CTCCTGATG CCATTCATTT GACGAACTAC CCAATCTTTC
CAACAGTGTC TTTGGAAGAA AGATAGTCAG AAAAGAAGAT AGAGTTGTTT TCTGTTCTTT
GCAACCAAGG AACTCTAAAT GATAGACTTG TTGCTAGGCA CTTTGGTTAT TTTTATTATC
TTGAATACTT CTGTGATATA CTTCTTTGTG CATGCCCTGTT TGTACGGATG TAGCTTTTTA
TATATTTTAT ATAATTCTC AGAAGTGGAA TTAATTAGTC AAAAGGTATG AACATTTTCT
GATTCTTAAT ATAAATTGTG CAAATGCTTT TTAAGAAGAT TATACCAGTT TACATTTTGT
GTTATATATA ACAGAAAGTA CTA CTGAAAA ATATTACAAA AATTGTCTCT CTGTTTCAGGA
GGACTTGTA TAGATGATAA AGTACTTGAA ATAGGAACAT AGAGCATTTT CAGTTTAAAA

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FIGURE 6 (115)

TAAATTTCATT GGGTTATTTA CGGAATCCTT AGAATTATGG CCAGACATTT ATAGATGATC
TGTACCAAAC CTAGTTGGTT ACATAAATTG CTTATTCAAC TGGCTTAAAT CTATAATAGA
AAGATGACAC TTAAGTGAATG TTTAATATAC ACTTTGTCAG GGGCTTTGTA TTATTCTATG
ACATCTTCAA AATGACCCTA CTTTCCCTATT TTATAAGTAA GGACAGGAAG GCTTCAAGAA
CATGACTAAT TTTCCCAAGG GCTGTACCAA AGCCAGAACC CAAATCTATA AGGCTTTTAA
ACCTGCATTC TAAAACTGCA TCTCGGCCAT CTTATTCCCTA CAGAACTTAA GGTAGAAAG
CCAGATTGGA GTCCCAATT CACCACCTAG TAACCAGACA AACTTGAGGA ATTCACCTCAA
CGTCTTTGAA TCTCCATTTC CTAATCTTTA AACTAAAAC AATAATACTG GCCCTACCTA
TTTCCCTAAA TTTCTGTGAG CACATAGAGC TAGTGTGGTA GAGTGCTGTA CAGATGTCAA
GTGTTAGCGT GAATTACTTA GATCCCTGAA CACCATGGAT GAATGTGTCT GACTGCTATT
AGAGGTCATA AAGAATATTG GGGCCAGGTA CATTGGCTTA TTCCCTATAAT GCCAGCACTT

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FIGURE 6 (116)

TGGGAGCCTG AGACAGGAGG ATCACTCGAG GCCACAATTT CAAGACCGGC CTGGGCAACA
TAGTGAGACC CCTTCTCTAC AAAAAAAAAA AAGCAGCCAC GTGTAGTGGC ACACACCTGT
AGTCCACAT ACTCAGGAGG GTGATTTGGG AGGATAACTT TAGTCCAGGA GTTTCAAGGT
GCAGTGAGCT GTGATTGCAC CACTGTACTC TAACCTGGAC AGCAGAGTGA GACCCTGTCT
CTAAAAAAAA AGAAAAAAAA AATAATAATA ATAGGCCCTTG GGATACCCAC
TCCCTCTCTT CTGCTCTGAG TTGTGAAGCA GTTGAGTTAC ATATGCATGT CCAATGGATG
AGGTTGAAA TATCAACTGG ATTGGAATGT GGCTTACTTG CGTGGCCACA ATGAGCTTCG
TAACACTTCC TGACAGGGTG AGAAGACAAA CTTCCCTCACC CAGTCACTGG CAGAGCTGGA
CACTCTGTGT CTCTCCACACA GAACAACCTC TTA CTGCA TG GAGTGGATG AAAAAAGTCAA
CCGAGAACAG GCTACTCCAA AAAGCAGAGC ACCAAAGGCA CCAGCTGGTC AGGTCCCCCT
TCCTAAGTAA ACAATCACGT AATTCATTG GGACAAAGCC AGAGAGGTGG TGTGGAGAAA

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FIGURE 6 (117)

GAGAGGGCAG TTTCTCTCCA AGTTTTCCT GGAATTCCTT ATGGGAATAT GAGGTTTAGG
GGAATAAGAC TTCCCTTTAA CAGTGAAGAA TCCCCAGCTC TATTGGTAAT AGGAAATCGC
TTACAAGGAT CATGGGGAGT ATTTCCCTCAG CTCGTTCTGC CTCCTACTTG GCTGAGTGGA
ATGGAACCAT CTGTGGCTGC TGCATATGAT ATTGTCAACT TTGTCATTCC ACACCCACTC
CTTGACGCCC TACCATGTGG TCATAAGACT CCTTTAAAG TGTTCCCTTA AAAAACAAAA
TGTGTTTGT TTCTATAAAA TACAGCTCAA TGTGAGAACC CTTGTCTTGT TTGCTCTCTG
ATGTAACCCCT TTCACAAATGT TTGGGCAGCT TATTCTCTCT ATTTCCCTGT AGGGTCCCAT
CCAGGCCAAA GTGAGTGCCA GCCTCATTTG GGCAGCACAT GCCCTGTGGA AGGGCAGGAA
GAGACGAAAG CTAATTGTAA CTTTGTGATT AGCTGTCATG GATGCCCTGGT CCTGTCAATA
GCGCTCAATA AAGCCAGAAG GCCAAGCGTT CGCTTCTGCA TACTGATTGC TGAGTCAGAT
TTCTCAGTGC AGAAGGGCTT TCTAGGCAGT CAATTTTGA ATATTAGTCT TGGTTCCTAA

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FIGURE 6 (118)

GTGGTTAAAA TCCCTAGCTG GTCCTTAAATC TGAGCCTGGA GAATTTAGTT AGGGCTGACA
TTCGTCTGTG ATATTTTTCG CCTCAATATA TATGTCTTTC CTCCATCTCT TAGATCCCTG
AATCATAGAG ATATATATGT TATATAATCA ACTGTCTCCA GTCCTAAGA GTGATAAGTA
CACATTGTGT CAGGTGAGG GGACAGGAGA ACTTCAAAA GCCTTTCTTG CCCCTTTTC
CTTCTCACTG CCTCCCCTA AGTCCAGCCA CTTATTATTC AGCTGACACT ATCATCATGA
CCATGAGTCT TTTGGGGCTA CCCTGGTTCG GATCCTTTTG GAGGTTTGTT GCTTAACCTCT
GTCCTCAGTC CTATGGAGCT GCTTTTTCAT TAAAGTTTCTA TTTTGGCTAA AGTTGGCCAG
AATCTCCTTG TAACCAAAGA ACAAATAAAA TACCAGCTTG CAATGTTCTA TGTGCTTCC
ACCAAACCTA TGCAGCACTT CCTATCTAAT CCACCTACTA GTCCTTTTCTT TTTTATATTT
TTTGGAGACG GAGTCTCGCT CTGTTGCTCA GGATGGAGTG CAATGGTGCA ATCTCGGCTC
ACTGCAACCT CTGCCTCCCG GGTTCAGCA ATTCCCCGC CTCAGCCTCC TGAGTAGCTG

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FIGURE 6 (119)

GGACTACAGG TGCATGCCAC CACGTCCGGC TAATTTTGT ATTTTAGGAG AGAGAGGGTT
TCACCATGTT GCCCAGGCTG GTCACGAACT CCTGAGCTCA GGCAATCCGC CCTCCTCGGG
CTCCCAAAGT GCTGGGATTA CAGGAGTGAG CCACCTCACC TGGCCCCGAC CTACTAGTCT
TTAGTGTTTG CTTCCTTCTA TTGGGTAATT GTCTGTTTAT ATGCATGTCT TGTTCCTCA
AATAAAATGT GGTCTTCTCA AGGTATTGG CCCATGTTCT ATCCATCTGT AGATATCACA
GCACCTAGCA GTGTCTTTCA CAGAGGAAGT ACACAACTGG CATATTGAT TCATTGCTCC
ATTTTTCCT TCTTTATCCC CAGCATTTCT CAATAATTTC AAACATCTCC ATTGGAGTAC
CGGAGAAAGC AGGTAGCTTT ACTTGCAGCT ATGTTTCTAT CCCCATAGTA ACTAAAAGAG
GACCCAGAGA AACATGTTTA AATGCTGTCC TGTTATCAGG ACCTCAGCCT TCTGATGCTC
CGTGGCTTG GGTTAATGC TTGATCATTT CCTCCCCAAC CTACACTGTG TACCTATGCT
AGTCTCTCA TGAGGACTAA GCCCCATAGT AAAAGGGCTA GATAAATAGA AAATCATTTT

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FIGURE 6 (120)

ATGTAATTAT AAGAATGAGA ATACTGAGTA TTA CTGGTGT TTGTTTAGGA TAAGCACATC
TTTATTTGTA TGAGAAAAG AAAAGAGAG TGAAAAATAT ATTAACGTGC ATATAGTTCA
GGACCATGGA TTGCAAGTGA CAGAACTCA ATTCAAACCA ACGTAAGTCA AAAGGAAAAAT
ATATTGGCTC ATGTAACCTT CTCACAGAGA GGGCAGGATG GAAGGGGCTT TGGGAACAAG
AGAAATTGTC TCAAATTCTA GGAATACTAG GATTAGTCCA GGATGGGTCA CCTTCCCTGTC
CCTGAGGTGG TGGTAGCGAT GG TAGAGTCT TATGGGAGGA AAGAGTGCAT GTTAGGATGA
AGGTAGGGCT AAGCAAACAA GGGCAAGGC CACTATATCA TGCTAAAAAT GGTTTTTTTT
GATGCTTCC TTAATTTCAC AAATGCTTCC AACAAAGTAG CACACAGGA AAAGAACATA
GGGACTCTAC TGGTGGGTGC TTTTATCTTA AGCCTTGTA CAGCTTACTC
ACTGCTTGT CCTGAGGCCA TATGCCCTGT AAAAGCTTCT GCAGGGTTTC TACTAAGCTG
GGTCCCTTAT ATGGCTCTCT CCCATTCTG TTGCCCTCACT CTAGTGATCT TTCTCTTTTC

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FIGURE 6 (121)

CTCACCTCTG GGA CTGGTGG CTGTTTGAT GGA CTGCCCTT AGCTTTGCTT TGGGTTTTTT
CCTGGGGACA ATGTCTTCAG ATTATCCTAG ACCAAATAAA CTACAGCCAC TGGGCCAGGC
TCTTCCCTCCT CCAACTGGAC CATGTTCCCA GGGCTCTTCA CCTTAGTTA GTCAAGCAT
TCTTGGCAA AGAAAGGCCT AGTTAACAAT AGACATTCTA GCAATTGATT CTTTTTGACA
TGTTGTAAGA TCTATTACA TTTTGTAAT AAAGCATTC CCTATGAAA CCAACACGAA
CTAAGCTGCT CCTGGAATGC AGGTGGCCT CCTCAATACA GGATGTTCTA GAGAGCTGTA
TTTTGGGCAC TTAACATATC TCCACTACTT AGGGCACAGC ACTGAAATTA ACACCACTAA
GTTTGTCATG TCCATGTAGT TAGTCTCAGG CAGTGCAGCC TCAGGAGTGG AACTGACCTC
TTATGTGTGT CCAGCCTTTC TTCCCTTCAGA AGTCAGCTGT GTTTTCTGCT GACTCTCCAT
AGGAACATCA GTCCCTGAATC CTCAGACCAC CATCTGGAGT AGTAAGTGCT CTGACAGTC
CTAGAAATTG TCTACCGCTG GATCTCCAAA GCGTGTGACA CACCGTGAGA GAGAAATGAG

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FIGURE 6 (122)

AAAGCTGGGC TCTTCAGGTA AATCTTGCTT TTTCACAAGC CCCCTAATTT TACTGCATAA
TTATTTTGAA TTCACTGATA ATTTCTACAA TTTTCCCATTA AGTCATCTAC ACACAATACC
CTCTCATGCA ACACTTGGCT TTGCTAATAC ATATCTATTA TGAGAGCTGT GCTTCTTAAG
CGTAAATGTT TTATATGCAC TAAGGCTCTT GGCTTACATA TAAAAGGGGT ATTGAGCAAT
GTGATACAGA AGTCTTTTCT CCACAGGTCT CATATGTAAA GAATTCATTA GATGGCTGA
AATAGACTGA TCTGTCCATT TCTCTGCTCA CTTATCATTA GGAAGTCATT AGCTAAGGAA
CAAAAACACTAC AATCTATGTA ATTAGAAGAA CAAGCTGGTT TTGCTCAATA TAAAAATAAG
AAAAAGAAAC CATGTGAAAG TCAAAAATATT TGTTTAATCA GGTCAATTGAG AATCTATTAA
AAAGTATTG AATCTTTTAT GATGAGAACT ATCTTGACTC AAGTGGACAG TGGTGAGCTT
TTTGGCCCTGT GGTCCTTACG TAGAAAGGAG GCTTTGTCTAT AAAGTCTTAT ATGGTACAGG
TGCCAAGTTA AGTGCCCAAG CTGTCTCTTA AAAGCATACT GGATTTTGT TTAGACTTTT

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FIGURE 6 (123)

AGTGAACTGA AGGGAATAAA CAAATCCCTC TGGGAGAACT TCTCCTCCAT CCTTGGTGAA

GTCATTCTGC CAGAAATTC

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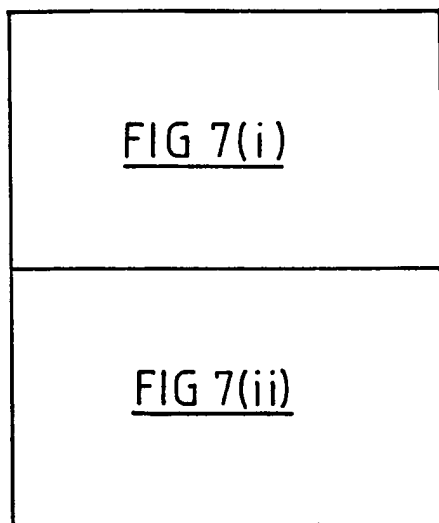


FIG 7

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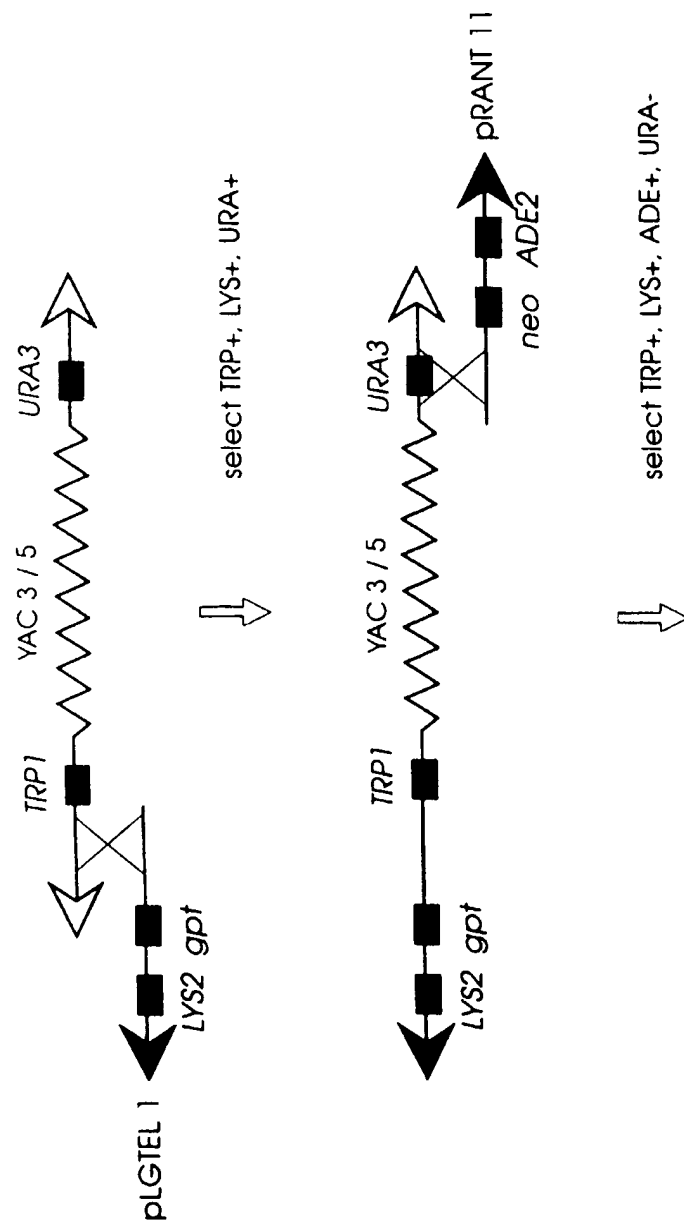


FIG 7(i) Procedure used to retrofit YAC 3 and YAC 5.

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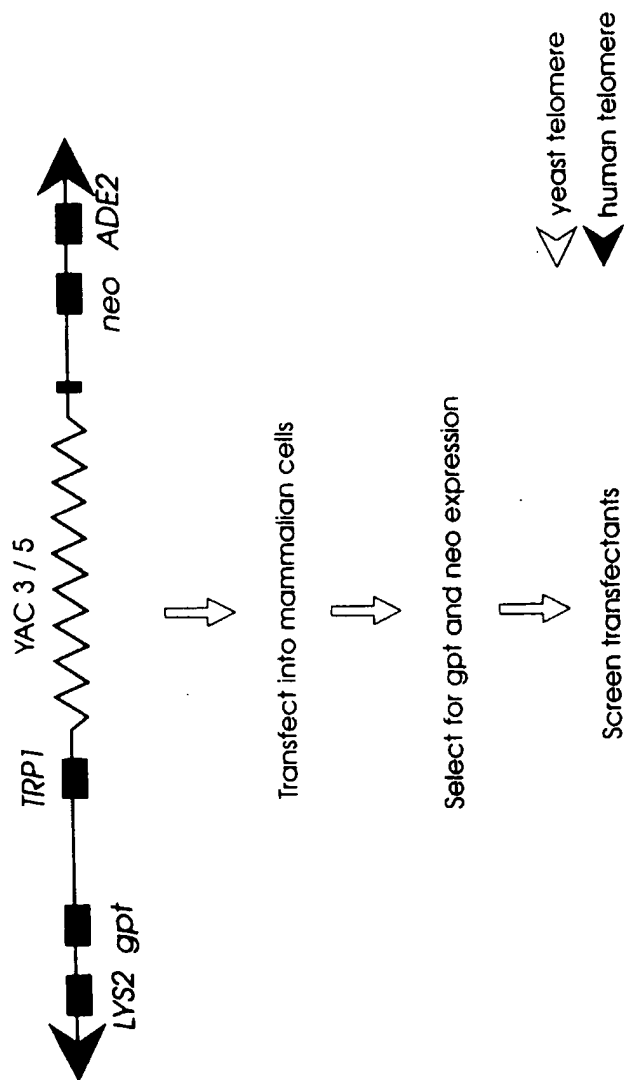
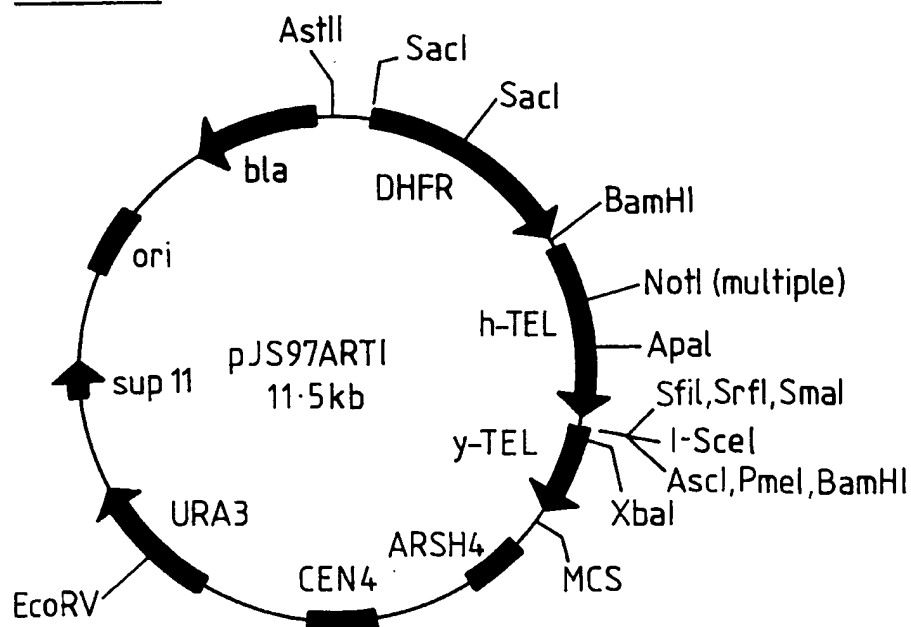
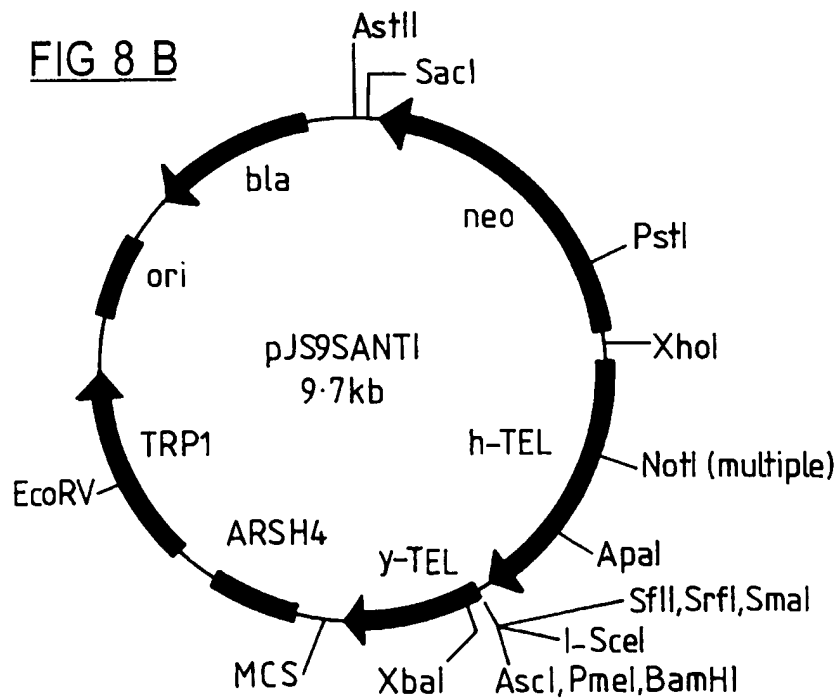


FIG 7(ii) Procedure used to retrofit YAC 3 and YAC 5.

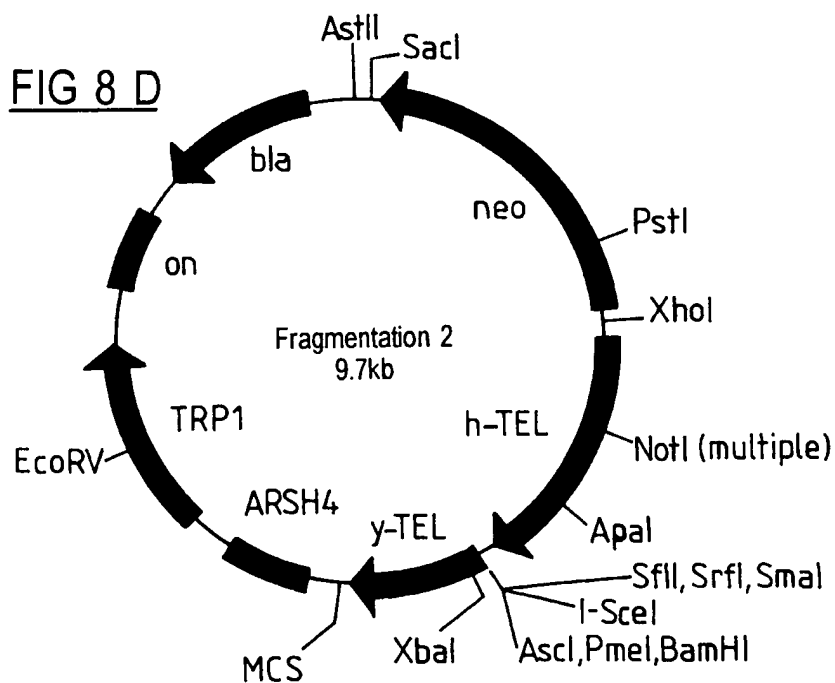
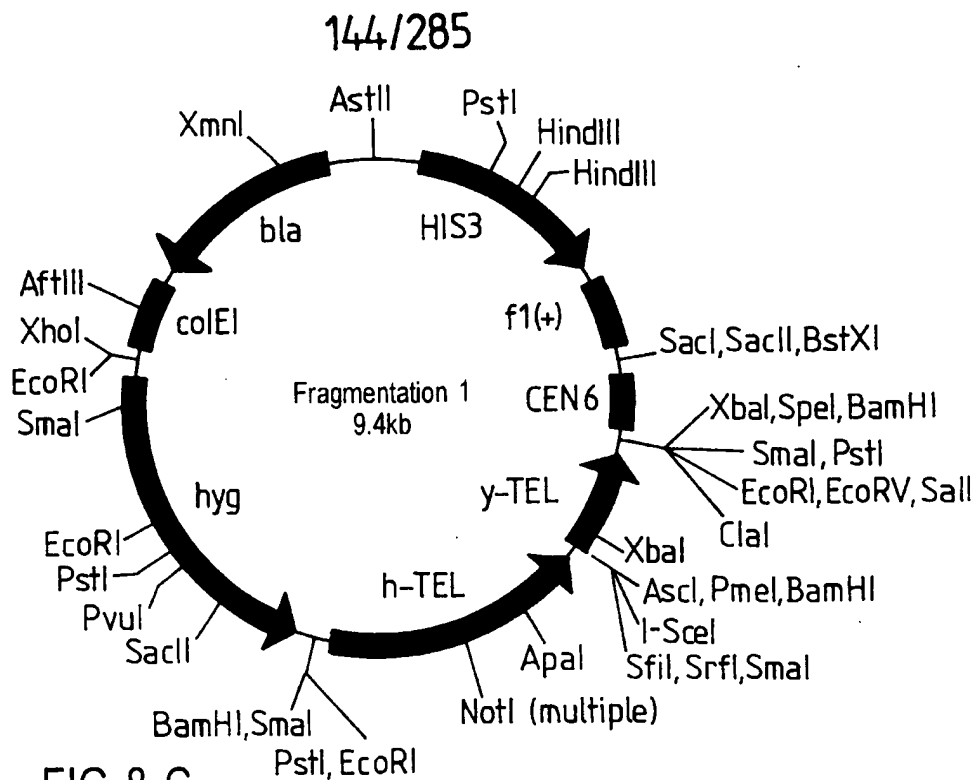
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FIG 8 A

MCS = T7, EcoRI, BglII, NotI, XmaII, SstII, SalI, NruI, NheI, BstBI, ClaI

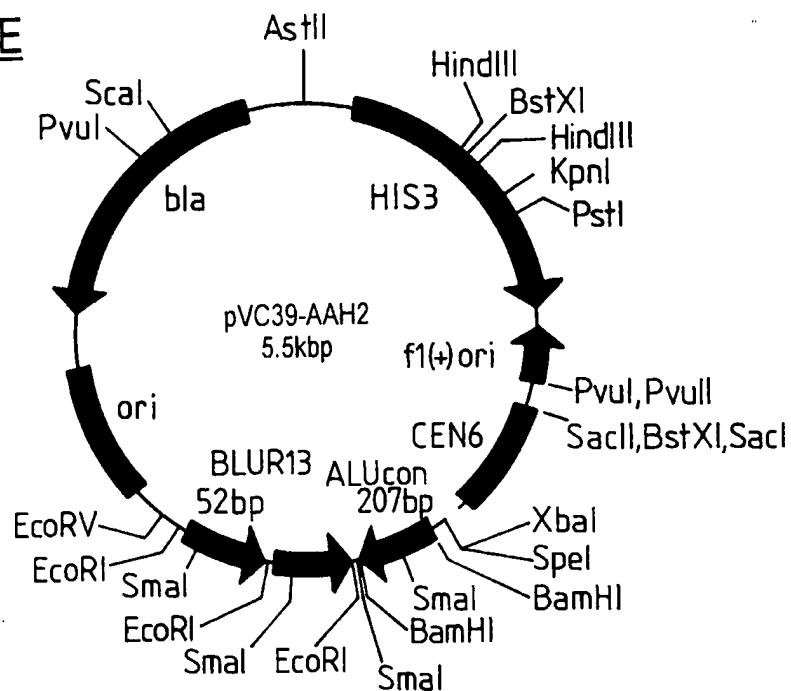
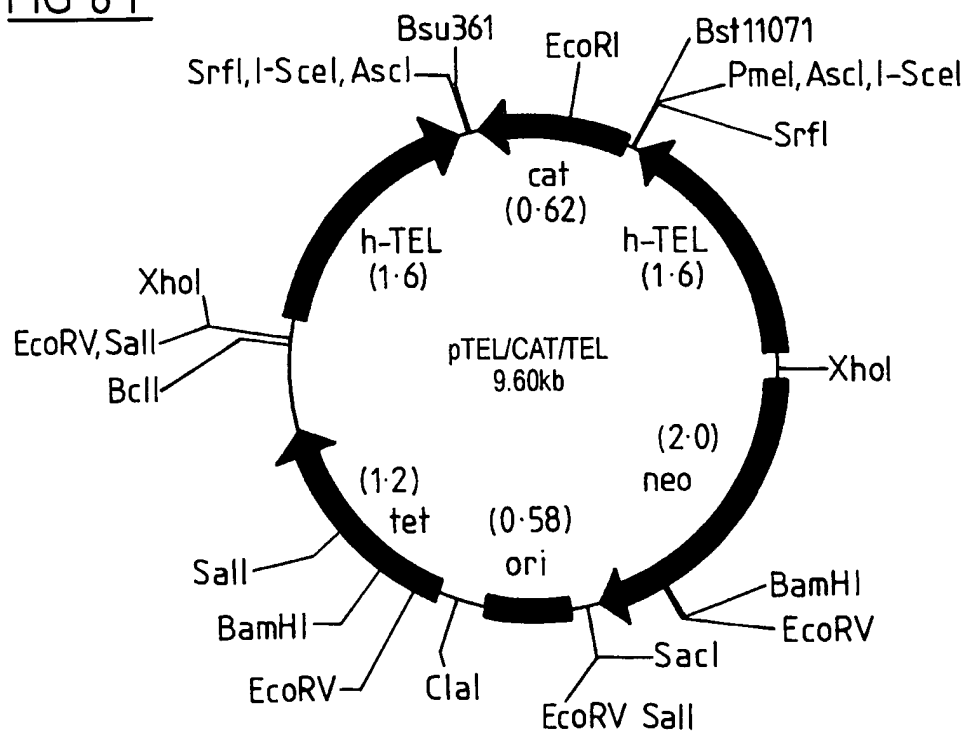
FIG 8 B

T7, EcoRI, BglII, NotI, XmaII, SstII, SalI, NruI, NheI, BstBI, ClaI

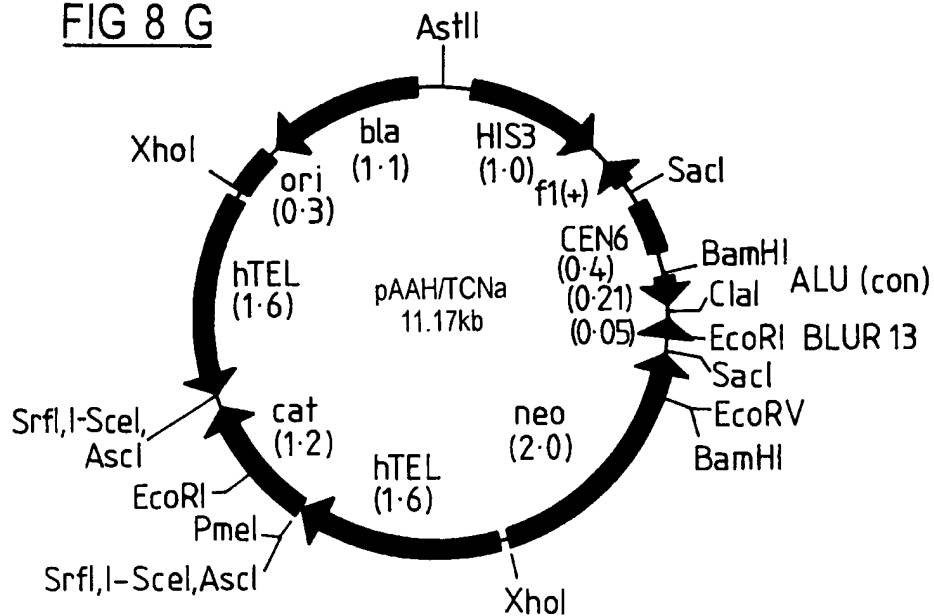
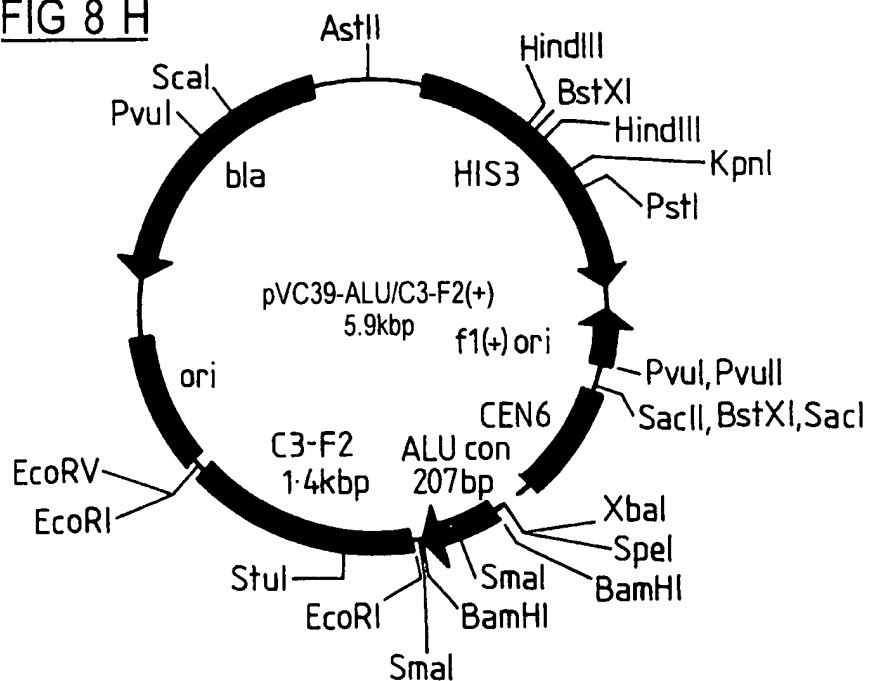


T7, EcoRI, BglII, NotI, XmaII, SstII, Sall, NruI, NheI, BstBI, ClaI

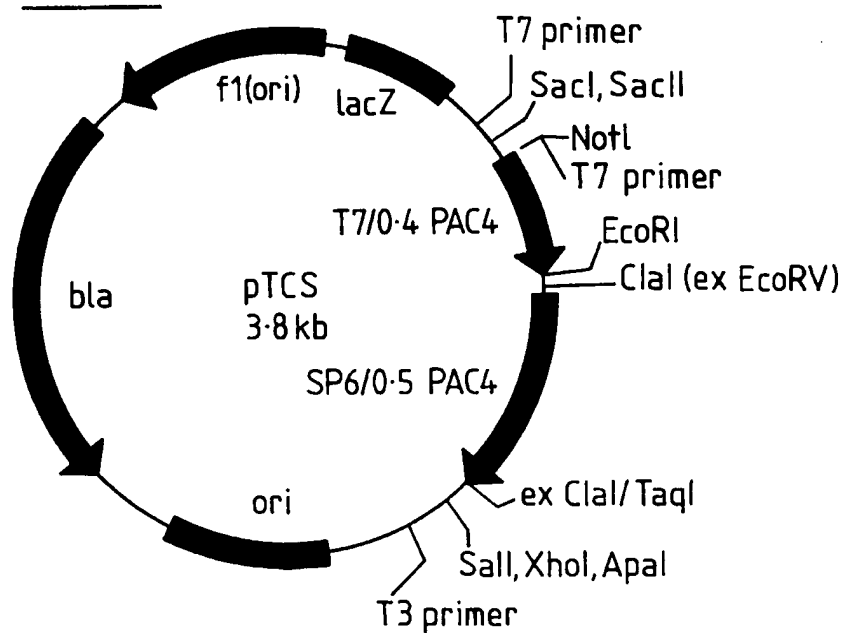
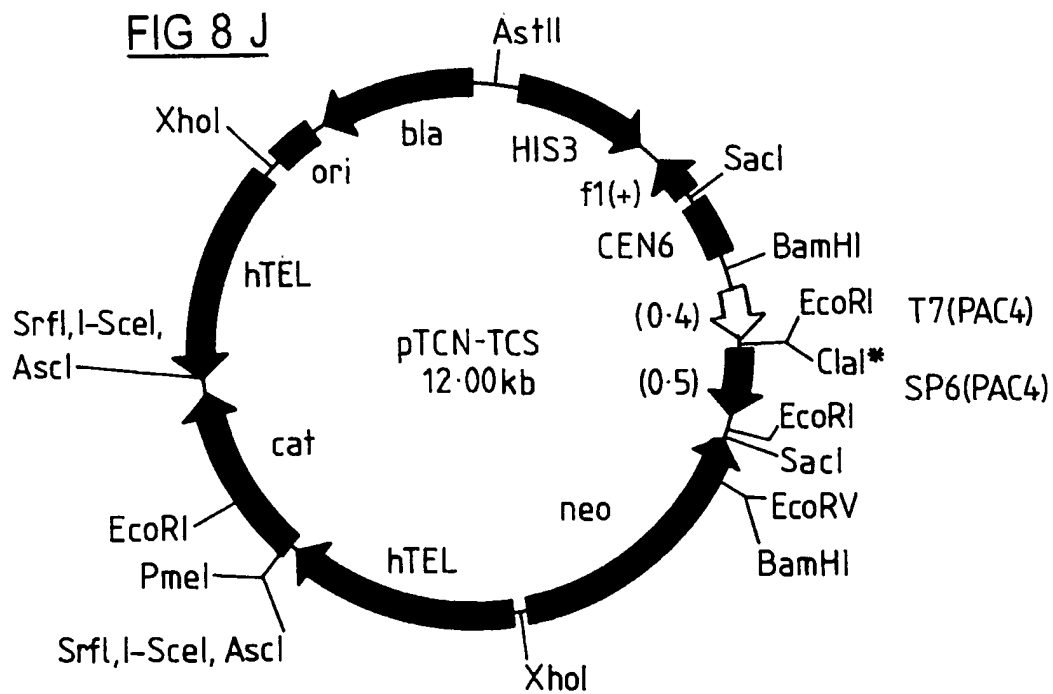
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FIG 8 EFIG 8 F

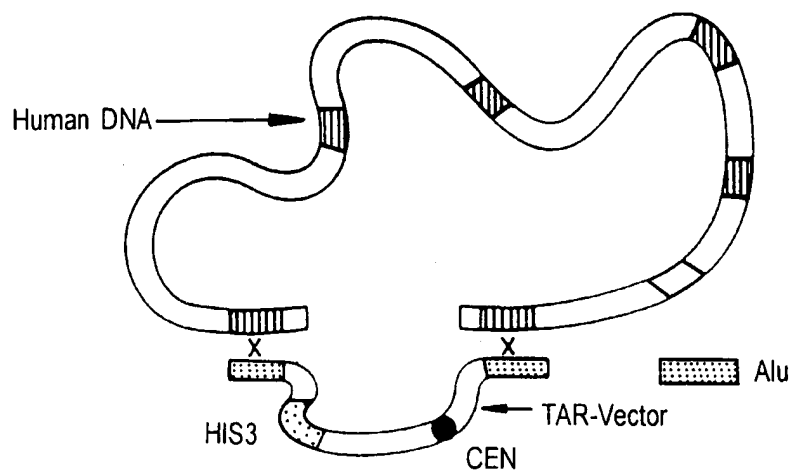
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FIG 8 GFIG 8 H

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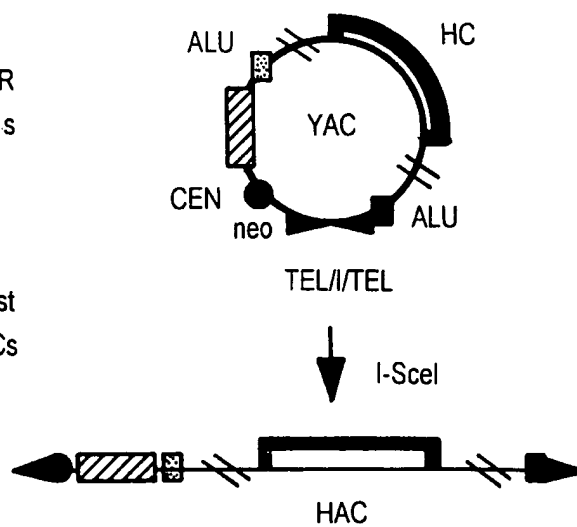
FIG 8 IFIG 8 J

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Circular TARFIG 9FIG10Shuttle YAC to HAC

1. Circular TAR
to create YACs

2. I-SceI digest
to create HACs



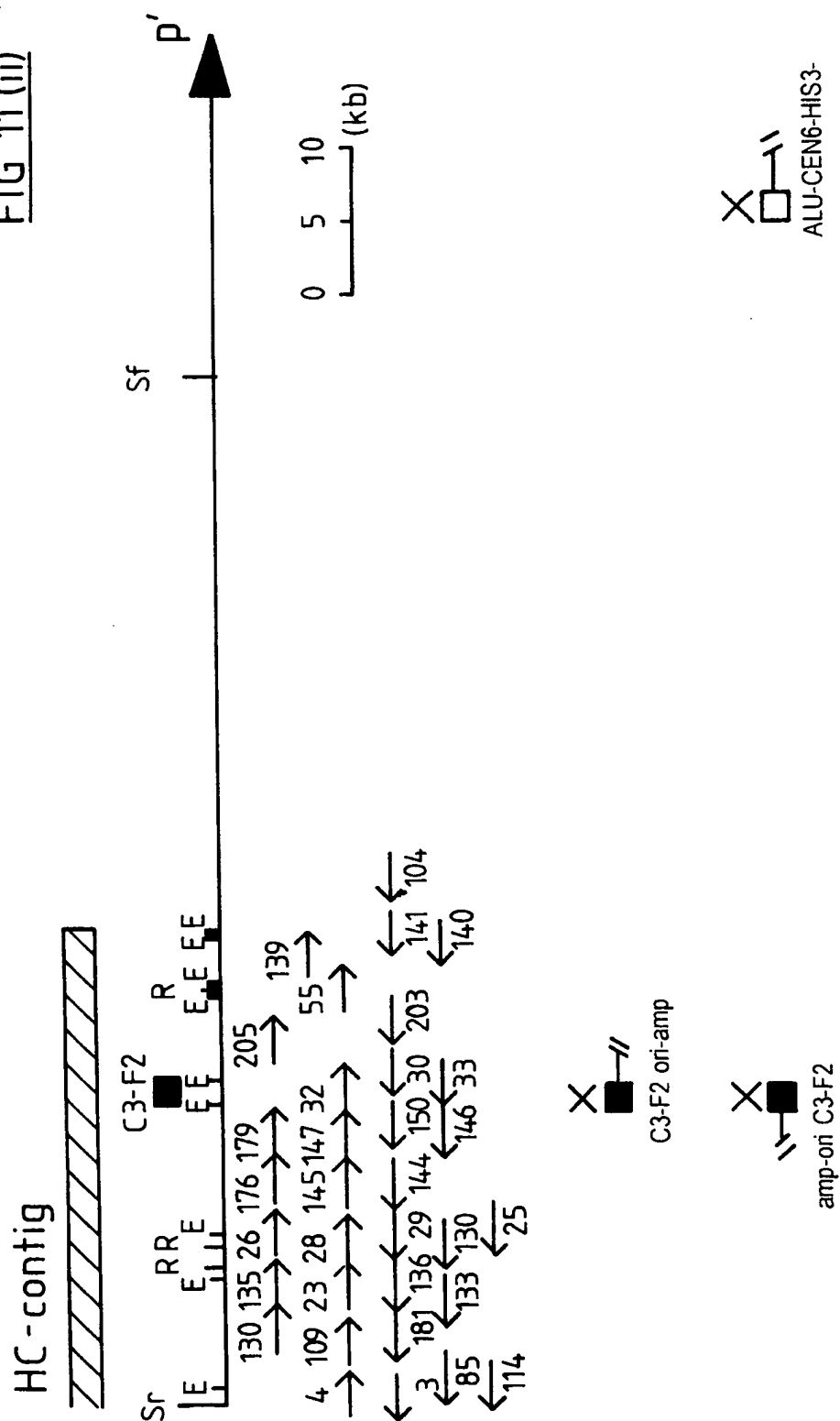
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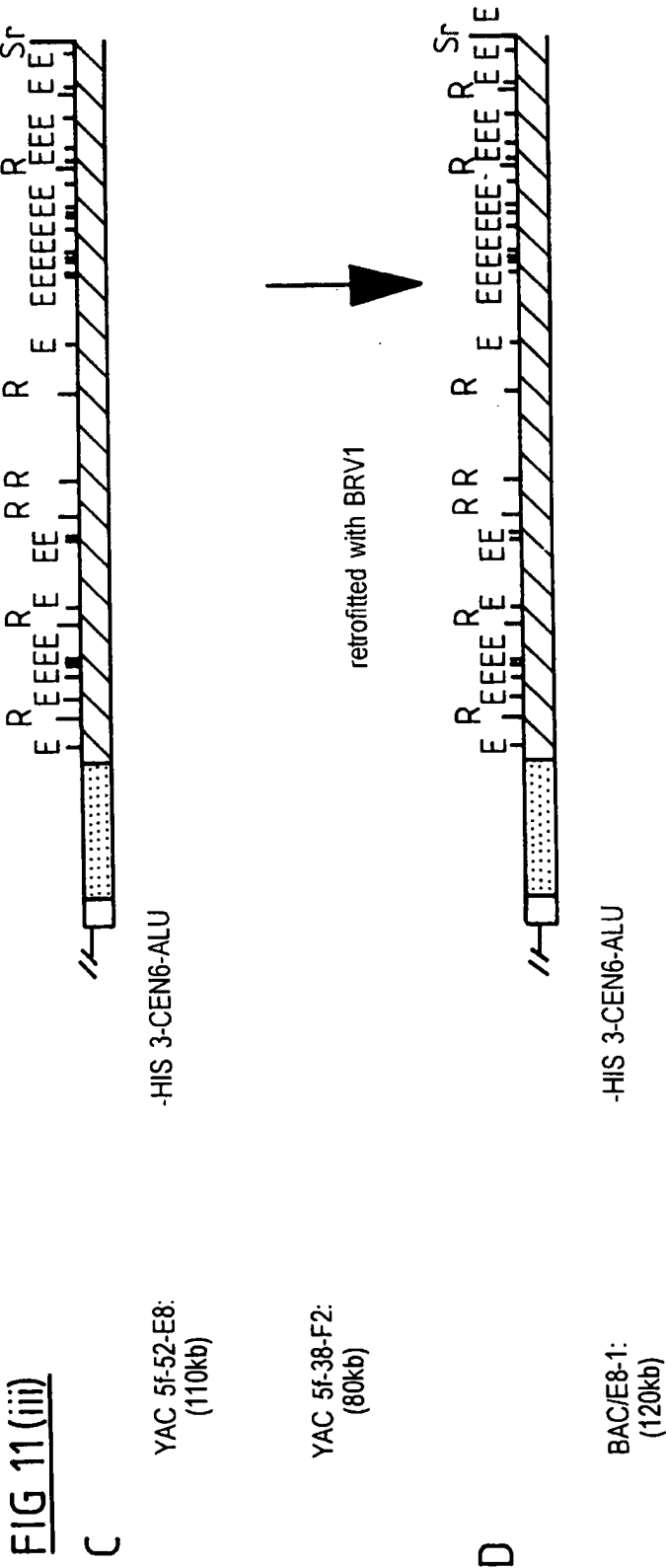
<u>FIG 11(i)</u>	<u>FIG 11(ii)</u>
<u>FIG 11(iii)</u>	<u>FIG 11(iv)</u>

FIG 11

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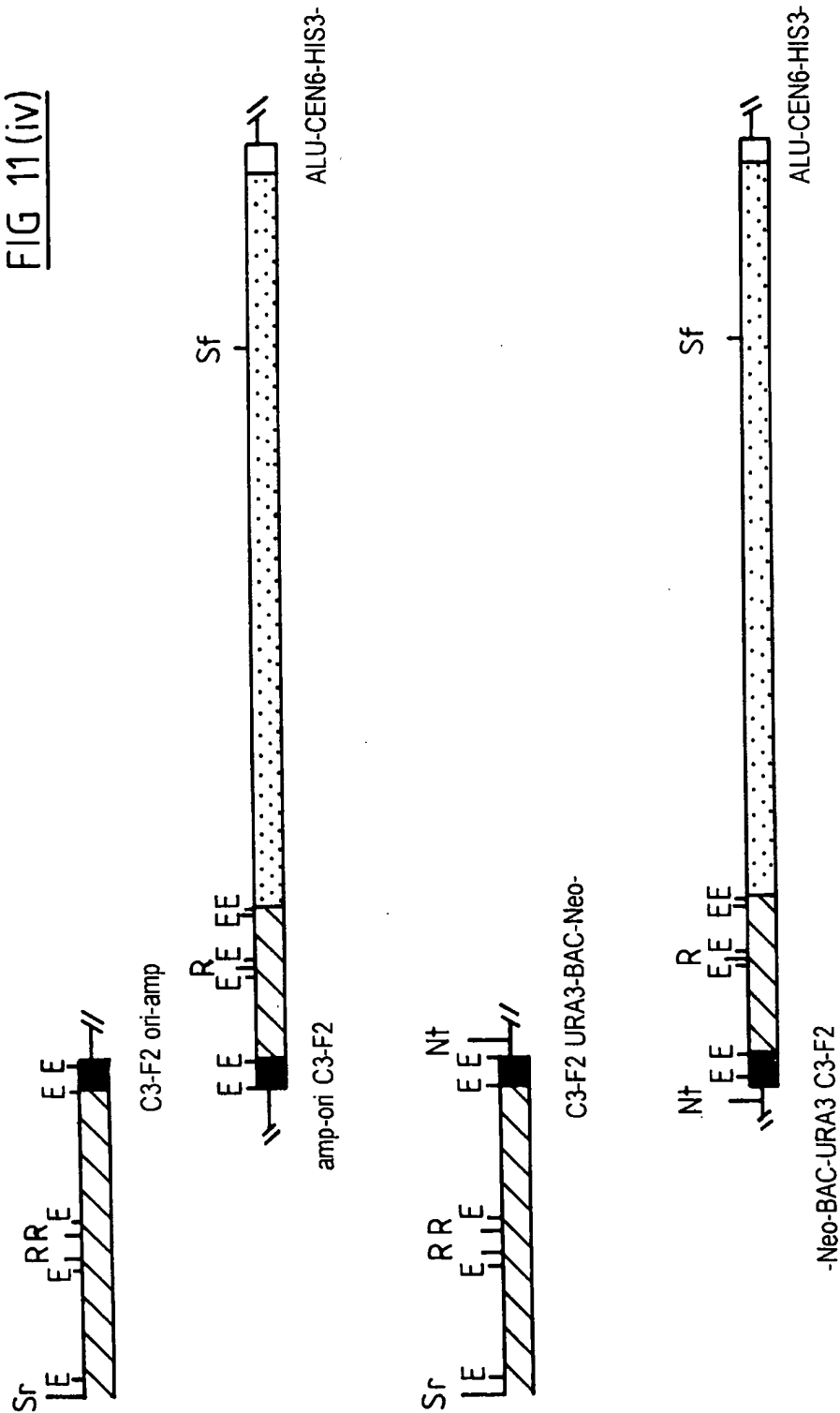
FIG 11 (ii)





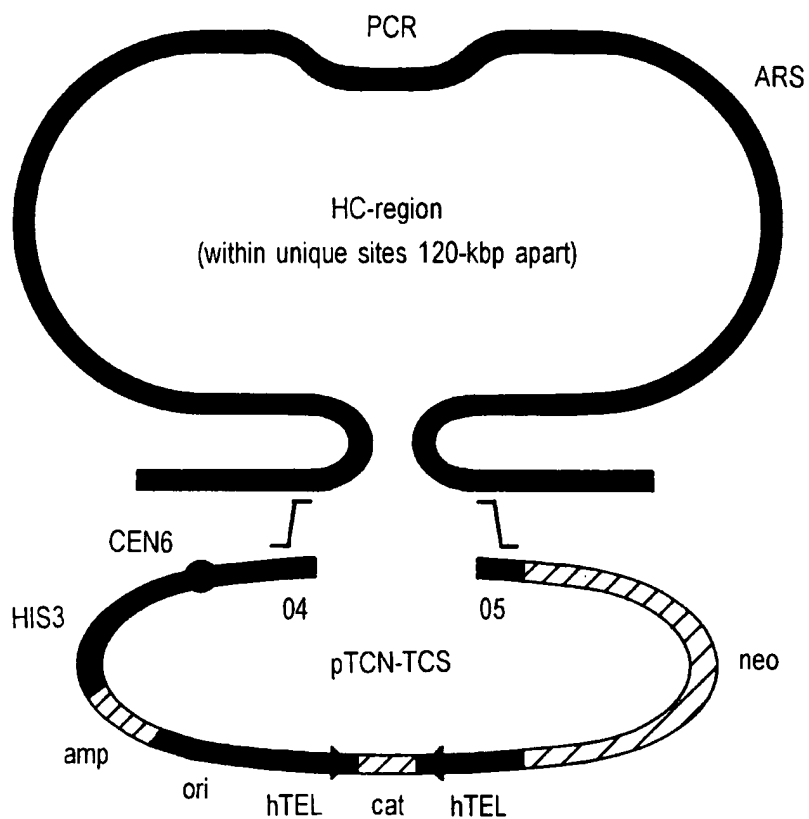
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FIG 11 (iv)



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Specific TAR of HC-region from mar (del) 10



1. Co-Transformation into YPH857
2. Select for HIS⁺ colonies
3. Screen for HC-region by PCR
4. Prepare high-MW DNA
5. Digest with I-SceI to expose hTEs
6. Transfect HT1080 cells
7. Select for G418^R
8. Analyze by PFGE and FISH

FIG 12

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Cloning in Yeast as YAC/HAC

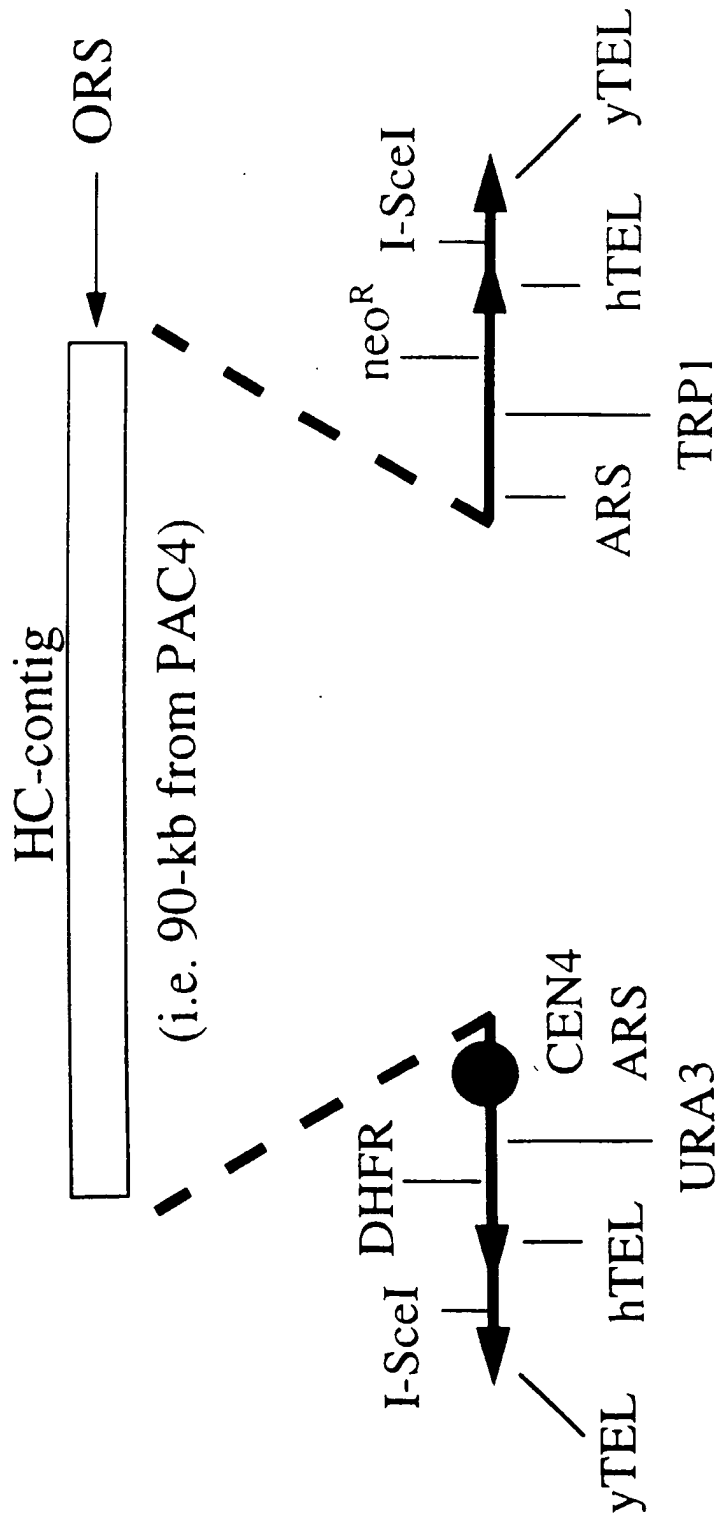
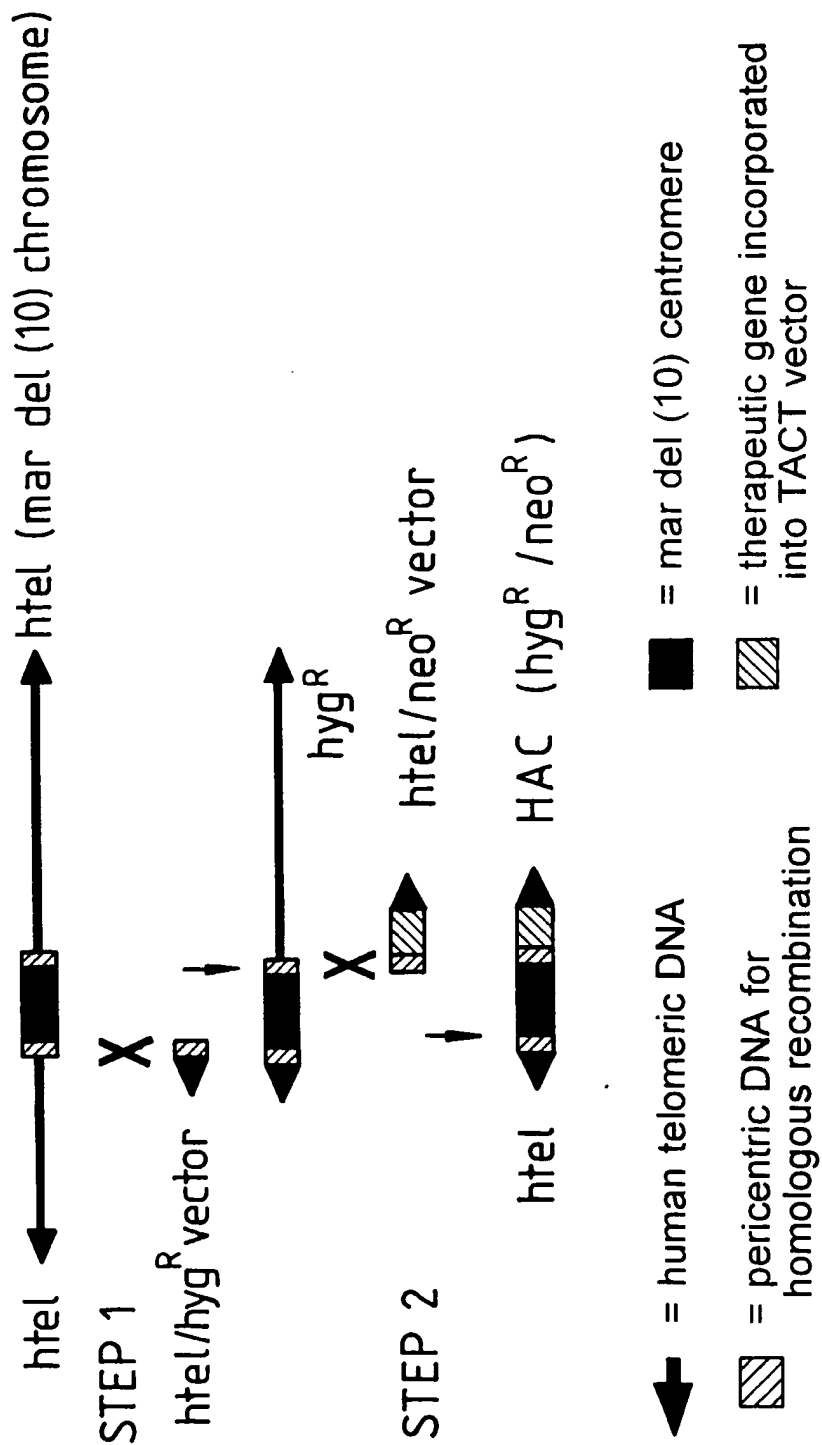


FIG 13

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FIG 14 Outline of TACT procedure



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TACT constructs

FIG 15A

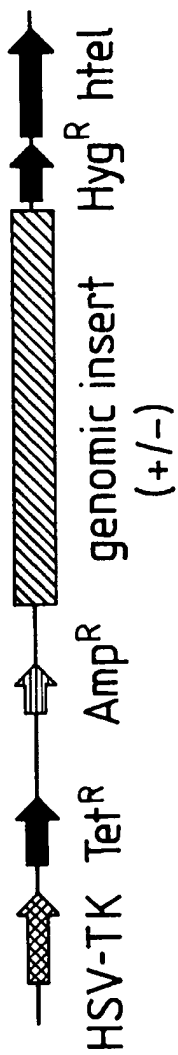
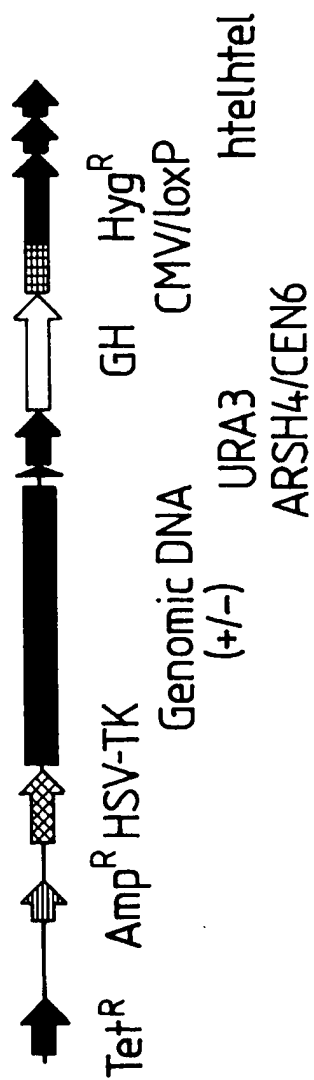


FIG 15B



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161/285	172/285
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163/285	174/285
164/285	175/285
165/285	176/285
166/285	177/285
167/285	178/285
168/285	179/285
169/285	180/285

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FIGURE 16 (1)

TGGTTGATT GTNNATAAGG AAGTTTGGA TCAATCCCGG AAGGAATTT TTTTAA
AATTTTGG AAGGTTGG TAWTAAAAA RCCAATTGG GTTTTAAAA ATAGGAATT
TATGGGAAA AATTTCCCT TTTTTTTTT TTAAGTTTA GATGTATGT TTCCTATAC
TTAAAGTGG TGTCTTATAG GCAGCATATA TCTGGGCTT GATGTATTAT TTAATCTGAT
AATCTCAACC TTTTGTGG AGTGTTAGG CCATTACAT TTAGTGTAAT TATAGACATG
GTTTGATTG CTATACCATC TTTTCATTG TTTTATATGT GAGCCATCTT TTCATTGTT
TTTTTTCATC TTTGACCATT TTCTTTAGTA CTGAATACTT TTTTGTAT TCATTATATC
TATTGGCTT TTAGTTATAC CTCTTAAAT TTTTTTTCT GTTTATGTA GGATTATAA
TATACATCT TAACTTATCA CAGATTACCT TCAAATAGTA TTTTACCAGC TCAAGTGTA
TGTAGAAACC TTACAAGAGT ATATTTTCAT TTCTGTCTCC TAATTTTAT GCTATTGCT
ATAATACATT AGGTTGTG TTGTTTGTT TTACCTTATT GCTGTGGCT GGGTCAGCA

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FIGURE 16 (2)

AACATTTTCT GTAAAGGGCT AGATAGTACA GGCATACCTT GGAGATACTG TGGGTTTGGT
TCCATACCAC CACAATAATA CAAATATGCA AGAAGTGGAT ATCACAATAA AGTGAGTCAC
ACAAGTCTTT TGGCTTCCCA GTGCATATAA AAGTTTGCT TATACTACAC TGTAGTCGT
TCAGTGTGCA ATAGTGTTAT GTCTAAAAA ACACATACCT TAATTTTAAA ATGCTTTATT
ACTAAAAAAT GCTAACAAATC ATTTGAGCAT TCAGTGAGTT GTAATCTTTT TGCTGGTGGA
AGGTCTTTTC TTATTGATGA CTGATCGGGG GTCAGGTGCT GAAGCTTAGG GTGGCTGTGG
CAGTTTCTTA AAACAACAGT GAAGATTGCA ATATCAGTTG ACTCTTCCCTT TCATGAAAAGA
TTTCTCTCTA GTGTGTGATG CTTTTTGATA GCATTTTATG CACAGTAGAA CTTCCTTTGAA
AATTGGAGTC AATCCCTCTCA AACCCGTGCTC TGCTTTAACA ACCTAAGTTA ATATAATATT
CTGAATCCAT TGTGTGCATT TCAACAATT TCCACAGTGC TTCACCAGGA GTAGATTCCA
TCTCATTTCC TGAGATGGAA TCTTTGCTCA TCCATAAGAA GAAATTCCTC ATCTGTTCAA

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FIGURE 16 (3)

GTTTTATCAT GAGATTGCAG CAATACAGTC ATGTCTTCAG GCCTCAC TTC ACTTTTAATT
CCAGTTCTCT TGCTGTTTCT ACCACATCTG TGGTTCCTTC CTCCATTGAA GTCTTGAACC
TCTCCAAGTC ATCCATGAGG GCTGGAATCG ACTTCTTCCA AATCCTGTT AATATTTATA
TTTTGACCTC CCATGAATCA TGAATGTTCT TAATGGCACC TGGAAATGGTG AATCCTTTCC
AAAAGGTTTT CAATTACTT AGTCCAGATC CATCCATCCA GAGGATCCAC TTTCAATGCC
AGTTATAGCC TTATGGAAATG TATTTCTTCA ATAATAAGGC TTGAAAAGTTG AAATTACTCC
TTGATCCATT TTCTGCAAAA TAGATGTTGT GTTAGCAGGC ATGAAAAGCAA CATTAATCTT
TTTGTAATG TCCATCAGAG CTC TTGGGTG ACCAGGTATA TTGCCAGTGA GCAGTAATAC
TTTGAAAGGA ATTATTTTTC TTAGCAGTAG GTCTCAACAA TGGGCTTAAA ATATTGGTC
CACCATTCTG TAAACTGATG TGCTGTCATC TAAACTTTGT AGTTTCATT ATAGAGCACA
GGCAGAGTAG ATGTAGCATA ATTCTTAAGG GACTTAGGAT TTTCAGAAATG GTAAATGAAC

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FIGURE 16 (4)

ATTGGCATCA ATTAAATCA CTAGCTGTAT TAGCCCCCAA CAAGAGAGTC AGCCTATTTT
TTGAAGCTTT GAAGCCAAGC GTCGACTTCT CCTCCCTGGT TACAAAAGTC CTAAATGGCA
TCTTCTTCCA ATATAAGGCT GTTTTATCTA CATTGAAAAT CTGTTGTTTA GTGTAGCCAC
CTTCATCAAT GATACTATCT AAATCTCTTG GATAACTTGT GCAGCTTCTA CATCAGCATT
TGCTACTTCA CCTTGTAATC TTATGTAATG GAGTGGCATC TTTCCTCGTA CCTCATGAAC
CAACCTCTGC TAGCTTCCAA CTTTTCCTTCT GTAGTTTCTC CGCCTCTCTC AGCCTTCATA
GACTTGAGGA TAGTTAGAGA CTTGCTTTGG ATTAGATTTT GGCTTCAGGA AATGTTGTGG
CTGGTTTGAT CTTCTATCCA GACCACTAAA ACTTTATCCA TATCAGCAAT AAGGCTGTTT
TGCTTTCTTA TTATTTGTGT GTTCACTGGA GTAGCACTTT TAAATTGCTT CAAGATATAT
TTCTTTGCAT TCACAACTTG GCTGACTGGT GCAAGAGGCC TAGCTTTCAG ACTATCTTGG
CTTTTGACAT GCCTTCCCTCA CTAAGCTTAA TCATTTCTAG CTTTGTATT AAAATGAGAG

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FIGURE 16 (5)

ATGTAGGCCA GGCACAGTGG CAGGCACAGT GGCATATGCC TGTAATTCCA ACACATTAAG
AGGCCAAGGT GGGAGGATTG CTTGAACCCA GGAGGTGGAG GTTGTAGAGA TCACACCACT
GCATTCCGTC CTGGATGACA GAGCAAGACC CTTTCTCAA ATAAATGAG AGGTGTGCTT
CTTCTTTTGG TTTGAGCCCA TAGAAGCCAT AGTATGATT TTAATTGGCC TAATTCAAT
ACTGTTGTGT CTCAGAGAAT AGGAGGTCT GAAGAGAGGG AGAGAGGTGG GGAATGGCT
GGTCAGTGGA GCAGTCAGAA CACACATAAC ACTAATAAAT TGTTTGCTGT CTTATATGGA
TGTGGTTTGT GATGCCCCCA AACAAATACA ATAGTTACAG CAAATATCAC TGATCACAGA
TCACCATAAC AGATATAAGA ATCATGGAAA AGTTGAAAT ATTTTGAGAA TTAGCAAAGT
GTGACACAGA GAAACAAAGT GAGCACATGC TGTGGAATA AATTGGTGT GATAGACTTG
CTCCATGTAA GTTTGCCATA CGCCTTCAAT TTATAAAAAA CACAATATCT AGGAAGTTCA
ATAAAGTGAA GTGCAATAAG ATGAAGTATG CCTGTAAATA TTTCAGGCTT TCCAGACCAT

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FIGURE 16 (6)

AGGGTTTCTG TTGCAACTGC TCACCTCTGC CATTATAGCA TGAAAGCAGC TATAGAAAAT
ATACATAAAT GAGGCCCTGTA ATCCCAACAC TTTGGGAGCC CAAGGTGGAT GGATCACTTG
AGGTCAGGAA TTCGAGACCA GCTTGGCCAA CATGGCAAAA CCCCGTCTCT ACTAAAAATA
CAAAAATGAG CCAGGACTAC GCATGCCCTGT AGTCCCAGCT ACTTGGGAGG CTGAGGCAGG
AGAATCTCTT GAACCCGGGA AGGGAGGTT ACAGTGAGCC AAGATTGTGC CACTGCATC
CAGCCTGGC AACAGAGTGA GACTGTCTCA CAAAAAAA AAAAGGAAA GAAAATACAC
ATAAATGAAT GTATGTGGCT GTGTACCAGT ATATCCTCAT GCTCTAGCTT GCCAACCCCTT
GCTTTACACT GTCAGTTACC TTCTAAAGAG ATTAAAAATC ATAACAATAT CTATTACGTT
TATTCACATC CTAGTGTAT TTCTTCCCTTA TGTAGAATCA AATTTCATTC TGGTATCATA
TTTCTTCTTT CTAATAAATT TCCTTTAATA TTTTATTATAG CACAGGTCTA ATAGCAATGC
ATTATGCAAT TCATTGCTAT TAGACCTGTG CTATAAATA GCAATGAATT ATGTCAGTTT

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FIGURE 16 (7)

TTAATTGTCT GAAAAAGTTT TTTGTTTTTG AAATATACTT TTGCTGGGTA TATAAATCCA
TGTTGCATAA CTTCTCTTTT CTTCAGCACT TTAATGAAGT CACTCAGTTA TCTTCTGGCT
TGTATAGTTT CTCTGGCTGC CTTCAAGATT TTTTCATTGT CTTTAATTT TAGCAGTTTG
ATGTGCTAG GAGTGATTTT CTTTGTAATTT ATCCTTTTGG GGGCCTCTTA ATTTCTTTGA
TCCCTTTTTT CTTTTTTTTT TTTTTTAAAC CATTTTGGGT CTTTCCCCC ATTTGGGGTG
AAAAA AAAAATAAAA TCATAGTTTA AAAAATAAT TTGGGAAAAT TTTCAGCTAT
CATTCTTCA AATATTATC CTACTCTATG CTCCCCCTCCT CCCCCTTCCCT TCTGTGACTC
AAATTACAGG TATATTAAAC CATTTTATTT GTTCACGGCA CTTGGATGCT CTGCTTTCTT
ATTTTTGTC TTTCATTTTG GATAATTTCT ACTGACCTAT CTTCAAGTTC ACTGATTCTT
TTCTCAGTCA TGCTAGTGT GCTCAACGCC TGTGAAGAA ATCCTTTGTC TTAAATATCA
TGTTTTTAT TTCTAGCATT TTCATGTAAC TCTTTGTCTT GGTTCATC TCTCTACTCA

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FIGURE 16 (9)

TGCACCAGAC TTCCATTTCAC TGCAAGAGTG GGCTGCTGCG CTTTGTGATT CATGTGAGGC
CTGAATTGTG GAAGGGTTTT TCCTTAGTGT GTCCCTCCAT GCTCAGATTT CAGCAAGTCT
TCATATCTGT GCCACAGAAG GAATCTGACC CATGCTCTTT TTGACCTCCC CAAGTGATCA
ACTGTGCTT GTTATAGCTT GTCATGGAGT AAGAGGGTGT TTTTTTTAGTT TTTCATCCTCC
AGCCTTGGTC TTGGGCCCTG AGCTCCTAGA CTCCAGGAGT GGATGGAATC CAGTGATTTC
TCAGTAATTC AGCCCCCTTCT CCAGTAGTGG CAGATCTCTG CTTTGTATCA GTGCAAGATC
CTGGGCTGAG CTCATTTTCT GCCCTTCCTC GAGTGGCAGA CAGCTCTTGC TTTCACCCCT
CTACCAAAGG CAGTGCATCT TTTCTTGGGC CTCCTCCCAT TGAAC TTATG ACTTTCACAT
AAGAGAAGG CTCATGTATC AGAGAAATTCT GTGACTTTGT GCCACATACA GAGTCTCTCA
GTTCTCTTGC CCGCCCCAG TCTTTTTTGT GAGCACCTAG TAGAGACCCCT TGGAGAAGAG
CAAGGAAGCG AGTATGGACT TCTTTTGTGT CTGTCGATTG CTTTGT TTCT CAACTGCTAC

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FIGURE 16 (10)

TC TTG GACTT TAAGAA TTCA TTA AAAATTTC AGCTG TTTTC TTT TTT TTTCTT TCGT TTTTCT
TTTT TTTT TTT TTT TTTT TTTT AGATGGAGTC TTGCTCTGTT GCCCAGGCTG GAGTGCAGTG
GTGTGATCTT GGCTTGCTGC AACCTCCGCC TCCCGGGTTC AAGCGATTCT CCTGCCCTCAG
CCTCCCAAGT AGTTGGGATT ACAGGTGCC ACCACCACAC CTGGCTAATT TTTGTATTTT
TAGTAGACAC AGGGTTTCAC CATT TTGGTC AGGCTTGCT CAAACTCCTG ACCTCATGAT
CTGCCCCCCT CAGCCTCCCA AAGTGCTGGG ATTACAGGCA TGAGCCACCG CGCCAGGCCCT
CAGCTGTCT CTTT TTACCT GCTGGGATGG CTAGTTTCT GTGTCAACTT GACTGGGCCA
TGGGATGTCC AGATATGTAA TTA AACAGTA TTTCTGGGTG TTTCTGTGAG GGTGCTTCA
GAAGAGATTT GCATTGAAT TGGTGA ACTA AGTAAAGCAG AGGGCCCTGT CTAGTAGGGG
TAGGCATCAT CCAGTCTGTT GAGGACTTGA ATAGAACAAA AGGCAGGGA AGGTGGAAT
TGCCCCCTCT CTGCTTGAGC TGAGACATCT ATCCTGCCCT TGGCACTCCT GGTCTCAGG

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FIGURE 16 (11)

GGTTCAGACC TGGATTCCCTG GTCCTCCACCT TGCCCATGGC AGACTGTGGG ACTTCTCAGC
CTCCTATCTA ATTAATAAAT TTTTTTTTAC ACACACACAC ACACACACAC ACACACACAC
ACACACACAC ACACACCCCTA TGTATCCCTTC TGTTTTTTCTG CAGAACCCATA TTAAATACAC
CTGCTTTTAT GACGATTACC TATCGATTCT GTATTCTGCC AAAACTGAAA ACAGTTCATT
TTTCCATCTC TTCTCAGAGA GGCTTGTCAG CCATTAGTTC TCTGATGGC TCAAGAAGTT
ATGCAGTTTT TTTTTTCTCA CTGTTAGGAT GGAATTGATA TTCTGTTGAA ACTTCTTATA
CCTAAGTGGA AACTTGTTTT GAGGTATATT TCTCTACTTA CTTTGTCTGG AAATGGAACA
CTCTGTATCT AGTTAAGACA CATAAACTGA CTTGTGATAC CATAATGTTG TGTGAATT
TATATTCTTA GAAATCATC TGTCAAGGTG TTAACCTAATG GCAAGCATT TAATAAATCA
GCATTCAATG ATTCAGGTGC TCTGAATTAT CTGACTTTTA AATCTTACT TTATAAATGA
GAAAATTGGG GCATGGAAA GTTAACCTC CTAACCCCGA ATTATTACAT TATTAAGGAC

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FIGURE 16 (12)

AGGACTTAGA GGCCAGATAT CTTAAGTCAT TAAATATTCTT TGGCTCACAG AATTGGCAGT
ATAACCCTAAA GGTAATAACT AGGTGATTTT CTTTATATATC AATTAAATAT GTCAGTTTTC
AAATATTTCAT AAGTACCTAC TGTGCAGGGA AAGAACATGC CATACAAAAG ATGTAGTCCA
GGCCTTTAAG AAACTTTCAT TTAATGGGAA CTCAAGAAGT GTACATATAA GGAGGGAAGT
AGCAGTATGG TACAAGATAA TACATACATA TCAGTGAATG ATATTGCCAA AAAGTGCTAT
TGATAGAGCA ATAAATTCATT TCTGCAACA GCTGCTGATC TCCTACTGAA AACAGAGGAG
GGAGAACAGG ACGCCTCGTG GTCAGGATAG AAGAGAAAGA CCTTGAGTTG AGCCTTGAAC
AGTATTTAAT ATTCAAAAGG TTAAGAGAGG AGAGCAATTG AGGAGGGGAG AATAGTTCCA
GCACAAATGA TGGTGTACAA GATGAACACA GTCAGTAAAG AGCAGACTGG TCTGGATGGA
GAGGAGGATT TGCATCATTT GGGATTACGT CATTAGACC CTTGAAAGCC AGGATTGAGT
AAAGCCACAG TGAAGCGACT GGCTCGTATG GAAGCTTTAT TTTAAGAAGA TTAATCTGGT

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FIGURE 16 (13)

AGTGACATGT GCCAAAACT GAATAGGTAG AAATGAGATG CAGAGAGCCC AGTTAGAACT
AAGTCTGGTG CAGTAATGCA GGATTGAGGC AATAAACACC AAATACAGT ATCACCAGAT
AATGGATGTT TGAACGGACG GTTTAAAGGA AAATGATGG TATTGGTAA TTTATTAGAT
AATCCAGGC CATGGAATGA GAGGGGAAA TGAATAACCA TAGTCATCAA ATGGTTTTTC
TTAATGAATC TGAATTTTGG TGTAAGAGCA ACATTTTCTT AGGCCTTGCC TAGTTGGTAC
AGCTGACTAT GATAATGACT GCTACCATGC TTGTTCCCTCT TTTAGCAGCT GTGAGTCCCC
CACCAGCCAA ACAATGAGCC TCTTGAAAAG GACGATGCCT TTTCACTTCT CTCCAAGTGC
TTGGCAAATA GGAGGCCCTT TGAAGTTACT TTATAGTTAG GGGTCCCAG TGAGTATTG
AAATATTAAG TCATGCCCGT GGTGACAGC ATGGCCCTAC TGCTCATCAT CAGTATTAA
CCTTAGGCAA GTTAATGAAC TTTTCTAAGC CCCAGTCTAC TCATTTATAA AGTGGATTA
TTAATAATGT CTAATTACATA AAATTATGAA GCCTGAGTTA GGTCAATCAG ATAGTGTTA

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FIGURE 16 (14)

GTCTGATTCT TCGAACCTAG TAAACAGTCA GTAAACAGAA GCAAATGCCA CATGCCCTGAT
TTATATCCAA GGGAGAAAG GTAAAAGTGA AATTTTCATG ATTTATGGAT TCAAATTATA
CATTCAAAG ATGCTTTATA AGCTATTGTT TTGGTAAGAA GAATTGAGCT GAAACAGAAT
TTTTCTGACAG CAGTGATTAT TAAATGGTGA AATAGGCTAT TGATGTCCTT AGAGGATATA
GATGTTCAAC TTTTGCATAT AAGTGCACAA AAATTCACTA AGTAGATATG TCTGTCTACA
CAGAGAGAGA GAGCGTGAGA GCATTAAAGT TAGTAAACAT CCCCCTCGCT TTTTTTTTTT
TGAGACAGGG TCTTACTCTG TTGCCTAGGC TGGAGTGCAG TGGTGCAATC GTGGCTCACT
GCAGTCTCAA CATCCTGGC TCAAGCGATC CTCCTCGCTCA GCCTCCTGAG TAGCTGAGGT
GTGCACCACC ACACCCGGCT AATTTTTAAA TTTTTTTTATT GTAAAGGTGA GGTTCACCA
TGTTGCCCAG GTCTCAAACT CCTGAGCTCA AGCAATCTGC TCACTTCAGC CTCCAAAAAT
GCTGGGATTA CAGGCGTGAG CCACCACGCC TGGCCAGTAA ACCCCATTCA TTTACATCAT

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FIGURE 16 (15)

CTTACTTGTC CCTCCAAAAT CCTGCAAAGT AGGTAGGTTT TGTCTTTATT TGTATTTAG
GTGAAGAACT TGAAGTGGTG TTGAGGGAATA GGTGTTTTC CAAAGATCAC GCAGCTGGAG
TGGCAGAGCT GTATACTCTT CTGATTCCAC CAACGCTGTT TACATCACAT CTGGAGAAAA
GTGCTCTGAG GCACAGATGT TTAGTGGGAG GGATGAGACA CAGGCTGCAA TGCCTAAAGA
TAATCGGGAA TAAAAGCAGA AAACAAGACG TTTGTTTCTG TTAAAAATGAG ACAGAAAAATA
AGGCGTTTGT TGTTTGGGAT TGAGCACTTG GAGAAAGTGGG GAGCGATTG ATTTGGGTGA
GACTGCTCCT GGAATGCTGC ATCTGGTTCT GGACTACTCA TTAGTAGGCT TATAGAAACT
AGCTGGAGGA GGTTCAAAGA AAAGCTCCAA AATGATTAGC GGGCTGACGG GATTGATTTA
TAAGAAATAT TAAAAGAATT AAATGTGTAT AGCTCAGCTA AGCAAGATG AAAGAGACCA
GCTAAATGTA TACAAATATC TGAAACGTGC AAACTTTAA AAGAGAGATT AATTATTTAA
CATGATACAC GGGGCACAA TATGCAGTCA CAGGATGAAA ATTTACGCTG AGTATCTAGA

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FIGURE 16 (16)

AGAATTCCCC GATAGTGAAT CTGTTAAGGC TGTCTGTAGT GTGGCCCTTTC CCTGGAGAGG
CAATAGAAAT TTCAAGTCTT ACGATTTTAA AAGTTTCTTG GGAAC TAGGT ATTAGATGAT
GTTAGAGAAT TATTATTAAAT TTGGTCAGGT ATGATAATGG TATTGTAGTT CTATAAGAAA
AATTGTATTT TTTAGAGTTA CATACCCTGA AATATAAGCA TAGAATATGA TGTAGGAGAT
TTGCTTTAAA ATACCACAGT AAGGAAAGAA AGGAAGGAGG AAGAAAAGAA AGGAAGGGA
AGAAAGGGAA AAAGAGGCAA AGAAGGAAGA GAAGGTAAGA GAAAGAAAAA GAATGAAGGA
AGAAAGGCTG GCACTGTGGC TCATGCCCTAT AATCCCAGCA TTTAGGAGGC CAAGTTGGGA
GGATCACTTA ATTAAGCCCA GGAGTTCAAG GCTGCAGTGA GCTGTGATTG CGCCACTGCA
CTCCAGCCTG GTGGCAGAG TGAAGCCCTG TCTCTAAAAA AAAAAAATAA GTTAAAAAGA
AAGAAAAGGA TAGATGAAGT ATGGCAAGAT GTTGGTAATG TTGAACCTGA AGGAAGTTAA
TATGTGAGTT CACTTTCCTC TTCAGTCTTC TTTATGTATG TTTGCCAACT TTCATAATAA

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FIGURE 16 (17)

ACAATTAAA TTATATTTTC CTGATCAAAA CTTAGTAGCA GTATTAAATCC CTGGGCTTCC
TGACTAGAAC AGCCTCATTA CCACATGGGC AGAGTTCTGG CCGACCAGGG ACCACGTAGT
GGTTCACCAT CTTGCTCTGG TAATGTGGTC TGGGCTGAAG GGCCCTTTCT AAGGTTGTAG
ATAGAAATCC AGGAAACTTG TTAGAACTGC AGACCTATCA GGTACCTGC AGGAGGTGAG
TCTACTAAGG TGAAAAAGCA GAGGGCAGAG GTCGTGATTA GCAGCTGACC GCCCCCTGCT
TTTCTGTCCC TCATTCTGTG AAAATTGAGT GGAGCTCAAT TTTGAGTGGA GCTCTAAGTA
GCTCCACTTG TAGACATTGA GTGGAGCTCT AAGTGTCTTC AGAATAGCAA AACACTAGTT
TTCTTTTCT TTTCTTTTTT TTTTTTGGG AGACAGAGTC TTGGTCTGTC CCCCAGGCTG
GAGTGCAATG GCACGATCTC CGTCACTGA ACTCTGCCTC CCGGGTTCAA GCGACTCTCC
TGCCTCAGCC TCCCGAGTAG CTGGGATTAC AGGTGCCAC CACCACGCC AGCTAATTTT
CCTATTTTA GTAGAGATGA GGTTCACCG TGTGGCCAG GCTGGTCTCA AACTCTGGC

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FIGURE 16 (18)

CTCAAGTGAT CCGCCTGCCT TGGCCTCCCA AAGTCCCTGGG ATTACAGGTG TGAGCCACCA
CACCCAGCTG CAAAACCCCTA TTTTCTCTGA ATGGAGAAAC ACTTCCCCCT TATTATTGA
GTTTGGGAAG CAAGAAGAGG GGTAATTTCAT TAAGTGAAA TTTCCAAAAT CCAGAAAACA
TCGATAAAGC AGCAGCTTAA TTTTCTTAAG GAAGAAATTT TTAACATATC TTCTTTTGAG
CCTCTTTAGG AAGACCTCAC GTCCCTTGCCT TGAATGTTGA GAGTGGGAAA TCCAGGGAGG
TTTTTGGAATG CATGCCCTTAT GTCTGCTTTT TTGTTTGTGA GAGAAATATA AATATTTTAT
CTAGGTTTGG CTGATGGCAG TCAAGCATGA ACACAACCCA CTGTTTGAGA AGCTGTAATT
TCTGAATTTC TGCAGAGTGC ACATCTAGGC CAGCAAATGG CAGTAAGAGT GAGGTGGATT
TAGCTCAGTG TAAGGATGAA CTCCAGAACC ATCGGCTCTG ACTGAAAAGTG AAGCGGCAGC
CGCGTTGTGG GAAAGCTGGC TGGAGTCTCT CTCATAAGCA GGCATTCTTT TTCTCCAGCC
CGTCACTGTG TTGGTTGGG CCCACGGTAA GCCTCCTGGC CTCAGGCTG TAACCCCCAC

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FIGURE 16 (19)

CATCCTCCTC TGCCTCGCCT CCAGAGTGAT TGTTCCTGAAG CACAACCTGGA TGTCACTTCCC
CTTCCTGAAC TCCTAGCACC TACAGGGACT CCATCCCCTTG TGCCCCACAT ACCTCACACG
TAGACATTCC TAATGAAGAT TTGATTGAAT TATTGTAAAC TCAGTGCCTC CCACTCTTCT
AGTTGCCCTCT CTGCCCTGCCT TTGTACATTT ATTTATTTAT TTATTTATTT ATTTATTTAT
GAGACAGAGT CTTACTGTAT CACCCAGGCT GGAGTTTAGT GGCACCATCT CAGCTCACTG
CAACCTCTAC CTCCCAGACT CAAGCAATCC TCCCACCTCA GCCTCCCGAG GAGCTGGGAC
CATAGGCACG TGCCACTATG CCCGGTTAAT TTATTGTAAT TTTTGTAGAG ATGGGGTTTC
ATCGTGTTC CCAGGCTAGT CTTGAACTCC TGGACTCAGG CGATTCGCCC GTCTCAGTCT
CCCCAAGTGC TGGGATTATA GCGTGAGCC ACCATGCCCA GCCGCTAGCA CTCATCTTAA
TCGTATATTT ACTTATCTGG CTTTCCCACC AGACTGCGGG CTCCTCAAGA GTAAATGCCA
TGTTTTCACC TTTATTTCCC CAGTTTGTGG CACATTCTAG GCACTCGCCA TCATGAAATA

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FIGURE 16 (20)

AACCTCTGGA GCTGTGATAT TACAAACGTG AAAAGATGAC GAGCACTCAG CAACTTTCAG
TGAGTAAACA AAGGCTTTCA TTCAGCATGT ATTTATTGAC TGCCCTGATC TGGGCTGCTT
CCTGTCTGTG GTTCAAGGAG AGCATAGTCT ACAGAACCAG AGACCTGGCT ACTCTGGAAG
TTAGACTTAA GCCCACCCTCG GTCCTTGAAT GGGGAAATAT TTCCCTTCAT TCCCTGTGTTT
TAGGGACAGA AAGATGAGTA ATGCAGTGAT ACATGCTGGA AATGTTTATT CCACTACCCG
AAGCTGCCTC TCAACTTAAC AATCCATGAA AGAAACAAGA TGGTATATATA CTTTTTCTAA
TTTGTGATGC CTTTGTTTAT TTGTTTCCGG TTAAAAGAGG AGGTGGCATT GAATTGTTTG
TTTGGTGTTGG TTTCTTCTTC AATAAGAAGC ATCTTAATAT AACTAGACTG GACATCTGTC
CCATTTTCAA AAATTACAAG TTTCGATCAT TGCTAAATTG TACAGATCCC AATCTGTCTG
CTCTGCATAC ATTTGCATTT ATAAAAGCAG AAGCAGACTA GCAGTCTTTC TAATGCAATC
CCCCAAATGC ATGAAGTATT AGATTGCTTC TCCCTATTGG TTCATGCATT GCTAAAGGCT

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FIGURE 16 (21)

TAAAGGATC ATTGATTTA ATTAATTTAAT GTGTACAGCA GGCTGAGCTT CCTTCTTTTT
TTAAGGAAG AACCTTCAGG GGCATTGCTT TAGTTTTTTA ATGTTAAATC TCATTTTTCT
TTGAAAATAA GAAGTTAAAG CTGTATTCAC ACAAGCTCTC AAAGTGCCAG ATTTTCATTG
TGTTTTTAAA CCATCTAGGA AATGTTTGAT TCTAATGAAA CATTACTGCT GAAAAATTGGG
CTGAAATTGC TGGGCTGAAA ATATTGTTAT AACTTCACAT GATCCAGTG TTGTATTATT
ATTTTTTCTT TTCCTTTTTT TGACCCGATA TAGATGAAGC GAAGAGACAA GGGAGCAATC
CCATGTGTAA TAAAAAAAGG CAGCCTGAAT TGTTGTTGCT GTTTTTTGAAA TTAAAGCTGG
TTTTCAATTA AATTCAGTAA ATGGTCCAGG ACTATAAATG TTGAACATTT TTACCCGTGT
GATTAAAAAT TTAGTTTTAA TGTTTTTTTT TTGGGTTTTT TTTTTTTTGA TGGTTTACAT
TTTCCCCATG GAAAGCAGCT ATGTCATGTC GGCATGATTC ATCATGGTAA CATCTCGGGT
TATTTGGTT TGTGTTATGT TCAGAAAGCG GAATGCCAAA AATAAGAGT GGTTGTGAT

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FIGURE 16 (22)

GTCTAGTGTG TCTTCCTTTA ACAAATCAAA GGCTTTTATT TAATCCACTT AATGGGACAC
TGCAGAAATT TAAAAAATGG AAGTCCCATC CACAGAAGGC AGTACTATG ATGTAAAAAG
TTTAGGTGGG GGATTAAATAG AGTGATCATA TAATTTATGA GCTAAACCGG AGGCACTTTT
TTTTTTGAGA TCGAGTCTCA CTGTTGCCCTA GGCTGGAGTG CAGTGACGTG ATCACAGCTC
ACTGCAACCT CCGCCTCCCG GGTTCAGCG ATTCTCATGC CTCAGCCTCC TGAGTAGCTG
GGACTATAGG CGCCACCAC CATGCCCAGC TAATTTTGT GTTTTGTGA GAGATGGGT
TTCACCATGT TGGCCAGGCT TGCTCAAAC TCCTGACCTC AGGTGATCCG CCCACCTCGA
CCTCCTAAAC TGCTGGGATT ACAGGCGTAA GCCACCATGC CTGGCCCAGA GACACTTTTG
AGAGTGAAGA GGAAGCTGAG AATAATTAC TGATCTACAA CTGGGACCAT CCAGGGCAAG
CCAGATGCCA TTACCACCTAG CTAGAAAGCT TGCCAAGGTC TCATTTACCT TGGTATATAG
CAAATTCTC TTTGAATTCT GGAAATTCTG GTAAAGTCATT GAGGTAGCTC TGTGCCAAGG

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FIGURE 16 (23)

AGCAATATGG TAGAATTCTA ATATTTTCAGG CAGTACAACA CTTTCCTGCA TTTGTAGCAG
GTAAAGGGAG GTCAGGGCAG AAGACAAAAC CACTGGGACT CGACAAAGG CATAAACGTC
TAATGCACCT GATGTAGCTG ATGGTAAATT GTTATCAGCT AAAGATCTTT CATAATAAAT
AAACTTATCA TTTGTAGGAG GGCACAGAAA TCGTGGAAG CTGGGATTCA GGTTGCCCTGT
GGCTTTAATT CTGGAATCAG AAATATTAGT CAAGGATATC AGTCTATGAA GTAAGTTTTC
AATGTTATAT GCCACAAGAT GCAGCTGTCC TATTTTCACT TCCAGTAATT CCTTCTGAAT
TAATACACCT TAAAAATAGC TGCAGCTTCT CAAATCTGTG AGAATCGTAT GTGCTGCTTG
CTACACTTTC CTTTTTCCCTG AAGGCCCTCTT TGAGGTCCTT CAAGAACTCA ATTCAATTCA
GCAACAATTA GGGGTCTAA GGTATACAGA CGCTGTGCAA GATGCTCCTG AGACACAAAG
AGGAGGTCAA GCCCCTGCCT TCAGGCACCT CTCATAATA TAGGAGGAGA AAGAGAAAGAA
ACACTAATAC ACATAGGTAG GTGCCATTAA AAGGTGCAT ACATTAAAGC CAGGTGGTAG

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FIGURE 16 (24)

GTGCAAGAAG ATTTGTAACG TGAGAATTTT CTGCATGTTT GAAATATCTT ATAATTTTTA
AAAAATTAAAA TGGGAGATAC ATATATATGT ATTTATGTAT GTATATATGT ATGTACATAT
ACACACATAT ATACATAAAT ATATACATAA ATATGTATAT ATGTGTATAT AGACATAAAT
ATGTATATAT GTGTATATAT ACATAAAATAT GTATATATGT GTATATAGAC ATAAATATGT
ATATATGTGT ATATAGACAT AAATATGTAT ATATGTGTAT ATAGACATAA ATATGTATAT
GTGTATATAG ACATAAAATAT GTATATATGT GTATATAGAC ATAAATATGT ATATATGTGT
ATATAGACAT AAATATGTAT ATATGTGTAT ATAGACATAA ATATGTATAT ATGTGTATAT
AGACATAAAT ATGTATATAT GTGTATATAG ACATAAAATAT GTATATATGT GTATATAGAC
ATAAATATGT ATATATGTGT ATATAGACAT AAATATGTAT ATATGTGTAT ATATGTGTAT ATAGACATAA
ATATGTATAT GTGTGTATAT AGACATAAAT ATGTATATAT GTGTGTATAT AGACATAAAT
ATGTATATAT GTGTGTATAT AATAATGTGT GTACATATAC ACACATATAT ACATACATAA

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FIGURE 16 (25)

ACATCTGCA TTATACCATT CACTTTGTAA CCCATCTTCC CTA AAAACTG TCTCATAAAG
AGTCTTCTTT TCCCTGTACC TATGCAATGG TAAGTAGCAA AACACACATT CTTTGGGTC
CCCATAACAT TCCCTGTAGT TTGCCCCTTAA CAGTCTTTGA TGTGAAATTT ACTGTTTCTG
TCTTAACCTT GCCTGCTCG CGTACATGGA GTTTTGGCTC CTGGCTCCTA GTCTGCATCT
TCACCCCATC CCTTGCCCAA AGAATCTGGT TATGTGACCA CTGCTCATCT TTTCTGCTGT
CACAACTCCA GTCCAAGCCA CAAACCTCTC TCTCCTGGAC TCCTGCGGG AGTTCCCTTC
TCTCCCTGCA TGAGTCTATT CTCCGCACAA CTGGCAGAGG TAAGTGAGAC TGCGGAAGAG
GCAAGTTTG AAGTCCAGAG GAAATGAAGA CTCTGCTTGT GCACATGCTG GGTGTGACGG
GTGCTGGATA TCCGATGGAT GGCCCTTAAG GTGAGCTCAA GGCTTAAGG AGAGATAGGG
GCTGATGATC TGAGATTCAT CAGTGTGTGG CTGATGTTA AACCCAGGG ACAGGATAAG
AAGGTTATC CAGGGAGAGC GTAGATAAAG AAGCTAAATG GCTTCTGGGT CCTTAGTCAT

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FIGURE 16 (26)

TCAAAATCGG ACCTCTGAGG CAGGAGGAAA GCCCAGAAAG AGTAGATTCC TGGGACTCAC
GGGATAAAGA CTTTCAAAAA GTGGGGGCTG GCCAGTGCTG CTGAAGGAAG TAGCAGGACC
GGAACAGAAG GGTAATCGTT GGACCTGGAG AACTTGAATT TGAATTTTAA GGTGGTAAC
CTTAAAAAAG AGCAATTTTA GATACCTTTT GAAATTATTT GCAAGATTTG TTTGGTATAT
GTGTTATTCC AGGCAAAGGG ACCAGAAAAG TAAAAAATAC TTACTGAACA GTTACTGCAT
GCCTGGCACT GTAACACCCCT GTTTAATTCT CACGGCAACC CTATAGAGTA GGTGTCATCA
TCCCCATCTT ACAGATGAGG ATATGAGGTG CAGCTAGATT AAGCAGTTTG CCTCAGGTTA
CACCAACTGG TTAACGTAGA GCTAGGATTT GAACCCGGAT GGGCTGATCC CAGAGCTCAT
GCTTTAAATC GCTAGACTGG TGCTCACAGA AGACTGGGAC CGAAAAAAT TAATAAAAAA
AATAAGGAGC CCCCTGGGCT AGCAAAATTAG GAGTTGTTC A GACAGATGTG AAAAGGAAAG
CAAGGCAGAG GAAAGTCAC TGTACAGAAG AGAGAGACC ATGACAGCAG AGACAGTGAG

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FIGURE 16 (27)

CTGATAAGT GGCTGGCGAT CTAGCCCCTG AAAATACCTC CAGAGAGGCA GGCTCACGCC
TGTAATCCA GCACTTTGGG AGCCCGAGGT GGCAGATCA CCTGAGGTCA GGAGTTTGAG
ACCAGCCTGG CCAATGGCGA AATCCCGTCT CTAATAAAA TACAAAAATT AGCCGAGCAT
GGTGACAGGC ACCTGTAATC CCAGCTGTTC AGTTGGCTGA GTCAGGAGAA TAGCCTGGAT
CCGGGAAGTG GAGGTTGTAG TAAGCCAAGA TTGCGCCACT GCATGCCAGC CTGGGCGACA
GAGCAAGACT TTTCTTAAAA CAAACAAACA AAAAAGAAAA AAGAAAAAGG AAGAAGAAAG
AGACAAAGAA AGAAAGAGAG AAGGAAAGAA AGGAAGGAAG GAAGAGAAGG AAGGAAGGAA
AGAAAGAAAA GGAAAGAAAG AAAAAGAAAG AAGAAAGAAA GGAAAGAAAA GAAAGAAAAA
GAAAGAAAGA AAATACCTCC AGAGAGCCAG GTCTCTTAGG CCTTCTGAGA AACTCACATC
CCTTTTGATG AACACAAATG CTTCACACTC TCAATGTTAT TGGTAATCCA AGTTATCAAT
ATACCTAAAT CACTTAGTAC TGAATCTGGC ATATAGTAAT CACCTAATGA AGAGATAAGA

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FIGURE 16 (28)

GTCATGGAGT ATTCTGAAGC AATTAGAATC AATAGACTCA ATATACACAT GGCAACAAAG
TTGGATCTTA AAAACCGACC TGAGTGAAAA AGGAAAGGGA AAGATACATA ACACGGTACC
ATTATGTAAA TTGATAAATAT ATGCTTACAC AATTGTAAAG AACACATACA AATAGATACA
TGTATATTAA ACATACTCGA ACGGTTACCC TATGGGGTGG TGGCTGGAGT GGGGGTAAAGT
CCGTAAGCTG TAATGGAACC TAAACAAATA CATGAAACGA GTAGGAATCA GAAGGAGTAA
CAATAAAAAT GTGCCATGAA CTGAGGAGTG TAAATTAATC AACTCACTGC ATCTGAGGTT
AAAAATAGAA AGATGATAAT TGTATATCTT ATTACTCCTA GGTCTTCCAC TTGCACTCAG
CTTTACAATG TTGGACTATC CTTCAGATGG CACCCTCCTT GCACTTGCTC AGGCAGGAGA
GCTTTTTCCT CCAGCTTTCT AGGTGATTTA ATATATCAGG GAATAAGTAT AAAAAAAGGC
ACGGTGCTCC CTGGGTAGCC TTTCTGGACT TCAGAGCTAA ATTGCAAAAGT CAGTTTTTACA
CATGTGATTT CATCTATGAA ATTAGGGCAA GGTATAAAC TGGCACAGAA AAAATGTGAT

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FIGURE 16 (29)

TTATTATGGT GTTACTATCC CTTACAAGCG GAGTGTGAGC TGCCTCTTTT TGTCCACTGA
TTTAAGGCAA GATGAAGTGA AAGTGGCTAT GATCACGTCT TCAAAAGCAC ACTCTGGCCC
CTCGGCTGCA GCGGCCCTGC ACATTCCCCA GCTGCGTGTC CCGTGGTGAC ACAGTGCATA
ATTGTGGCGC CTTCCCTGGTG CAAACTGTCT CACTTAGCTC CGTCTTGCTG GCACAGCAGA
AAGGAAGAAA TCGAAAATGT TTGGATTCA AAGGTAACAA GAAGCTGGAA AACAACTACT
GGCCGAGTCT GAGAGTTTCA GCGGAGACTG GTGCAGCCTT GTGTTTTCC ACTGACAGCT
GAAAATGAGC CCAGCTTCAG TGAAGCTTGT TTCCCTCCCT CCTCAAGGTT ACCCACAAAT
CTCAGTTCTC TCAGGAAAGC CAAAAATGA ATTTGAGGGT TTAGGATTGT GGTCTTTTA
TCTATTACAG GATTGATAAT ATGTTCCCTCC ACCAGATGTT CTGCTTGTA CAATACTCAC
TTCCCTGACAC TACTGCATAT GCAGGAGTGT CACTACCAAG GTAAACACAG AATTGGCTGC
CCAATTCCAA ATCCCTGAAC TGAGTGAGAG AAATCAGAA TATAATAGGG GATTCAACAG

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FIGURE 16 (30)

AGCTGGCTAC GGATGTGCCA GTGGTCAGAT ACTTTGCTCA TCATACGCAG GTGCTGCTGC
TCTAGCAACT GCTCACTGCT TCATTTCCTG CCTTGGTCTT TAAATACTGC TTTTCTCAGC
TCAATTGGCT TTCTTCCCCTC TGGCAGTCAC GTTCTCTTTGG GTCAAACAGC AAATGATTCT
TTAGAAATCAC CTGGTACTCA AAGGAGCTAC AAGACATTGG GCATCCACTT CCACTCTCTT
GGAAAAACAA TTTTATGGAA GCCAAGGTTG CCATAGTGCC TCTTGAGGTT GTTTGCTCAG
CCAAGGCCCA AGCTTTGTGC TTCAAACATG AAATTAGAGA GCTTCAGAAC AAGATCCACA
TTTTTCAATGG CCTCACCCCA CTGGATAAAA GAACAATTGC CATATCTCAA TGACCACCTT
TTCTCAGGTG GGATGGTAGA TGCTGGAATG GGTCACAGCA TTGCCCAACC AAACTTTGCA
AAAAAGGCTG GAAGCTCTGA CTGGGGACCC TAAATATGCA AAAGTTAATA GGCTCTTCAT
GCAGAATATG AACCCCGTGT ATGGATATAG CTAAAGGGTT GGCCTTTATG TTTCTATTCC
TTCACAAACC TGGTAGAATA GATATGCTTG TTTCCCCTTA AAAAAATGTCA ACAATTGCAT

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FIGURE 16 (31)

TTATGATGCT GTGTATAGTA ACTCACAGAT CATGCTCCAT GAAATGCTT CAGAACCCAA
TATAAGGAGA TTTTTTAGCC ATGTGTGACA AAAGAGAGGC CATTTCAGTG TTGAAATTGT
TCAGAGAAGT ATTTGATTAT GTTTTCTCAG ATCTTTTAT TTTTATTTT TTTGAAACAG
AGTCTCACTT TGTCACCCAG GCTGGAGTAC AGTGGCTGTG GTCTCGGCTC ACTGCAACCT
CTGCCCTCCA GGTCAAGCG ATTCTCCTGT CAGCTTCCCG AATAGCTGGG ATTACAGGCG
CATGCACCAC CATGCCTAAT TTTTGTATT TTAGTAGAGA CAGAGTTTCG CCATGTTGAC
CAGGCTTGCC TTGAACTCCT GACTTCAGGT GATCCACCCA CCTCAGCCTC CCAAGCACT
GGGATTACAG GCATGAGCCA CCGTGCCCAG CCTGTTTCT CAGATCCTGT ATTTGTGTTT
TGAAGCCTTC ATTTCTATCT TCTTATTTCAT TTTGGAAGTA GTACACCTAA GTAAGGTTTT
TAACAATCAA ATATCTTTGG AAAATTCCCT GGTCCCTTC TTATTCCCTAC AAAAATATGT
TCAGTATAGC TGATGTTATG TTTCTTTCAA ATTATTCATT TCTCTATCTC AGAATTTATC

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FIGURE 16 (32)

TCATGCCCTAA TTGTTATTGA ATAGTCTTCA CTTCTTGTCA TCCAGTTTCT GGTCTCTTAT
TTCACCTCTAA GTCTAATTGG CTATTAGAAT AAAGAGCTTG TAACAGATTC TTTCTCCAAT
ATGTCCTATC TTTTGA CTG ATGCCAGTGA CAAACTGTTA ACTGTTTGA TTCCTCATAA
CATTCACAG AACATGCTGA CTCCTCTCTT CCTGAAAGCA ATGCCCAAGC ACAGCATTGT
TAGATAGTAT GTACGCAACA GGGACATGGG TGCATAGCAA AAAC TAGAAG GAAGGAGGAC
CTTCCTTAGC AATGGGTGAT ATGGTCCCCTG GACTTAGACT CCAAAGGGTC GTGAGGTGAA
ACACACATCG TCCATACCCA GGAAGCACAC AGGTGGGATG GAAGAGCTGT GCCTAATGAA
ACTTCATCCA CGTGGAGGTG GAGGAGGCTG CAGCTGCAAG AACTCAGAGC TGCCTTACCC
AGACCAGGGA CCAGGGAGGG CTTTCTGGAG GAAACAGCCT CTGAAC TGCC AGCTGATAGA
GGAGCTCTAC CTCAACTCTT CTGGTTCCCC AGGGCTGCTT TTCCACGTCC ATTTATTGGC
ACTGAAGTTT GAATACCTTC AGGGGCCCGA AAGCCTGCCA GGTCTCTTC TCTGCAGAGC

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FIGURE 16 (33)

AATCACACCA ACCTGCAAAG GGCTAGGAAA GGGCTGTGTCAT CATCTCCTAC TCAGAAACTG
GTTCACTGGA AGGACTCAGG GGCCACTGAA TACATCCTGG CAGCTTTCAC AAGAAGGGCT
TCTGACTCAA GGATGTTTCC ATCTTTGCCA GGTGCGCCTTT TCTCCTTCTC TTAGAGTTTG
GAGGACGCAA ATGTGCTGAG AAGTCAACCT TTCCCTGCAAG GTGAGACACA AGGGCCTTTC
CCAGCAGAAA GAAGAGAGCA AATGGAAGGT CCTTCTTCCT CCAGTAGAGG ATGGACTCTG
TCTGGCAGCC ACCCAACAGG AAAAGCACAA TGCATGCCCTG CCTGCTTCCC TCCCTCCCCC
CGTTTCTCCC TCCCTCCCTC CTTCCTCCCT TCCAATTCTCT TCCCTTCCCC TCCCTTCCCT
TCCCCCTCCCT TCCCTTCCCC TCCCCCTCCCC TTCCCTTCTC CCTCTCCTTC CCTTCCCTCT
CCCTTCCCTC CTCTTCCCTT CCTTTCCCTT CCCCCTTCCCT TCCCTTCCCTC CCTCCCTTCC
TCCCCCTCTT CCTTCCCTTC TTTTCCCTTCTT CATTTCCCTCC CTTCCCTTCTT TCCCTTCCCTC
CTTCTTCTT ACTTTCCCTAC CTTTAGGGCT CTGTGTCTTT GGAGTCCATT CTGATTATGC

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FIGURE 16 (34)

TGTAATGTCT GCCCCTTCCT CTTCTCTGTC AAAAAATGAA AGACATGGAA GCCACTTGCC
TTTTACTGAA TTAAAAATTA GTAAAAGAGC TAAAAATTAA TGGTTAAAAA TGTACGCATA
AATTATGCAG TATACTAACC AATGAAAAGA TACACTTCTC TTAATTAAAA GCTGACAGGG
AGGGAAACAA GAAAAGAGAA ACACAAAACA ATAATCTAAA TGACCTATTA GTTGGAAAGAA
CAACATCAGA GAAAATAGAT ACTGTGTATA GTCATGTGTA TGCTATGGA ATAACATTG
TAGAGAAATC TGGACTGATC CTTTCTGAGT AAAGAGAGCT GTGGGTACAA TTAAGGGGAG
ATTGAAAGGA ATCCAAAAGC ATAGCAGATG CTGTGCCCTCA CTGGAATGGT TGCCGATCTC
CTCCAAACTA TGAAGTGTTT GAGGCTCAAC TTTAATATAA TTAAGATACA AAGACAGAAAT
GAGAGAAAGA GAGAAGGGAG CTCACTGGAA GAACACTCAA GATTCCCTTAC TACTCATTTCT
CTAAAATTAC AATTGTTCTA GATGGAAGAAG AAAAAAGCT TCTCTGTTAA AAAAGGAGCT
TGTGCTATAG GAGGTTTAAA ATATACTTCT GACCCATCTC CAACATTCTA AATCCTTCCC

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FIGURE 16 (35)

AGAAAAAGTAT GCCAATCCCA AGAAATATTC AATCAAAATG CTGGAAGAA AAATACAAAA
TATTAAAATG TATTAGGAAG CGACAGTAAT TAAATCAGAA CTGGAGCAGG AATAGACCAG
CAGATCAATG AGACAGACAT CAAGTCCCGG AATGTGACT TGCAAAATGCA TTAAGTAATA
TGATATGCAA TAAAGGTGGC ACAGTGAACC AATGGGAAA AAATTAATCT TATAATAATT
GATATTGCAA TAAATTGTCTA GTAATTGGGG GAAGAAATAA GCTTATTCCCT TATCTCATTT
CTTTTTTCT TTTTGAGACA GAGTCTCACT CTGGTAGCCC AGGCTGGAGT GCAGCGATGC
GATCTCTGCC CACTGCAACC TTGCTCTCCC GGGCTCAGGC GATTCTCCCA CCTCAGCCTC
CCGAGCAGCT GAACTACAGG CGTGTGCCAC CACTCCCGC AATTTTTTTT TCCATTTTTA
GTAGAAATGG GGTTCACCA TGTGCTCTGG GCTGGTCTTG AACTCCTGGG CTCAGGCAAT
CCACCCGCCCT TGGCCTCCCA AAGTGCTAGC ATTACAGCA TGAGCCACCG CGCCTGGCAG
CTCATTTTTT AGACTAAATA AATTGGAGAT GGCTAAAAGA TTTTATATGA GGCCAACTAT

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FIGURE 16 (36)

GT'TTTTAAAA AG'TTTT'TTTT TTTAAGGATA TCTGCTGGAA CCAATCATGC CACCAACCAA
AGATGCAAGA CTATAAAACA TACCCAGT'TT TTCAAAGCAT TTAAAAATTA TTCTAAAAAT
ATTTT'TTCTC CAGAAATTTT GCATTGATTC CCTGAAGAAG CATTAATATG GGACCTGACT
TATAAAATGA TGAAC'TCAAT CTCCCCACTC AAGGTAGGAG TCTCTCAGAT TTAAAAAATA
AGCATCC'TAG TCCTCTTGTC CCTGTAAAAG TTAACCCCTTA CACCTGAAAC ACCAGGAGAC
TGGCGG'TGT TTGCATAGGG GTTACAATTA AAGTTGAGCT ACCTCTGACA TCTATTAAACA
CCAAAA'TTAG TAAACTATGC ATGTATGGAG ACTTTTATGA TTGAAC'TTGT TTATTGAGTC
AAGAGATATA GTTTACAATG AAAATTTGGG GCATATCAAA ATGACCTTGG CTTAGCTTAG
CATTTGCTGA TGTTAACTAT TTTTCTTCATT GGGCTGATTT TAGTTGCTTA GGAAAAATAC
AAACACACAC ACTTTAAAAT TATATTAAAA TCCCGTCCTA AACCTCAGAG TCCAGAACCG
CATCCTAACA CTGGTCATGC ATAATATGTT TAAATTTT'TG TGCTTTAAAA ACTACAAATA

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FIGURE 16 (37)

AGGAAATGTAT TAATAGTTCC ACAATCAATG GTCAGTTAGC CGAGGGAAGA TTAGCATAGT
TAAAGACTTA AAATGGCTTA ACAACATATA TCAAAAGGAC AAAATAAGGG GAACAGAGTC
TAGAAATGAG GAAACTGGGA CACAGGCAA AAAAATAAT GAGAACTGGG ACATGAATAA
CGCAAGGGAT AAGACTAATA CACAAACAC CCCAAATAAA TAGCCAGCAT TTGCTGAGCT
CTTACTGTGA GCCTGTCTTA AGCACTTTAC ATATATTAAC TCATTTTCATC CTCAAGGAAC
CATCTGAGGC AGGCACTGTT ATCATCTCCA TTTTACAGAT AAGGAATAGA CCCAGAGAGG
CTGAGCAACT GGGCCATTTC CACAGCTACT ATGGTGGAGA TGAGATTAA ATCTAATCAT
TGGCTCCAGA GCCCATGCAC CCAATGGCTG CACTAAGTGA ATGCATGCGC TATCAACGTT
GCCAAAAGTG GGCCACAGCT CGGATCTGCG TTTTCCAGTA GCCAAAGCAG AGAGTGTGAT
CAGACCTCAC TTAAATAAGC AAGTCTCAAG CCAGAGAGAG GTGGTATCAG GCAGCAAACA
GGCTGCTAGT CGAAATCCCA CTTCTTCTCT GAGTGGTCCA TACAGTTTAA CTCTACTTGC

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FIGURE 16 (38)

TTACAGAATG AAAATAGCTG GAGTTCAGGT GCGCTTTCAA TGCCCTGTG TCAGGATGG
GCTTTTCAAG TTTATTTTTT GTTGTTGTTT TTAATAGACT GTACTTTTTA GAAAAATTTT
AGATTTACAG AAAGATTGAG AGGATAGTAC AGAGAGTTCC CGTATACCTC ACACCCAGTT
TCTGCAATTA TTAACCTCTT ACATTCAATG GGTACATTTG TTACAATTAA TGAGCCAGGG
CCGGCCGGGC ACAGTGGTTC AGGCCCTTAA TCCCAGCACT TTGGGAGGCA GAGCAAGCG
AATCACTGA GGTGAGGAGT TCGAGACTAG CCTGACCAAC ATGGTAAACC CTTTCTGTAC
TAAAAATACA AAAAATTAGC CAGGCATGGT GCTGGTTGCC TGTATTCCCA GATACTCAGG
AGGCTGAGGC ACAAGAAATTG CTTGAACCAG GGAGGCGGAG GTTGCAGTAA GCCGAGATCG
TGCCACTGCA CTCCAGCCTG GGCAACAGAG CGAGACTCCA TCTCAAAAAA AAAAAAAA
AAAAGAAGGA AGGAAGGAAG GAAAAATTAAT GAGCCAATAT TGAGACATTA TTATTACTAA
AGTCCATGCT TTATGCAGAT TTTCTTAGTT TTTACCTGCT GTCATTTTTC AGTTCCAGGA

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FIGURE 16 (39)

ATGCATTTCAG GATGCCATAC CACATTTAGT TCTCATATCT GCTTAGGCTC CTCTTGGCTA
GACTGAGTTT TAATCTACTT TCTGCAGAGC CTGAGAACTT TAGCATAATT TCCTTGAAAT
TACAGCTCAA TATTTCAAG CACTTATACA AACAGCCTAA TGTACGTTG GCCCATAACA
GTGTTTCAAG GTAATAAACT TCTTTGTTTT CTGTGCCGAT TGAAAGAACT GCTGCTTAGC
CTCCTGCCAG ATGATGAACT GGTACACAC GAGCATTTTT CCAGGTAAAG CATATTTCGT
GCGACTTCTT AAGCTGCAGC CTTATATGCA ATAATTGTCC ATTTACAAGA CTTATGTTTCG
AATTTCAGGC ACTCTGTTTT CACTAACCAT ATCTTCAACT TTGATAAGTA CTGCTTTAAT
CACTCAGAAA ATTTAACTTG ACTAATTTTT TTTCACCATC AGTTTTTTTT CTGTTGACTC
TTTCTCCTTT TTCTGTTTGC CCAGAAACAT GCTCAGGATT CTCACAGGCT TTAAAAAATG
AAAAAATGTT TCCTGCAATC TAGTTACTCC TTGATTCTCT TGTTCGTGTT ATCGCTGGAA
TTCTTGAAAG CTGGTGTAT TAGTCTTTTT TCATGCTGCT GATAAAGATA TACCTGAGAC

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FIGURE 16 (40)

TGGATAATTT ATAAAGAAA AGAGGTTAA TGGACTCACA GTTCCACGTG GCTGAGGAAG
CCTCACATC ATGGTGAAG GCAAAGGCA TGCTTACAT GGCAGCAGAC AAGAGAGAAT
GAGAACCAAG GGATTTCCTT TTATAAAACC ATCAGATCTT GTGAGACTTA TTCACTACCA
CAAGAACAAT ATGGGGTAAA CCGCCCCCAT GATTCAATTA TCTCCCACCG GGGCCCTCCC
ACAACACGTG GGAATTATGG GAGCTACAAT TCAAGATGAC ATTTGGGTGG GGACATGGCC
AAACCATATC ACCTGGCCTA TAGCATTATT TCCATTTCTT CCCCATCCTT TTATTCCTCA
AACCGGTACA ACCAGACCTC TTTTTTTTTT TTTCTACCTG AAACCTGCTCT TTTGAGGGTA
GCTGATAAGT CCAAATACT GTCACCTTTT CTCAATTCG TTCCTTCTTA TGCCTTTGGA
GCAATTGACT GTGTTGGTTG CCCCCTCCTT TAAAGTGCTCT CTCACCTTGGT TTTTATGACT
AATGATCATG ATTTTCTTTT TCCTCTCTAA ACATTCCGCT ATCTTTT TAG CTTCCTTCC
CCCTCCCATC CCTAAATGT CCTTGTTTCC CAGAACTGCT CTCACCTCTT TGACTTCTCT

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FIGURE 16 (41)

ATGCCCTGTC ATTCACTCAT GGGTCTTTTAT TACATTATTG CATCTGTGTC AATAACTCTG
GTCTTTCTCT TAAGTTCCAG TCTCCCATTT TCAAATGTCC CCAGACATTT CCAATTGAGT
ATCTCTCCAA TGTATTTAAC CTGCTAAATA TCTAACACAT AATCTTTCCC ATCAAAATCGT
TTCCCTCTTAA GCTTTTCTTA TTTCCCTATTA GTACTCCCTGC ACTTCTCCCA GGAGCCCAGA
CTTAAACCT TGAATTTCTC ACCATAACCT CTCTTTTGTC TCCCATATC AATTAGTAGC
AAGTGTTATC AATGATTAAT TGACAAATATC TTTTCTTAT TCCCTCCCTG CTATGATCAT
TCATCTAGCA AGAAGAGTTG GCCCTTTGTA TCTGTGGTTT CTGCATCCCT GGATCAACC
AACTGTAGAT GGAAAATATT TGAAGAAAAA AGCGTCTATA CTGAGTATGA AAAAATTTA
TTTCTTGTC TTAATCCCTA AACAAATACAG TATAACAACT ACAGCATTTA CACTGTAGCG
TATAGATCTT ATAATCTAGA AATGATTTC AATACACCAT TATATATAAG GGACTTGAGC
ATCTGTGAAG TTTGGTATTT GTGGGGCATA CTGGGACCAA TTCCCCCATG GATACAGAGG

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FIGURE 16 (42)

GACAACTATA TTTACTCAGT GCTTACTAAA TACCAGTTGG CCAATGTGTT TTTCCTTTTC
TGTTTTCCCTG TCTTTAGTTT GCCCCTTGCC AATTAATTCA ATAGTGCTGC CAATGCCAGG
TGTACCTTCA GAATATTCTA TTCTAATTTT GTCATCTCCA AGCTTAAAAA TATTAAATGG
GCCAGGCGCA GTGGCTCACA CTTGTAATCC CAGCATTTTG GGAGGCCAAG GGGGGTGTA
TCACTTGAGG TCAGGAGTTC CAGACCAGCC TGGCCAACAT GCGAAACCC TGTCCTACA
AAAAAGTATA AAAGTTAACC AGGTGCTGGA GCATTTGCCT GTGGTCCCAG CTACTCACGA
GGCTGAGGCA AGAGAAATCGC TTTAATCTGG GAGGTGGAGT TTGCAGTGAG CCAAGATCTC
TCCACTGCAC TCCAGCCTGG GTGACACAGC AAGACTCTAT CTCAAAAACA CAATAACAAC
AACAACGAAA AACATTTAAT GGCTGCACCT TGCCCTGTGAA AAATGCATTT CTGTGCCAGA
TGTTGGTGGCT CAAACCTGTA ATCCCAACAC TTTGGGAAGC TAAGGCCAGG AGTTCGAGAC
GAGCTGGGAT ATATAGGAAG ACACAATCTC TACAAAAAAA AATCCACAAA ATTAGTCAGG

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FIGURE 16 (43)

CTTAGTGTTT ATGCCTGTAG TCCAGGTAC TCAGGAGGCT GAGCAGGAT TCCTCAAGCC
CAGGAGTTCA AGGCTTCCGT GAGCTATGAT GGCACAACTG CACTCCATCT TGGGTGACAG
AGCAAGGTCC TATCTCTGGA GAAAAAATAA AAAGAAGCA TTTCTTAGGA GAGTTCTTCT
CTGTAGAGTC CTAAGGGTTC CATGGAACTC CTTAAAAAGCA TCAGAGTATG TGAGTGCAAT
GGGAGGAAGC ATTTAGCCAG AGCAGTTGTG CTCCCATTGC ATATTAAATT TTAAAAAACA
AAGCTATAAA AAAAAGTTGA AAATACTAC GTTAGCATCA GCCTGACATT TAATGGCCTC
GTAAATCAA CCTTAATTGA CTTTTTAGCC AGTTATGCTA CTAGCCAACT ACAGACAACA
CACTTTTAA CCAAATTAGA CTAATAGTTG TCATCAGTGG AAATCAAGTT TGCCATTCTT
CCATGCCCTT GCTCACACCA TTACCTTTTC TGGAAATGTCC TGTACTCATC TTCCCTGTGTT
GAACTCTATA CCCAACTTTA AAAACCTAGC TCAAAGTTCA AACTTCCAT TCCATTTCAA
AAAGAGCTTT CCTCTTCCCTT AAAGTTTAAG AACTCATTTT CATGAATCTT TTTGGCATTT

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FIGURE 16 (44)

ATTGCACACA TGCTTGCTTT GTGTTATTG TGTTTCATGCC TCATATGCCC CCAAGGTGTT
TTAGACTCCT TAACGGCAAA AATGATGCTC TAAACACCTT TCTATCTTC ATAGTGTCTT
AGTCGTGTTG TGTGCTATA AAGGAATACC TGAGGCTGGG GAATTATTT AAAAAAGAGG
TTTATTGCGC TCACAGTTCT GCAGCTATAT AAGAAGCATA GTGTCAGCAT CTGCTTCAGG
TGAGGGCTTC AGGAAGTTTC CACCCATGGT AGAAGGCAAA GGGAGCAGG CATCACATAT
CAAGAGAGGA GGAATAAAG GAAGGAAGAA AGGAGGGTGC CATCTCTTT CAACAATCAG
TTCTTGTTGG AACTAATGGG ACAAGAGGCT GGGCACGGTG GCTCATGCCT GTAATCCCAG
CCCTTTGGGA GACCAAGGTG GGTGGATCAC CAGAAATCAG AAGCCTGAGA CCAGCCTGGC
CAATGTGTG AACTCCGTC TCTACTAAAG ATACATAAAT TAGATCTAGC TGGGCCCTGGT
GGCGTGTAAC TGTAGTCCCA GATACTCAGG AGGCTGAGGT AGGATAATCA CTTGAACCCG
GAAGACAGAG GTTGCAGTGA GCTTGTGCCA CTGCACTCCA GCCGGGGCAA CAGAGTGAGA

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FIGURE 16 (45)

CGGTCTCAA AAATTTTAAA AACTTTTAAA ATAATAGAGC AAGAAAGCAC CAAAGTTATTC
AGGAGGGATC CACCCCCAAT GACTCAAATA CCTCCCACCA GGCCTCACTT CCAACACTGG
GGATCAATTT CCGTATGAGA TTTGGAGGAG ACAAAATATCC AACTATATC ACATAGTAAT
GAACATAGTA CCTTATCTAT AGAAAGCAAT GGCTAGACAA CTGTTGAATG GCTAACCCAAA
TCTGCTTTCC TATGGTCTCG CTCTAGAGGG GGTCAGTATG AGTTTCTGTC AAAAGGAGAA
AAAAAAATGT ATAGTCAGTT TTGTGTGTGT GTGTGTTTAT GTAAAAGAGA TCAAGAGAAA
AGAACAAGAG AAATCATGAA AAGGAGGGG AATATAAGAA TAATACATAG AAAAAAGCAA
ATTATCTGT TTATCAGTAA TACCCAAGG GTAGAAATG GTAAGTAATA ATCCTTCTTC
ACTTTGTCTG TAGTTCACTT TTTTGCACCT TTATTTTGAT GAATTCACAT CGAAGACATT
AACTCATTA GGCTTCCAAT ATTTTGGAG ATAAGAAGG CTGCTATGCT CTTTATAGAT
GGAAAACTTG GGTCAATTAAT AACTCAAACA AGGACATAAC AAAGAAATGG AGCATAAACT

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FIGURE 16 (46)

GCCAGGTCCT GACTGTAGAT TTGGATTCCC AGTTGGTGTC TTGTCACCCCT TTGTTACTCT
TCCATAAGTT ATGATCTTTT CTTGTGCATA GGAAATTTCAT AGTGATTTC CATCACCCCTT
GGGATTATCA TAGCTCCCTT AAGTCCCCCT CTATGCACTC AATAACATCA ACAGTAAGTG
TTCTTCGAGC ACTTACTGAG TGTATATCAT TGTGTTCTCA CGCAGCACCC ACAGATCTCA
CCAAGAACCT AGCTGAAGCC TGAGAAATGA ATAGGTAAGT ACTGCCATGC CAATCTGGAG
TACTCAAGCG ATGCAAATGA TTCCTTTAAT TGTACTTTTG CAGGCTTGTC AGTTTGCCTC
ATGGAGAAGT GGCTACTGCA TCCATGTTAT ATCTATGTAA TGTGGA CTG CGAAGCATCA
CTTGACTTTT TCCAAGCAGA AATTACAGCT GATGACAAGC TGCTGCTGAG AAAATGGATA
TTTTTCTGAA TTCAGTTCTA CGTGGAAACA GCTGACTAGT TTCCATTGCT GTAAGATGGC
TCTTTTGCTC TTGGTTGATT TTGAGTAAATG GCTTACTTC TGAGAAAGG AGATTTCATT
TGAAGTCCAC TCAGGGATTT GGTTCACAA ACTGGAGTAC AGGTTTCAGA AAATATCTCT

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FIGURE 16 (47)

TTAATCCTCC AATAATAAAT TTTCTCATCT ATAATTCCCTG GAACACTTCA TCCTTTGCAG
CCGAGCATAT AGATAGATTT GTTGCTCACT GTGTCTGAT TGCCACTTTG ACCTGCTTTT
TCAACTTAGG TTACAAATAG AACAGAATCT CTCGTATTTT TCTCATTAAT TGTTTGAATT
CCCACCTTTC CTCATTAGCA AGAAGTCCAG TATCTTCCCTG AGAACTTCCT TTTCTCAATC
TAGGAACTTA CTTGGTCCAT AAGGTAACAG TCTTATTTCT GACTATCAAG GAGAGAAATA
ACAGGAGCCA TTATCATCTT CATGGTGTCA CTTTGTGAAA CTGGTCCCTCT GTAGATCTTC
AGATTCTTGC GTTAGTCCAT TCAGCTGCTA TAACAAAATT GCATAGACAG CATGGCTTAT
AAATAACAGA AATGTATTTC TGACAGTTCT GAAGGCTAGA AAGTCAAAGA TTAAGACACT
GGCTGATTG GTGTCTGGCG AAGGCCCATT TGCTCATAGA TGGACGATGA CCTTCACTC
TGCTGCACA TGGCAGAAGG GCAAGAGAGC TCTCTGGGTC TTTTATTATA GGGCACTAAT
CTCATTTTG AGGACCCCTGC CCCCATGACT TAATCACCTC CCAAAGGCAC TGCTCCCCAA

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FIGURE 16 (48)

TACCATCACC TTGAGGGTTA GGATTTC AAC ATATGATTTT GGGGGGACAG AAACACGCAG
TCCATCTCGC TTGTCCACTC CATGGTGGTA TTCTTGCTGG ATCAGTTTCC TCCTTGGGGT
GCATTGTGT TCCATGTCTA ACTTGCAAGT TATAGCAGGC CCGATAGCAA AGTATTCCAA
TGT'TGGTATG CAGAGGCATT GAATAATCAG AATGAACCCA CGCCATAAAC AACTGGTAGA
GCTGCAGAGA GTACCAGCTG ATTATGAGCC CTGGGTAACA GTGGTTTTTA GTTCCCTATGT
CCGTCAGCCC TTTTCTCCTC TAGTAGCCCC ACTGTGTGA AGTGGCTGAA TCGACAGAAG
CTTCCAGCTT GGGCCACATG CTCATGGAAC CAATTCTCCT TATGAGCCGT ACAAGAGCTG
GGTTGCCATT CTGGATACCC TCTTCTTCA AGAGATTTTA TTTCAAGGAT ATTTTTCCTT
TTATCAACTA CAGGATTAT TTAGAATCTT AGGCAGTGG TGCCCCAACCT TTTTGGCCCC
AGGGACAGGT TTTGTGGGAG ACAATTTTC CATGGACCAG TGTGAGGGG CTGGGAGGCA
TGGTTTTGGG ATGAGTCAAG TACATTACGT TTGTTGTATA CTTTATTCT ATTATTATTA

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FIGURE 16 (49)

TATTGTAATA TATAATGAAA TAATTACACA ACTCACCATATA ATGTAGGAAT CAGTGGGGAG
CCCTAAGTTT GTTTTCCTGC AACTAGACAG TCCCATCTGG GGGCAATGGG AGATAGTGAC
AGATCATCAA GCATTAGATT CTCATAAGGA GTGCTCAGCC TAGATCCCCG GCATGTGCAG
TTCACAAATAG GATTGCTCA CCTATGAGAA TCTAATGCCA CTGCTGATCT GACAGGAGGT
GGAGCTCGGG CAGTAATGCG AGGGTTGGG AGCAGCTGTC AATATAGATG AAGCTTTGCT
CGCTCGCCTG CCACTCACCT CCTGCTGTGT GGTCCACTTC CTAACAGGTC ACAGACTGGT
ACTGGTCCAT GGCAGGGAG TTGGGACCCT GTCTTAGGGA GTAGGGGTGG AGTTCCCTTC
ACTTCTAGAA GGCCCTGGAT TAGTATCCCA GAGCTGTCTAT TACAGAGTAT CACAAACCAG
GTGGCTAAAA ACAGACATGA ATTCTCTCTT ATTTTGTATG GCTTGGGAAGT CCAAAGTCAA
GGTGCTGCCA GGGCCATGCT CCTCTGAAA TGTGTAGGGG AGAATCCCTC CTTCCCTCTTT
CTAGCTTCTG GTGGTTTGCT GGCAATCACT GGCAATCGCTT GGCTTGCAGC ACTTCAACAT

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FIGURE 16 (50)

CTGCCCTTAC TGTCTCATAG TGTTCCTCCC TCATGCTCTC AGGTCTCTCT GTCTCTCTCTC
TTTGTATAAG GAAACTAGTC ATATTGGATT AAGGGCCAAC CCTACTCTAG TATGACCTCA
TCTTAAGGTC ACATGCAATG ACTATTCCAG ATAAGGTCAC ATTCTGAAGA ACTGGGAGTT
AGGACTTCAT ATCTTTTGAA GGAACACAGT TCAACCAATA ACAGCCCCTG TACTGTTTAA
CAAATAGGTA TTCCCTCTCCT TCCCAAAGTT CTTCATAGCA GAGACAACTT GTACCAAAAG
GCAAAATACC TTATTATGTA ACCTTAACCT AGGATCATAG ATCCCTACTT GTCTGGTGCT
TTTATAAGCC ACAGAACCCAC CCGGAAATC ATTATTAGA CAAGGAAAGG CCAAGTGCAG
TGGTTCATGC CTGTAATCCC AGCACTTTGG GAAATTGAGG CGAGTGGATC ACCTGAAAGTC
AAGAGTTTGA GACCAAACTG ACCAGCATGA CAGAACCCCA TCTTTACTAA AAATACAAA
ATTAGTTGGG CATGGTGGCA TGTGCCCTGTA ATCCCAGCTA CTCAAAAGAC TGAGGCAGGA
AAATCACTTG AACCGAGGAT GCCAAGATAG CAGTGAGCCA ATATCGTGCC ACTGCACCTCC

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FIGURE 16 (51)

AGTCTGGATG ATAGAGCAAG ATCCTGTCTC AAAAAATTAA TAAATAAATA AAAAGACAAG
GAAAGCCTTT TCCAAGGAGA CCTTCTGCT TTGCTAGTTC AGAGAACTTC TCTTTGGAGA
AAACAAACAC CCAGTCCATT AGCAGCAACG TCAGGGATTG AATTCTTAGG GCAGCAGGCT
GGGCACAGTG GCTCATGCCT GTAATCCCAG TACTTTGGGA GGCTGAGATG GGTGGATCAC
TTGACATCAG GTGTTGCGA CCAGCCTGGC CAACATGGTG AAAACTCATC TCTACAAAAA
ATATGAAAAA AAAAAAAAG CTGGGTGTGT TGGCTTATGC CTGTAGTCTC AGCTACCTGG
GAGGCTGAAG CAGGAGAATC ACTTGAACCC GGGAGTTGGA GGTTCACAGTG AGCTGAGATT
GCCCTACTGT ACTCCAACCT GGGTGACAGA GAGAGACTCC ATCTCAAAAA AATAAAGAAT
TCTTCGGGCA GCAGTCTTTC CTCCACCTCA TAGACCATGG AGGTGAGCCA GCTCTGACAA
ACCATGAGAA CAATGGCAGA GACATACCTG TAACGTAACT GACTGGGGCA AAGACAAAGG
TGAGGAAAAT GACAAGTTTG AGGAACTATG AGACCAGGCA GTGGGGAACA CCACTAGCAG

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FIGURE 16 (52)

AAATGATGGA AGTTCTCAAG AATAACAACA GAGAAATAGA CCATGGCCAG AGCTAGAAC
CCTCCAGGGA AAGGAGATGG GCTCCAGAGG CAGAAGAGGA CGTTGAAGGG AATGGGGAGT
GGGTGAAATA TATAGACGAT GGGGACCACC CAAGAGCAGT CGCTATTGCA AACTGAGGA
GAAGGAGAGT CTGGAGGGGG TGGTGGGAAG CTGGGTCTCC TAAGGAGGTT TTGACAAAAG
CAGTCATGGA GCGGGCTTAG AAATCACAGT TGGGGACAGG GTAAAGTTCC TCGGGATATA
GAGGATGAGA TTAGAAGAGG TTCCAACTAG GGTAGTGTGG AGAAAAGCAC TATTGACCCA
AAAAGGAAGG AGAATGTGGG TGGAAGTGGC AGAGAAAGAG GGGTTTGAGC AGAGAGTGGT
GATTTTCTA ATGCAGAGTT GTGGGAGGTG GAGTGCAGGG AGCCAGGCTG GGTGGCTGTG
CTGATGTGAT TAAGCACTTA CTGACTGCCA GGCAATGGC TAAGTACCTG AGATGCTTTG
TCTGTTATCC CTCCCCGAAAC CCTCTGAGC AGGTGCAGTT ATTATTCTCA CTTACACAGT
AAGGAAATTG AGGCACAGAG AATTGAGTAA CTTACCCCAAG GTGACATAGC TCATATATGG

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FIGURE 16 (53)

TAAAGCAGGC TTGTGAACCTCA GTCTAGCTCC CGAACCTAAG CTTGTAACTA CTATGCTTTT
CCCAAAAAA GGGGGCTGGC ACAAAGAG CTGAGGGGG CTGGGCATGG TGGCTCATGC
CTGTAATCCC AGCACTTCGG GAGACTGAGG CAGGTGGTTC ACCAGAGGTC AGGAGTTCGA
GACCAGCCTG GTCAACATGG TGAAGCCCTG TCTCTACTAA AAATACAAAA ATTAGCTGGG
TGTGTGGTG TGCACCTGTA GTCCCAGCTA CTTTGGGAGG CTGAGGCAGG AGAATCGCTT
GAACCCAGA GCGGATGTT GTAGTGAGCC AAGATCATGC CACTGGACTC CAGCCTGGGT
GACAGAGTGA GACTCCATCC AAAAAAAGA AGAGCTGAGG TGATGGCCAC CATCAGCATC
AGCCTGGAAG TTATAGCAGG ATGCTAAGTT TCTCTAAAGC TGTCTTTCTT AGGACTTGAA
AAAGATAACT TGGGTTTGTA TCCCATCTCT GCCATTAGTA GTTTACTGGC TTTGGATAAA
TTTACTAGCC TTAGTGAACC AACTTTGGAT TTTTATAGAG ATACTGTAAT GAAAGGAATA
AGGTATCAGT CTTAGCAGAG CATCCAGAGT GTTCCCTATTA AAACCTAAAT CATATCCCTGT

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FIGURE 16 (54)

CATGCTCTG CCCAAACCA TTCAATGGCT TCCCAACTCA AAGTAAAAA CTCATCTTTC
CAGTGGCCTG CAAGAGCCTA TGCTATCCGG TGTCTGACCT CATCTGTTGT TCCTTTCTCC
CTCCCTTTCT TGGCTCCAGA CGCACTCTGG TCTCCTTGCT GTTCCCTTGAA TACACCAGGC
ACACTCTTTT CACCTGAAAC ACTTTACCCC AGATATCTTA GCTTACTCTC TGCCTCCCTC
AATTCATTGA TGAAATGTCT CAGTGAAGTC TTCTCTCTCT CCTCTGTAAA AGTATACTCT
CTGTTCCTTCT TCTTTACTGT TCTAGCTACT ATGCTGTGT AACAAATCAC TCCCCAAATT
TAATGAGTGA AAACATCAGC CATCATCTTA TTTCTCACGG TTTCTGAGGG TCAGGAATTC
TGGAAGGGCT CAGCTGGGAG GTTCTGGCTC TATAATCTCT TATGCAGTGA GAGTCAGATG
CTGGCTAAAA CTGAAACAAA GCAGGGTTCT AGTAGCTGAG GGCTGGCTGG GTCTCTCAGA
TATAGTTCAG ATCTCCTCCA GGGGGTCTCT CCACGTGGGC TAGTCTGAAC TTCTCTCACAG
CATGGTGGCC TCAGGGCAGT GGA CTCTGCA TAGTGGCTGA AGGCTTCGCA GCTGAGTATT

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FIGURE 16 (55)

CCAGCAAGCA AAGTGGGAGC TGTATTGCCT CATATGACCC AACCTTGGA TCCACACAGC
ATCACTCCG TGTATTCTAC GGGTTGAAA GTCACAAAA CCAACCAGTT TCAAGGAGAA
GGAACAGAGA TCACATTCTT CAATTGGAGA AGGGTCAAAG TCACATTGTA ATCAGAGCCT
ATGGGATACG AAGTATTGCG GTCAGGTATG AAAAATTGA TTTGCTGCAT CTGCTTTACT
TTCTCCACAG CGTTCATGAT CTGCTTCTCA CATGATATTG ACTTACGTCA TTTCTGCATT
TCCGTGCTTC CACACTAAA TGTACGCCTG TTTTGTTCAC TGCTGTATCC CCAGAGCCTA
GCACGGAGCC CAGCATGTAG TGGTATCCAA TAAATACTTG TTGCATGAAT GAATTCTGTC
TTTTAATCCT AGCTATAGGT TTCTAAGTTA AATATTACTA TAATCATCTT ACAGACGAGG
GAAATGAGC TCAAGAAGAT TTGGTAACTT ATGCGGGATC ACTCAGCCAC ATAATGGAAG
AGACAGCATT GAAGTACACA TGCTTGCTCT GTCTGCTCTT CCAAGCTGCT CATCACACAG
CTGCACCTCT GAGGACTTCC CTCCCCAGTC CACCTCCACC CTTACCCAGA GACACACATG

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FIGURE 16 (56)

GCCACAATCC ACTAGCAGAC CAAAATTCAA TTTTTCCTCCCA GTTGGTTGCA CTCAAGCTGA
GAGCAAAGCA ATTGCACCTT AAATCCCCCTT ACAGCAGATA TTTCAGAGCA TGTTCGGAAG
AACCCTATCAC ACTTGGCTTT TAGATCTTAT TTCTGGTTTG TTACAAAAAC ACAATTAAAT
GAAAGGTTAG GTAGCTTTTG AATGGCCAGC TCAAAGTTT GGCTTATTTT TGCCCTTGCTG
TCTTTATAGG CATTTTACCA ATATTTATCA CTATTTCCCT TAGGGAACCC TTAGATCTGT
GATATTTGAA ATAATAAAGC CTCCTCATTG GCCCTTTAAA AGGTTTGTTG TAAAACCACA
CCATTAACAT TCACAGTTCC TTATTTATGA GGCTGATTG CACTTATTC CATATTTCTC
ACTGTTTCTC CGATGAGGAT TTCACATAAT AGTGTTTGAA GGCTAAAGAC TTCAAAGCAG
ATTCTTTACT ATTTTATCT TGAATAATAT TCAATATTG TGTAATTAAA GTGAAGTCTT
CCTAGAGAAA ATGACAACTC AAATAATCTT AAATGTACCT CCAAGAAAAA AGCTGTCAAA
GTGACATTTA GTAGTAGAGT CACATCTCT AAGGCCTTTG CTCTCCTTC TGAGTTCTTA

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FIGURE 16 (57)

TCATCTTTGA AGTTATGTC ATGGCTGACT TCAAATCACT TTAAAAATTA TTATGGCCTT
CTTTAAATGT GAGTCTGAA GGTGAGGGC TTTATCTTTC TTTTGCTCCA GATTTTCT
ACCGGTCAT TACCAAGCAT CTAAACAA AACCTAAAA CAAAAATCTT CCTTGACCTG
GTTTTTCCCA CTAGCTAACA TCCTATTTTT ATCTTCCCT TTGCACATAA GGTTTTTAA
CGGATCTTTA TACCCCTCTGT CTCCATTTTC TCATCTGCTA ACTTATATGG CAAAGATTAC
CACTGCCTTT CAACATAATT GGCCAACTCA CAGAAAGTTT TCAAGTTCTC TTTTTAATTG
ACCACCTCCT GCCTACCTCC CCACCTTTGA CATCTTGCTT CTCACTTGGC ACCTTACCCA
GTGTTCAAGA TTCCCTCCTT TAGGATGTCT TCAGAGCAGC TACACAGTTG GTACTATAAT
TTATACATCC TTGTACACAG GGCTTGCTGG GATATTGATG GAGAGAAGGA GGAAACTGGA
AGTAGTTCAG GCCAGAGCTA GGGAAATTGA CCCATCTCCA GGTCTCAGGT CTGCAAGGGG
AGCTCACAGC TTAACACATG GAGTCTAGAA ACTTGTGCTG GACCTTGACC AACACCAGCC

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FIGURE 16 (58)

CATGGAGTCC AATACAGTGC TCAATAGGGA TTTCCAGGAA ATTGCTATAT TTATTCAAAG
AGAACTTACC AAGGTCAGC TACGTGTGG GCATTGTGTT AGGCACAGG ACCACAAAGA
TAAGACATTG TAGCTTTCCT TAAGTTGCTC ACTGAGTAAA TAGAGAGACA GAAAGGTAAA
CAGGTAAGTG CAAAATACA TACAATTCTG CAATAGTGTT CATAGTGGCT ATGGAGAGAA
CGCTCACTAA CTTTGTTTAA ACAGTTGTTC TTTCAAGGAT TTGACATGGA TTTGATTGGA
AAAGCATGAT ACCATTTTTT GCAATTAAAC ACAGGAATAC ATAAATAAAA TGCATCAGTA
TTTTTTTACAA ATAGCTACTA AGAGCTACTA GAAAACCTGG GAATTCTTAA AACCTTACCA
TGCTACTTGC TCTAAAATAT TTTATTTTAT GTTATTTTGT ACATTTCTTT ACCTACACAA
ACACCACTGT TTTCTTTCATT TCTTAGTCTA TTTAAACCTC ACACCTTTC AGCATCTCTT
AATTATTTAC TACCATCTGT TAGTTCTCCT GTCTGAATG AAACAAAAAT GGCAGAATGT
AAAACGAGGG CGAACAGATT TTTGACAGGA AGTATTCAGA GGTAGAAGGA AATAGTCAAG

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FIGURE 16 (59)

ACACATATGA TAAACGAAA CAATAATAAC TTTATACATA ACAACTTATA GACACATTTA
AAAAGTTTAA GATCTCAAGA GCTATGTCTG AATAGATAGA AGTAAAAACT CTATTAAAGTA
ATTAGGAAAA TAACAAGAAC AGTGAATTTC TTAATGAATG GCATGTAATC AAAACTGTAC
TTATCGTCTA ATTCATAATC TTGAATGTTT TTATTTTATT TATTTATTTT TTTATTTTTT
GAGACAGAGT CTGTGCTCTGT CACCCAGGCT AGAGTACAGT GGCGTGATCT CAGCTCACTG
CAACCTCCAC CTCCCAGGTT CAAGCGATTG TGCTGCCCTCA GCCTCCTGAG TAGCTGGGAT
TACAGAGGCC TGCCACTGCA CCCGGCTAAT TTCTGTATTT TTAGTAGAGA TGGGGTTTCA
CCATCTTGGC CAGGCTGGTC TTGAACTCCT GACCTCATGA TCCACCAGCC TTGGCCTCCC
AAAGTGCTGG GATTACAGGC GTGAGCCACC ACGCCTGGTC GAATGTTTTT ATTATTTGAA
GAGACAACAT GGGCCTTAAA TCTGTCTTCT ATTTGACAGA CTTTGATGGA GTCAAAATCCC
AATGCTGCCA CTTACTGAAC GGCCTTAAAT GACTTAGTCT CTCACGCTG TCTTTCTGCA

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FIGURE 16 (60)

TATGTAAGGT GGAATAATGA TGGCTTCAAG GAGGAATAAA CCTATGAAA GTGTTGAGGA
TAGTGTCTGA TATGAAATAA GGATTCAACA AGTAGTAGCT GCTATTGAAG ATTAAAGAGT
TATTTATTAC AACTATTTAA TAAAATTTTA AAACTAATA CACTTAAATT ATTAAAGAGC
TTTGAAATGG GCCAGGCGCA GTAGCTCCTG CCTGTAATCC CAACACTTTG GGAGGCCAAG
GTGGGCGGAT CACCTGAGGT CAGGAGTTTA AGACCAGCCT GGCCAACATG GTGAAAACCCCT
GTCTCTACTA AAAACGCAA AATTAGCCAG GTGTGGTGGC ATGCACCTGT AGTCCCAACT
ACTCAGGAGG TTGAGGGAGG AGAATTGCTT GAACCTAGGA GCTGGAGGTT GCAGTGACCC
GAGATGTCAC TGCACCTCCAG CCTGGCAACA GAGCAAGACT CCATAAAGAC AACAAAAGCT
TTGAAATGT GTAAATGAGT TGTACCTATC TTCATTTAAG AAATTCATCT TTGTTCACTCT
ATTTTACTT GACATGAGAG CTTCCAGCAA TTTTTAATTA AGCCCTCACA GATTTTATGT
CACTGGCTAT GTGATAAACA AATTATTGC TAAAATAATA TTCTTGCTTC TTTTTTAAGG

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FIGURE 16 (61)

AATTGTCTCC CTAGAAACGG TTTGTACCAA ACAATACACT GACTTTACAC AAAATCAGAT
CTGATTGGCA ACAGTTGCAG ATGTTTTCAG AGGATTTTCA TTTGAGAAAGG GGCCCATTTG
GGTTATTAG ATTCTAAGAA CTGAAACTGC TTTGTTCTGT TTTTCTGGCT TCTGGGAGAG
GAGGAGACAT GAATTCAGTT AGCACCTTGG TATTTTCTTT ATCCTTCATT TCAATACAGA
AGATGCTTCA TATGCACAGT GGTGTCAGGT CACATCAAAA GAAAGAGAAA CAGTTTCTTG
GTTTTTAATT TTCAACCCGA AAGGAAAGGC ACCCATTTTG TTCCGCTCTA ATTAGCCAGT
GCATGACTTA GAGAGCAGGC AGATGCTTTG AAGGCGTGGT AACACAGGTC TTCATTAAATC
TCCACGCAGG ACTTGCACTT CTAATATGCC TAGGCTGAAG AAAATGGCTC AGGAAGATGA
ACAATCTCAC AGAGCCCTAA CTAAGTGAAG CCAGGTGTTA TAAAGCACAA GTCAAGAGGG
TGAGAAACTA ACGTTCTTGA AATCTCCAC TTCTTTCTAC GTCAGAAGAG CCAAGCTGAT
TATTTTAGTT GGAATTAGA AATTTTAA AATTATTTA AAGTCATGAA CAAGCCTAAT

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FIGURE 16 (62)

TATAAAGATA GTTGCTGTGA AGTGCTGAA ATAACCTGAT TTACCAACC CCGTCTTCTG
GAGGAAGCCA GAATGGAATC CTGTAGAATG TTCACTCTAC CAACGAACTC TTGTTTTTCT
AATGAGGAAA CAGAGGCCCA CAGTAGTAA CTATCTTAAC CAAGACAAA TGA TAGTGC
TCTGGTCCTT TTATTAAGCA CTAAAATTTT GATCCAATAA TAAATCTGTC CAGTAGAAGG
AGTTTCCCTA ATGTA CTGGT TCTA ACTTGT TCCCTTCAAG GGGCAGTGT CCGTACACA
TAGCTAAATG GGA CTCTCT TCAACTACCA TTACCCAGAG GGCAGAACCT AAAATGCTGT
GAATGACATT CTGCTGTTCA CATCTCAGCA GCAGTGTTCG ATTTGAGCTT CTGCAGGGCC
ACCCAGGACC TATATCTGCT CAGATGTTTA ACTCATCTAA TTCAGTGAAC ACTTCATTCT
AGTTAACTGA ACATCTACTT TGTACAAGGC ACTACAGCGG TTCAGAGATG AATAAAATCA
TGAGATTCCA CTGCTCCTA TAAACCATCA CTTTGGGAAA TTTTAGAAAT GTGGGTAAGC
TCCAGGGCTT CCTGCAGCGT AGAAGTCACA AACTCAAATG CCTGCAGAGG CCCAGCTGAC

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FIGURE 16 (63)

AACATAAGTA AATGATTCTG GCTGGGCGGA AAACAATTAC GGGTGGGTGG GTTTCAGCT
GGGGAGTGCA CGCCTGTGTT AAAGGACA
GCTGCTACTC ATTTCCAGCC AACTGTGTTT CCATGTAGAA CTGCGGCCCA GTGTAGCCAG
TACCGAAGAT TTCTCAGAAA AAGCCGGAGA TCTCAATGTT AGTGAAAAAT CTCTCAAATT
TCCAAGAGGA TTATATGGGG CAAAGGTTCT CAGATCAGTT TGCAGTCTCT TACTTAGCCC
ATGTGCAGAG CAGTCGTAGA GGGTAGCATG CAGTGTCCCTA CATAATAATT CTTTTTTATT
TTATTTTATG CCTTCCTCCT TCCGTGTCCT CTTTAACCTT TCTTCTTCCC TCAGGCTGGC
TTCTTCCCTC AGCCTCGTCC GACCCAGCC TGGGTCAAT GAACATTGG TAAAGGAACA
CGGAATGTCA AGCGATTAG AGACAACCTT GAGACACATT CCTCTGCGG TAAGCACTTC
ACTGTAGATT TTTAATTTA AACAAAGACAA TGTTTACGAC TTGCTTCTTT CAGGGAAGAG
CGATATCAAT TTTAGTGAAC ACTTCAAGGC TGAGATACGC TAGGAGAGTC GTGTGGTGT

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FIGURE 16 (64)

GCACAGCAAA GAATTCCACT TTGAAGCGAG TGGGAAAAAA AGCATCAAAT GCCACATGTA
ACTCACC GCC TGAAGGTTA CATTGGTATG AAACCTGGGT TTAAAAAAGG ACCGAATAGA
CTAGCCATTA AAAGACCTGC GTACAACCTC TCTCTCTCTC TTTGAGAGAT AATGTATCTG
GACAATAAC ATGAACAGAG TGGAGTCTAT CCTGTTTAA ACATTGCCCTA CTGTACAGGC
ACCAGGAGCT GAAGGGTCAG AATATTAGCA GTGGGAGCTT GATTAGAAGT TGATGAGAGA
TGGGTAGTAG GAGGAAAGAG TGAGATAGAG GAAGAGGACA TGGGGGTAC CCGTAAGTGG
AGAGTAGAAA AGTAGAATCA GCTGGCCATC AAAGGGCGTG GGA CTGAGGA ACAGTATGGC
ATGTATTAAA TATACTAAGC GCTGACATTG GAGGAGAACT AGGAAGGTAA ATGAAATCAA
TAGGGGATGA TGGAGAATAG TTAGGTGTGC AGGGATTAGG GTTATGATAG AAATACATGT
GAATACATGC AGTATTGTCC TGGAAAATGG TTAACAGTTG GTTCTCTCTGG GGGGTGAGGG
GAAGCCCTGA TTTGTAATAT TTGCCCTATT CTGTGGTGCA AATACTCCA CCATGACCAG

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FIGURE 16 (65)

TTTCAAGCTA TGAATGTGAA TCACAAAAGC AGGTTGGGAG GAGATGCGCA CATTGTGTCC
CCGGCAAGGT GGAAGGTAAG GAAGGTGAAA TCAACAAGGT CAAAGAAAAC TCAAGATTTC
GAGGTGCCCTC AGGTCTGAGG GGCAATGAAG TCTAGGAATG GCTGTGCTGA GGTAGCTGAA
ATAGAAAGTGA CTGCAGAGGT CATGAAGCTG AAGAGGTGAA AACAGAAATT AGAAAGGCAA
ACCCCCACCG CCCAACCCCC ACCCCTGCAG CCAGTTTCTG AGGGTGACAA TAGAGGAAAG
GGTGGAGATG GAGTTCAGGT CCAGAAAGCCA TAGAAGCGAG TGTGACATTG TGCTCAAGGT
CAGCACATGT CAGTGTGGGG TGTACACATGC TGTGTGAAC CATCATTTAT CACCAATTAT
GGAAGACCTC CTATGGGCAT CTGCCCATAT GCATTATAAA GATGTGTAAG AAGACATTTC
CCTCCACTTG GTGAGGAGAA TTAGGGCTGT ACACAGATAC TGTAGAGTGC CATGTGCCCTG
GTACAGATAA GGTGTGTTAG AGGTTAAAAG ATGAGGCTCT TAAATATTAAT GATAGATCCC
ACTTACCTGA GTCTGACTTA CAATGTGCCT AGCATTAAAGT GTTTTACCTG CATCCCCTTT

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FIGURE 16 (66)

GACCTTCAGA ACAACCCATT TTACAGATAG GGAATTTGGG TCAGAAAGTT TCAGTAACTT
ATCCAAGGTC ACACAATTGG CAAGTGCCAG AGCTGAGCCA GGAAGTGAGG TCCTTCTAAC
ACCAAACAGC TTGTCTCCCC AATCACTGTG CTATTTTCCC TCCCCCAGAA GATAATACTC
TGATGGAAAT GAAGGATAGT GTAATAGGAG ATTCGGTGTT CCTTTTTTTA AAAAAAATTC
AGCTTGCGATA TTCCCTAAAGA GTCATATCAT GTTTAAAAAA AATTTCCTT GTGCTTGCAT
GTGACATGTA TTTTATAGGAT CTGCTGTAG CAAGTGATTT TTTGTGTGAT TGAGTGGGAG
AGTGGGAAAA GTTTTGCAGA GCTGTTGAAG CCAGAAATGCA GGGGGGCTGC GCAGCAGAGA
CTGTAAAAATC TCTGCCATCT CAGGCTCTGG AACAAAGCACA AAGAGATGTG TTCTCGATTT
ATTATTCTAT GTACATCCCC AGATGAATGA CTAGTTAAAG GTATTGTTAA AGCATTTTAA
ATGACCCACT TCCAGCAGCG AACAAAATCA CTTGCTGTGC CAAGCCAACT GGCATTTCTG
AGATGATAAA ACCACAAAGT GAGGAAAACG TTAAAACTGC TAAAGCAAAA ATGATACACA

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FIGURE 16 (67)

ATAATGGAGA AGGAGAAAAA TTGAGCTTTA TTGTCTGCCT AGGCAGATGG CTGACCCACTA
GGTGGGCTCG GCGTCACGTC CAGGGTAATT GGTGCTGGG GTGTTTCTGG CGAGGAAGAT
TCACGCTTCA GCTCGGTCCA CAAGATCCTG GCTCATTTCT TCCTAGATTC CATTTTCTGC
CTCCCTCTCCA TGA CTGGGTC TGATGGTTGA TCCAAACGGG CAATTGAAAT CAGAAGGTTA
CCTTTACCTT AAAATGCTTT TCTGGAAATA AAAGGACATG AAAAGTAACT AAGGACCGGA
TTTCCTAGCC GTCTTTCTCT CCTGCATGCG CAATTTATCC CCAGATATAA AATTGCCTGC
TTTGATAATT ATACCCCTCTA AATGAGGGGC AAGTGGCTAA TTATGCCCCAC ATGTGGCCGA
TTGCACTCCC CATAGCCAA TTATGTGCTC AATTATTGT GCACATGAAT AATTGCACCTC
ATGGAATA GCGGCCCTCC TTTCAAATCC TCGTGCTTG AGTGGCTGAT GGAGTAATTG
TCACACTGGA AATGCACCTG GTGGGAGGG AAAGAGTATC AGATACCAGG AAACGCATAA
GTGACCAGAG CTCGCAGATG TTCACTGCCA CAAATGGCCT TAGGAGCCAG AGAGAGCGGG

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FIGURE 16 (68)

AAGGACCACA GGATGGAACG GGCCAGCCTG TGAGTTAGGA AGCCTGCTTC TGAAGTTGCC
TGGGCAGCTC ATGTGCCGGTG ACCTTGGGCA AGTCATTAAAC TTTCCTTCAG GTCTAACTGG
TTCTGCATAC ACAATGAGGA TGGTAATAAC GCCCAATTCC CATCACTATC GTGGGATGGA
TCAGACTATT TAAAAGGATT TACAATCTGC TTGGGTAAAA GCTTTACATA AATATGAGGC
ATTATCATGT CGCTTGGTAC ATCTCCAATT ATGAAGGAAG GGTAA TGACC CTCCACAGCA
ATGCAGGACT CCTGGTTTGG AGGAGGGAA AGTTGAGAA GGACAGGAAG CTTGTTGCCC
CAGCACTGAT GTTCTACTG AGGTACCAGA AAATGTCATG TGGTCATACA GAATTCATTT
ATTCAATCAA CAAACATCTG TCAATTGTTA CACTGTCCTG AGAATTGGA AAAATGATGA
AAGACTCAGT CCTGCCCTTAG GAGGTCACTG GCACATTGGC CCGGGCCCTT GTTTTGGGCC
TTTTACTCTG ACCTGTGCTG ATTTGCCAAAT AGTGGGAAAT TTTATCTCAA GTCTAGGAAA
TCTGGCATGC ATTTTCACGG TTTGATTGCC AGGTACATTC GATGGCAATG AGTCTTATAA

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FIGURE 16 (69)

TGTTTGGTTA CCTTCATTTA CCTAAAAACT GTGGTTGTTG CTGTGGTTGT TGTTTITGTT
GTTTTTGAGA CGGAGTCTTG CTCTGTCAATC CAGGCTGGAG TGCAGTGGCA TGATCTCCGG
TCACTGCAAA CTCCACCTCC CAGGTTCAAG CGATTCTCAT GCCTCAGCCC CCTCAGTAGC
TGGATTACAG GCGCGCACCA CCATGCCCGG CTAATTTTGT TATTTTGTAGT GGAGACAGAG
TTTCACCATG TTTGGCCAGG CTGGTCTCGA ACTCCTGATC TCTGGTGATC CGCCTGCCCTC
GGCCTCCCAA AGTGCTGTGA TTACAGGCGT GAGCCACTGT GCCCAGCCAG AACTGTGGTT
TTAATGACAA TGCTAAAAG TGGTATATGT CACAGTGTCG GGTGGGGCTA AGAGGCACAT
TGCTGCAGTG ATCCATCATT CATTTCCAC CATCTCGCC TGGATTAGCG CAGCAGCTCC
CAGAGAGGCA CCTCACTTTG ACCTTCTTCC TCAAAGACAT TCTCTGTGAC CTGCCCTGGCC
CTTATTACCT CTCTAGCTTT GCCACTTCCC TATGTCTCCA TCTCCCCCTCT CACACGTAGT
AAGAAAGAGA CTCTACCTCC ATGGAAGTTA AGGAGAGGTT TCACAGAGGC AGGATTGCTT

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FIGURE 16 (70)

ATTAGTCTTC AAAGATGAGG TATTTGCTAA ATGAATGAGA CAAAGGGATT GGGGCCACAT
TACAGGAAAT TGAGGTATGT AATAGCCTGG TGCAGGTAA GAGTGTGGAC TCTGAAACCA
GACTCAGCCT GGAATTGAAT CCTGGCTGTG TGATGTTGGG CCAGTGACTT AACCTCTCTG
TGCTTTTATT CACTCTTCTA TAAAATGGGG ATTATAATAA ACCTACCCTA TAAGGTTATT
ATAAGAGTCA GTAAATATAA AAATAGAAGT TTTTGGATGA TGACTAGCAC AGAGTAAACA
CTTGTTTGCC ATTATTTTTA TTAATTGACT AAAAAATATAC CAAAAGACC ATCCAAGAAA
AGCCTTTAAG CTGCTAGTGC AGAAAGATTC CCCTTGTTGT TGTGTGCTGG GGGGTCAGTG
GTGCCCTGTGG CCCACTGGAG AGGAGACAGC TATGGCTGGA GTGATTCTCA AACTTCAGAA
TGCTTAAAT CATCACATGG ACAACTTATT AAGGAAAGCA AATGCCCTGGG CTCCATCCTC
AGAGAGTCTC ATTCACCTGGG TCAGGATAGA GCCCAGGAAT CTTTACCCTA AAGAACCATC
CCACCTCCCA CCTCATATGA TCCTTATGCA GGTGATCTGG GGGCCCACAC TTTGAGAAAT

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FIGURE 16 (71)

AGACTCAGGT CAAAGTGGGC TCTAACTGCA TCTCATTTCT TACCTGGCAT ATCTAATAGT
AGAGAAGAAG ACAATGCTAA GATTTTGTGTT GGAGATCTTT TGCTGGGATT GCTGCTTCAT
TCATTCACTC ATTTATTTAT TTATTTATTT ATTTGAAAC AGAGTCTCAC TTTGTCACCC
AGGCTGGAGG GCAGTGGCAC AATCTGAGCT CACTGCAGCC TCAGGCTCCT GGGTTCAATC
GATTCCTTG CCTCAGCCTC CCGAGTAGCT GGGATTACAG TCATGCACCA CCACGCCCAA
CTAATCTTG TATTTTTAGT AGTGACAGCG TTTCACCATG TTAGCTAGAC TGGTCTCGAA
CTCCTGACAT CAGGTAATCT GCCTGCCCTCG GCCTCTCAAA ATTAGTAGCT GCAATTACAC
GTGTGAGCTG CCGTGCCCTGG CCTGCTGTTT CTTTTAGTTG GGCTCTTCT GTAAATAGAGT
GTGAGAATTC TGACTTGCTG CAACAGTCTG CTTTGAAGCA GGGCTGTGTT TACACTGGTC
AGATGTGGAA TTGTGGGGCA CACTTAGCAG CTTCTTCTC TAATTTTTCT GTATTTTCAG
GAGAACAATT TTAAAAAATT TAATAAAAAT GCCTTAAAA TTAACATTAT TATAAGATGA

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FIGURE 16 (72)

ATCCCATTTT TCTAATCTTG TAAATTAAAA ACAATCATAA GCATATGAGC ACCTGCACTT
AGGGAATCAA GGTGGCAAAG CTAAACACTT CCAGCTCTAG GTGATTCGG GCAATACAAA
TGGAGCTGGA CTTTGGCCAC AGTGCAAAA TATTGATCTG TTGTTAGATG CTCTGAAAGT
TCCACAAAGA ATTGTTCTG CCTGCTGTGC TTCAGTGCTT AAGGGAAGTG GTTCCTCAAA
ATGTTAGTTT TTAAGCCCAG CTTTCTTAAA TAGGAAGATT CTAATAGTAG CAAAAATATA
AACTGCTTCT AGGTTTAAAA AGGACCAGCA CACAATGGTT ATCACACACC TTTCTCCTCA
GGTGATGAGT GGATGAGTGG CCTGGTGTAT TTCATAACAT CTCCCAGGGT CCAAATGCTA
AAGCAATTGC TGA AAAAGATA CCATGTGTAC CGGAACCTTG CAGAGGTATT TTGTTGGCAT
AAAAAGAAAT ATTGATCATC TATAGTAAAA ATGGTTCTAC TTTAATACTA CTGAGAAAAAG
ATTTTCTTTT CCCAGATCTA CATCCTGAAT CTTCATGAAG ACAAGATCCC CTAAACTTCC
ACTAACACCA TAATGTGTGC TGTCTTTGT AATGTAGTCC ACAGATCTCA TAAACTGTCA

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FIGURE 16 (73)

GAAATAGCAG AGATTGTAAG GTCAATCCACT TCCCCTGTAA GGCCTGCCGC CCTCACTTAC
ATCCCTAATA ACGTCCTCTA ACCTCTGCTG GAGGGCAGAT TTAGCTGCCA GCTGGGAAGA
GCTCTGCCCT AGTCAACATT TTTATCTGTG GCTTTCAGAT GAGAACACTG GATGCTTATC
TGAAAAAAGC TCCTCAGGCT GGAGGGAGGG ATTGGCTCTA ACAAGATGCA ATGTGATAAG
AATAAAAGCG AAGCCAAACT CTAGGCCCAA AGGCTCTAGC AACACACTTT TGAGAACCTT
GGAGACGAGT TTTGGCTGAT GCGAGCTTCT CCGCCTGCTA AAGTAGCCCA TTCCAATTGG
ACGGCTCTAG AGGCTGGCAT GTTCTTCTCC ACGTTGTGTT AATGTA CTCC AGTTTCTTCC
TGCCATGAAC TGGCATGCCC TGGCTCCTCC TACCTTCCCC ACTTTAAGTC TTCCCTCCCT
CCTTCTGACC TTCCCATTTCC AGCCACACTG GCCTTTGTG TGGTCCCTAAC AAACCATGCC
TTTCCCTGCCCT CCAAGCCCTA CACCTGCTAT CCATCCCCTCT GTCTGAGAGA CACTCCCACC
CCTTCACAAA GCCTGTTTCT CATCCTTCCA GTTCAGATGT CTTCTCAGCT TGCCTCAACT

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FIGURE 16 (74)

GACCTCTTTC AGCTATTCTC ACTCTTTGTA CTCTGTTTCAT TTCCCTTCCTG GCAGTCACCA
TAATTTATCT TTATTTGAAT CAATTTCTTA GTTGATTAT TTAGTTATTT GCACACTCTG
TCTCTCTGTG CCTTCTTTAT TCACTGCAGG CTTTCTTATG TAAGTAATTT ATTACTTAA
ATTTTAAAA ATAATTTCAA CTTTGGCCG GGCACAGTGG CTCACGCCCTG TAATCCCAGC
ACTTTGGGAG GCCGAGGTGG GTAGATCAGC TGAGGTCAGG AGTTCGAGAC CAGCCTGGCC
AACATGGTGA AATCCCATCT CTATTTAAAA TACAAAAACT AGCCGGGCGT GGTGGTATGC
ACCTGTAATC CCAGCTACTC GGGAGGTTGA GGGAGGAGAA TCACTTGAAC CGGGGAGGTG
GAGGTTGCAG TGAGCTGAGA TCACGCCATT GCACTCCAGC CTGGGGCAGC AGAGTGAGAC
TTCATCTCAA AAAACAAAA AACAAAAAC CCTGCTTTT CAGAGGGGCT GAACTAATTT
ACATTCTCAC CAATAGTGTA TAAGCATTC CCTTCTCTA CAGCCTCACT AGCATTTACT
TTTTTAAAA ACTTTTAAAT AATAGCCATT CTGACTGGTA TGAGATGGTA TCTCCTTGTG

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FIGURE 16 (75)

GTTTTCACTT GCAATTCTCT GATGATTAGT GATATTGAGC ATTGTTTTAT GTTGTGTTGGC
TGTTCTGATG TCTTCTTTTG AGAAGTGCT TTTTCATATAT TCTGCCCATT TTTTGAATGG
AGTTGTTTTG TGCCTGTTGA ATTAAGTTCC TTATAGATTC TAGATAATAG ACTTTTGTTC
GATGCATAGT TTGTGAATAT TTTCTCCCAT CCTATAGTTC TGTTTACTCT GTTGATAGTT
CCTGTTTTGT TATGTTTTGT TTTTTTGCTG TACAGAAAGCT GTTTAATCTA ATTGGTCCCA
CTTGTC AATT TTTGTTTTTG TTGCAATGGC TTTTGAATTT TAAATAATAA TTCTTTCCCTA
AGGCTGATGC CCAGAACAGC ATTTTCTAGG TTTTCTTCTA GGATTCCTAT AGTTCAAAAGT
CTTATATTTA AGCTTTTAAT CCACCTCAAG TTAATTTTTA TATATAGTGA AATGCAGGGG
TCCCTGTTTCA TTCTTTTGCA TGTGGCCAGC CAGCAATCCC AGAACCATTT ATTGAATAAG
GAATCTTTTC CTCATTGCTT ATTTTGTCAA CTTTGTCAA GATCGGATGA CTGTAGGAGT
GTGGCTTTT CTGGGTATC TACTCTGTTA CATTGGTCTA TGTGCTGTT TTTGTATCAG

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FIGURE 16 (76)

TATCATGCTG TTTTGTGTAC TATGCTCTCA TAACATAGTT TAAAGTTGGA TAATGTTATG
CCTCTGCTTT GCTGTTTTTG CTTAAGATTG CTTTGGCTAT TGAGGCTCTT TTTTCACCTTC
ATATGAATTT TAGAATAGTT TTTTCTAATT CTTTGAAAAA TGACCTTGGC AGTTTGATAG
GAATAGCATT GAATCTATAG ATTGCTTTGG GCAGTATGCT ATTTAATGA TATTGATTCT
TCCATCCAT GAGCATGGAA TATTTTCCA TTTGTTTGTG TCATCTACTA TTTCCTTTAG
CAATGTTTTT TAGTTTTCCCT TGTAGAGATC CTCCTAGGTA TTTTCATTTTT TATGTGACTA
TTTTTAAATGG GATTGCAATC TTCATGTGGC TCTCAGCTTG AATGTTATTG GTGTATAGAA
ATGCTACAGA GTTTTGTACA CTGATTCTGT ATCCTGAAAC CTTACTGAAG TCATTTATCA
GTTCTAGGAG CCTTTGGCAA AGTCTGTAGT GTTTTCTAGG TATAGAATCA TATCATTAGC
AAAGAAAGAT AGTTGACTT CTTCCTTTCC TATTGGAATG CCTTTTATTT CTTTCCCCTTG
TCTGATTGCT CTCCAGTAC TACGTTGAAT AGGAGTGCTG AGAGTGAGCA TCCTTGTCTT

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FIGURE 16 (77)

GTTCCACCTC TCAAGGAAA TGGTTCCAGC TTTTGCCCAT TCAATATGAT GTTGGCCATG
GGTTGTGAC AGATGGCTCT TATTATTG AGGTGATTC CTTTGATGCC TAGTTGTCA
AAGGCCTTA TCATGAAGG ATGTTGATT TTATTGAAAG CTTTTTCGG GTCTTATTG
GTGAATTGCA TTTATTGAAT TGTGCATGTT GAGCCAAACT TCCATCCCAG GGATTAAACC
TACTTAATCA TGGTGTAAAC TTTTGTGATGT GCTGCTGGAT TTGGTTTGCT AATTTTTTTT
TTTTTTTTAA AATGGATTCT CCTCTGTCC CCCAGGCTGG ATTGCAGTGG TGTGATCTTG
GCTCACTGCA AGCTCCACCT CCCGATTCA TGCCATTCTC CTGCCCTCAGC CTCCCCGATTA
GCTGGGACTA CAGGCACCCG CTACCATACC CAGCTAATT TTGTATTTT TAGTAAAAAC
AGGATTTCAC CATGTTAGCC AGGATGGTCT TGATCTCCTG ACCTCGTGAT CTGCCGTGCC
CAGCCTCCCA AAGTGGCTAG TATTTTTTTA ATTACTATT TTCTCACCC TTGCTGCCAT
CTTATGATT TCTAGTATTT TGTGAAGAT TTTTGCATCT ATTTTCATCA GGGATATTGG

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FIGURE 16 (78)

CCGTGAATT TCTTTTTTCA TTTCATCTTT ACCACATTTT TGTATCAGGT TCATACTGGC
TTCATAGAAT GAGTTCAGGA ATGGTCCCTC CTCCTCGAAT TTTCTCTGTA GAATTAGTAC
CAGCTCTTTG TGTGTCGTGG AGAAGTTGTA TGCCAATAAT TTAAATGCAG TTAATATTTA
CTGGACAATT TCCTCCAGAT AATTGTATAT GATTTTGGT CCACCCTGAG TTGATACATG
TATTTTAATT GTATCATGGT ATGAAAAGAG CAAGAGTATT TGGTCACCTA GTCTTGCCCTA
TAGATGTGCC TAATGATTCA AAGTAGATAT TTTGGGAGCC TAACAGGTGC CGTGACTAGG
CAGTTTGTGTT TTTTTTTTTT TTTGAGACAG AGTCTCGTTA TGCTGCCCCAG GCTGGAGTGC
AGTGGCATGA TCTCGGCTCA CTGCAACATC CGCCTCCTGG GTTCAAGCAA TTATACTGCC
TCAGCCTCCC CAGTAGCTGG GACTACAGGC TCACGCCACC ACGCCTGGCT AATTTTGTGA
TTTTTTAGTAG AGATGGGGTT TCACCATATT GGCCAGGCTG GTGTTGAACT CCTGGCCCTCA
TGATCCACCC GCCTCGGCCT CCCAATGTGC TGGGCTTACA GCGTGAGCC ACCGCACCCG

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FIGURE 16 (79)

GAGATTAGGC AATTTTATAT TCCCAAATAT CCAACTCTTC TGACCCGCTT TCTCAGCCTG
GGTGTATCAG GCACAAGGCC TGTTCAGATT ATGTGGTCTC TGAAGATATG GCTCTCCAGG
GTTGACAATG TGGATAAGGA TTCACCTGGT TTAGGATTTA CACATTGCGC TTGAAATGTCT
GTTGCATCAA GTAGACAGTC CATCCCAACT TGGCCATTG GTCAGAGCTG TAAGGAGACA
AGGAGGTGGG CAGCCGCTGC TGTGAACTGC TTGGACAAAG ACTGCCAAAT AGCTATCAGA
CAGTGTTAAC AACAGCTGAT TTAGGTTGA AGGGGCAGT CTCTTGGGCC ACTTACTATG
CTGCATCATC CTCCTTGGAA AATGCTCTTC AGGTAAGTGC CTAACAGACT GAGAAAATAA
AATGCTCACA GAGAAAAAAG ACCCGGAAAG TCTGACTTCT CAGAGCTCAG TGTTTAGGTG
CAGAACTGGA TTGTGAAAGG ATTTTAAAT TTTTATATATT CATTGCAGGG AACATTCAATT
TATTCCATCC TTCTCCACTC CCACCTGTCT GTCGTTGTCT TTGTCTCTGT CTCCCCACCT
CTCTCTCTAG ACACACACAC ACACACACAC ACACACACAC ACACACACAC ACACACACAC

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FIGURE 16 (80)

ACACACACAC ACACACACAC ACACACACCC CTATTCATTG CCAACAGTAA TAGAGTTGCT
TCTTTACTTC TTGGAGAGAA AAGCCTCAAT CTGAGGAAGC TGTGCTGACT AGCCTTGCTC
TTAATCATGG AGACAAATGCT TTATGCCCTTT ATCTTTGCAC AGCTGAAAGC CATGGCAGAA
GCAGTCCCTCT AAACGAAATA AAATAGAAAG GTTCCTGCTA AGCCCTGGCA AATGCAGCCT
TCTATCCCTC CCCC AACACT CACAGCTTCT GAGCAAGATG TAGCTGCCCTT CCAGGAGGCT
GGGTGATGGG CAATAATGAG CAGAGCCACG TGAAGGAAAG ATGGGTGAAG AAATGTGTGT
GGAGGTCATG CTGGCTGCAC TGACCATGAA ACAAGGATC TACCCCTCTA GTAAGTCCCC
TACTCCTTTG GTAAGTGTTC TGAATTTATA ACTTGCCAGA AGTTCAGAAG GACCTAGTGC
AGGTATTAGA GGAAATTTCGT AAGATTGAGC CATTATTCC TGCACAGATA CATAATAATG
GACACGGGCC ATGGTGGCCA GCATTCTTGC TCTTGACAAT GGTGAAGGGA AGGTTGTAG
GTCATGGCTA TGCTCTCAGA ATTATAATGG AAAGAAACAG CTCCTGAGTG TTTACTATGA

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FIGURE 16 (81)

GCCAAGGGCT GTGCTAAACA CTTTACCATA TGATGACATC TTTTCTCTAC AGGTATCAAA
AAACAATAGG ACATACCGGA TAGCTACAAT CTTTGGGCCC CTGCAAAACAC AATAATGTGT
ATTCTCTTCT TCAAATCCCTA CATATTGCTA CAAACTGTAT CCCTGAGGCA TATTCATTTGT
AAAATAAAA CATAAAAGT ACTACTTTTG TTTTGTGAGA TGGAGTCTCG CTCGTGCACC
CAGACTGGAG TGCAATAGCA TGATCGTGGC TCAC TGCAAC CCCCTGCTCC TGGGCTCAAG
TGATTCTCCT GACTCAGCCT CTCAAGTAGC TGGGATTACA GGCGCACGCC CCCATGCCCTG
GCTAATTTT GTACTTTTAA TAGAGACCAG GTTTCACCAT GTTGGCCAGG CTGGTCTCAA
ACTCCTGACC TCAAGTGATC CACCTGCCCTC GGCCCTTCCAA AGTGCTGGCA TTACAGATGT
GAGCCACTGC ACCCGGCCCA TATAAAGTAC TACTAATGTA ACAGGGTGCT AGTCCAGACA
GTGACCACAC GTGGTGTTCA TTGAAGGCTG GACTAACAAAC TCCAGCCCTCT CCGCCATCAC

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FIGURE 16 (82)

CTGCTCTTG TTGTATACAT GTTAGATGAT CAGGCCCTCAA GAAAAGTATA AAGAGATCTT
TGTGCTCTCT GGGACTCAAA AAGCTGCACT CTTTGGGGGA AGGATAGCCA GTAAAAAGTG
GCCCAGGTAA AGAGGGCCTG GTACACCTGG TTCTGCAAGA TGGTAGACAC AAAAATGAGA
GCCACATTG GAGCTTATGT GCCCCTAACT CTGTACATAA CCTGCAAGAT CTAATTACTA
ACAACTGGAA TCTTGGAAC ACCTGTAGTA CATCCTTGGC TAAGGTTAGC CCCAACAGAG
AGGGCTCTCC TCTTACAGAG AACCATTACA TTTGTGCCCTT CATCCTAGAG TAGAAAAAGC
ATGATCAGAC TACTAAAAAG ACATCAGGA AGGGCCCTGTG ACATCTGAGG GAAGTGGTTG
CCCTCTCTGG GATGTTGGTT CGGGAAGAGG GGCATGGAGG AGTGCCCTGCT TTAGATGGTC
ATTCAGGAAC CCAGGCTGAT AGTGAGAGGT GAAGCCAGCT GGGCTTCTGG GCTAGGGGGG
ACTTGGAGAA CTTTGTGTC TAGCTAAAG ATTGTAAATG CACCAATCAG CACTCTGTAA
AATGACCAA TCAGCACTCT GTAAAATGGA CCAATCAGCA GGATGTGGC AGGCCAAAT

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FIGURE 16 (83)

AAGGGAATAA AAGCTGGCCA CCAGAGCCAG CAGTGGCAA CTGCTCAGGT CCCCTTCCAC
GCTGTGAAG CTTTGTCTT TTGCTCTTCA CAATAAATCT TGCTGCTGCT CACTCTTTGG
GTCTGCACTA TCTTTATGAG CTGTAACACT CACCGTGAGG GTCTGTGGCT TCATTCTCTGA
AGTCAGTGAG ACCACAAACC CACTGGGAGG AACAAACAAC TCTGGACACG CCAACTTTAA
GAGCTGTAAC ATTCACCTGCG AAGGTCTGCG GCTTCACCTC TGAAGTCAGC GAGACTATGA
ACCCACTGGA AGGAAGAAAC TCCAGACACA TCTGAACATC TGAAGGAAGA AACTCCAGAC
ACACCATCTT TAAGAGCTGT AACACTCACT GCAAGGGTCT GCGGCTTCAT TCTTGAAGTC
AGCAAGACCA AGAACCCACT GGAAGGAAAC AATTCCGGAC ACATTTTGGT GACCCAGATG
GGACTATCAC CAAGTGGTGA GTACCATCAA CCCCTTTTCAC TTGTTATTCT GTCCCTATTTT
TCCTTAGAAT TCGGGGGCTA AATATTGGGC ACCTGTCAGC CAGTTAAAAG CGACTAGCAT
GGCTGCCAGA CTTAAGAGAC TAAAGACACG GGTGTCAGAC TTTCTGGGA AGGGCTCTCT

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FIGURE 16 (84)

AATAACCCC AACTCTTTGG AGTTGGGAGC GTTGTTTGC CTGGAACCAG CTTCCACATT
TCCGTGACTT CTGGGCTGAG ACGAGGGTCA ACAGAGAGGA AAGCCATTCA GCTCTGGGGT
CCCGACAGCA AGTTGGTTGA CCTGTGGCC ATGAACAGAA CTCTCGAAGT CATGTTGCCC
AAGCGAGACT CACCCATCTA TCCTATCTAT CCTGACTCTT GCTTCCTGGG TCCTAATGCC
TGGAAGACAA AACTTCCCTCT TGTCTCTGTT CTCCAAGGCT AGTCCCACCT CTAAAAACCA
CTCCCCTGTCT CTGGTGCTTT TCTAGTTTCT CCTATAAGAA TGATTCTAG TATAAACTCC
AGGACTCTAT TCTCTTCTTT AGGCACCCGG GCTCACCAAT CAGAAAGCCA TAATTTTTC
CCAAAGCCCC ATCTTAGGGG GGAATTTAGG ATCCCTCCTC AGACAAGCAG
GCCTAACAAA AGCTATTCCCT GAAGCTAGGA TATGGGGAGC CTCAGAAATG ATATCCTTCC
TATTCAAGTG AGGACAAAAG GCATCACTCT TCCAATTCTG GAAATCCCCT CCCCTCCCCTCA
GGGTATGGCC CTCCACTTCA CTTTGGGGC ATAACGTCTT TATAGGACAC GGGTAAAGTC

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FIGURE 16 (85)

CCAAATGCTAA CAGGAGAATG TTTAGGACTC TAACAGGTTT TCAAGAATGT GTCGGTAAGG
GCCACTAAAT CCGATTTTTC TCAGTCCTCT TGTGTGCTA GGAGGACAGG TAAGGGTGCA
GGTTTCAAA AATGTGTTGG TAAGGGCCAC TAAATCTGAC ATTCTTGGT CCTCCTTGTG
GTCTAGGAGG AAAACTAGTG TTTCTGCTGC TGCATCAGTG AGCGCAACTA TTCCAATCAA
CAGGGTCCAG GGACCATTTGT GGGTCTTGG GCAAGAGGTG TTTCTGCTGC TGCATTGGTG
GGCTCAACTA TTCCAATCAG CAGGGTCCAG TGACCTTTGC GGGTCTTGG GTCGGGGGGT
GGGGGGAACA AACAGACCAA AACTGGGGC AGTTTGTCT TTCAGATGGG AAACACTCAG
GCACCAACAG GCTCACCCCTT GAAATGTATC CTAAGCCATT GGGACTAATT TGACCCGCAA
ACCCTGAAA AGAGTGGCTC ATTTTATTCT GCACTATGGC CTGGTCCCAA TATTCTCTCT
CTGATGGGA AAAATGGCCA CCTGAAGGAA GTATAAATTA CAATACTATC CTGCAGCTTG
ACCTTTTCTG TAAGAAGGAA AGCAAATGGA GTGAAATACC TTATGTCCAA ACTTTCCTTT

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FIGURE 16 (86)

CATTAAAGGA AAATCCACAA CTATGCAAAA CTTACAATTC ACATCCACA AGAGGACCTC
TCAGCTTACC CCCATATCAT AGCTTCCCTA TAGCTCCCCT TCCTATTAAAT GATAAGCCTC
CTTAATCTCC CCCACCCAGA AGGAAACAAG CAAAGAAATC TCCAAAGGAC CACAAAACCC
CCTGGGCTAT CGGTATGTC CCTTCAAGC TGTAGCGGGG GAGGGGAATT TGGCCCAACC
CAGGTACATG TCCCCTTCTC CCTCTCTGAT TTAAAGCAGA TCAAGGCAGA CCAGGGGAAG
CTTTCAGATG ATCCTGATAG GTATACAGAT GTCCTACAGG GTCTAGGGCA AACCTTCAAT
CTCACTTGA GAGATGTCAT GCTATTGTTA GATCAAACCC TGGCCTTTAA TTTAAAGAAT
GTGGCTTTAG CCACAGCCCG AGAGTTTGA GATACCTGGT ATCTTAGTCA AGTAAATGAT
AGAATGACAG CTGGGGAAAG GGACAAAGTC TCTCCCGGTC AGCAAGCCAT CCTAGTG TG
GATCCCCACT GGGACCTAGA CTCAGATCAT TGGGACTGGA GTCGCAACA TCTGTTGACC
TGTGTCTTAG AAAGACTAAG GAGAAATTAGG AAAGAGCCTA TGAATTATTC AATGATGTCC

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FIGURE 16 (87)

ACCATAACTC AGGAAAAGGA AGAAAGTCTT GCCTTCCCTT GAGTGGCTAC AGGAGGCCT
TAAGGAAAT ATAACTCCC TGTACCCAA CTCACTTCAA GGTTAATTG ATTCTAAAG
ATATGTTTAT TACTCAATCA GCTGCAGATA TCAGGAGAAA GCTCCAAAAG CAAGCCCTTG
GCCCTGAACA AAATCTGGAG GCATTATTAA ACCTGGCAAC CTTGGTGTTT TATAATAGGG
GCCAAGAGGA GCAGGCCAAA ATGGAAAAGC GAGATAAGAG AAAGGCCACA GCCTTAGTCA
TGGCCCTCAG ACAAAACAAC CTTGGTGGTT CAGAGAGGAC AGAAAATGGA GCAGGCCAAT
CACCCAGTAG GGCTTGTTGT CAGTGTGGTT TGCAAGGACA GTTTAAAAA GATTGTCCTA
TGAGAAACAA GCTGCCCCCT CACCCATGTC CACTATGCTG AAGCAATCAC TGAAGCCAC
ACTGCCCCAA AGGACAAAAGA TTATCTGGGC CAGAAAGCCC CAAGCAGATG ATCCAACCAC
AGGACTGAGG GTGCTCAGGG TTAGCGCCAG CTCATGTCT CACCCCTCACT GAGCCCTGGG
TACATTTAAC CATTGAGGGC CAGGAAATTG ACTTCCTACT GGACACTGGT GCGGCTTTCT

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FIGURE 16 (88)

CAGTGTAAAC CTCCTGTCCT GGACAGCTGT CCTCAAGGTC TGTACCATC CGAGGAATCC
TGGGACAGCC TATATCCAGG TATTCTCCC ACCTCCTCAG TTGTAAC TGG GAGACTTTGC
TACAGATAGT AAGTATGCTT ACCTAATCCT ACATGCCCAT GCTCGGATAT GGAAAGAAAG
GGAATTCCCTA ACTTCTGGGT GAACCCCCCAT TAAATATCAC AAGGAAACTA TGGAGTTATT
GCACACAGTG CAAAAACCCA AGGAGGTGGC GGTCTTACAT TGCCGAAAGCC ATCAAAAAGGG
GAAGGAGAGG GGAGAACTGC AGCATAAAGTG GCTGGCAGAG GCAGGGAAG ACAAGCAGAA
AGGAAAGAGA GAAAGAGCAG AAAGTGAGAG AGAAAGAGAG ATAGGAAGTG ATAGCAAAGA
GGGAGTCCGA AAGAAAAGAG AGAGGAGAGA GAGAGGGGA AAGACAGAGA GAGACAGAGG
AAGAGACAGA GAGACAGAAA GAGAGAAGCA AAGAGAGGAA GAGACAAAGA AGGAGTCAAA
GAGAGGGAAA GAGAAGTAGT AAAGAAAAA CAGTGTAACC TATTCCCTTA AAAGCCAGGT
TAAATTTAAA ACCTATAATT GATAATTGAA GGCCTTTTCT GTAAACCCTAT AATACTCCAA

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FIGURE 16 (89)

TACCACCTTG TTGTCAGTGT AAACAAGGGT ATAGCCCAA AGCACTGAGG CCACTGACAA
CCCGTAGCCT TCTTATCAAA AATCCTTAAC ACAGCAGGTT TCCTAACAGG GAATCTAAAT
CTTAAGGTCG GACCAGACAT AGGAGGAACT GCCTTCAGGA CAGGATGATA GATGGTTCCT
CCCAGGTGAT TAAGGAAAAA GACACAATGG GTATTTCAGTA AGTGATAAGG AAACCTCTTAT
AGAAGCAGAG TTAGGAAAAT TGCCTAATAA GTGGTCTGCT CAAACGTTGA AGCTGTTTGC
TGTTTGCACT CAGCTAAACC TTAAAGTACT TACAGAAATCA GGAAGGAGCC ATCTATACCA
ATTCTAAGTT AATATGGACT GAACGAGGTT TTATTAAATAG CAAAGAAAAAT TAAAATCTCA
AACTTACAAG GTTTTCAACT AAAGTAAAGT TTGCTAAAAAG TTAAACAGCGT AACATGTATT
ATCCTACTAC CTCACACTCT CTCAAAGGAT TTCTCAGACA GTTTGC AAAA AAGAACGAAA
TCTGTCTTA CTCTACAATC CCAAATAGAC TCTTTGGCAG CAGTGACTCT CCAAAAACCGC
TGAGGCCTAG ACTCTCTTAC TGCTGAGAAA GGAAGATTCT GCACTTCTTA GGGGTAGAGT

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FIGURE 16 (90)

GTTGTTTTTA TACTAACCAG TCAGGGATAA TATGAGATAC CACCCAGTGT TTACAGGAAA
AGGCTTCTGA AATCAGACAA TGCCTTTCAA ACTCTTATAC CAACCTCTGG AGTTGGGCGA
CATGGCTTCT CCCCTTTCTA GGTCCTGTGA CAGCCATCTT GCTAATAGTC GCATTTGGGC
CCTGTATTTT TAACCTCTTG GTCAAATTG TTTCTCTCTAG GATCGAGGCC ATCAAGCTAC
AGATGATCTT ACAAATGTAA CCCCAAATGA GCTCAACTAA CAACTTCTGC TGAGGACCCC
TGGACCGACC CGTGGCCCTT TTCAATGGCC TAAAGAGCTC CCCTCTGGAG GACACTACCA
CTGCAGGGCC CCTTCTTCAC CCTATCCAG CAGGAAGTAG CTACAGCGGT CATCGCCAAA
TCCCAACAGC AGCTGGGGTG TCCTGTTTGG AGGGGGGATT GAGAGGTGAA GCCAGCTGGG
CTTCTGGGTC AGGTGGGGAC TTGGAGAACT TTTGTGTCTA GCTAAAGGAT TGTAAATGCA
CCAATCAGCA CTCTGTGTCT AGCTAAAGGA TTGTAAATGC ACCAATCAGC ACTCTGTAAA
ATGGACCAAT CAGCAGGATG TGGGCGGGGT CAAATAAGGG AGTAAAACT GGCCACCCGA

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FIGURE 16 (91)

GCCAGCAGTG GCAACCCACT CGGGTCCCCT TCCACACTGT GGAAGCTTTG TTCTTTTGCT
CTTCACAATA AATCTTGCTG CTGCTCATTC TTTGTGTCCA CACTACCTTT ATGAGCTGTA
ACACTCACTG CGAGGGTCTG TGGCTTCATT CCTGAAGTCA ACAGACCACG AACCCACTGG
AAGGAACAAA GAACTCCCCG TGTGCTGCCT TTAAGAGCTG TAACACTCAC TGCGAAGCTC
TGCAGCTTCA CTCCTGAAGT CAGTGAGACC ACAAAACCCAC CAGAAGGAAG AAACCTCTGGA
CACACCTGAA TATCTGAAGG AACAAACTCC AGACACACCA TCTTTCAGAG CTGTAACACT
CACCGCAAGG GTCTGTGGCT TCATTCTTGA AGTCAGCAAG ACCAAGAACC CACCGGAAGG
AACAAATTCC AGACACAGTA GGAAATCTGT ATTTTGTATC TGTGGCTTCC AGGGTTACTC
CAGTCATTGA AGTCTCCATT GCAGCCTTAA GGAAACAGAG AATGGTTTGG AGGAGCACAT
GTGGGAATTG TTATGGACCA GGCTTGAGAT GCACATAGGG CATTTCTGAT CAAACCTAGC
TGGAAGCAGG GCCAGGAAAT ATAATCTAAG GAAGACAGTT TTTGTAGACA GTAGTAGTCT

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FIGURE 16 (92)

TTGCATCTGA GACATGTAGA TTATCAAGCA ATTAATTAGA AAAAATATAG CCAGGTGCCGA
TGGCTCATGC CTGTAATCCC AGCACTTTGG GAGGCCAAGG GGTGTGGATC ACAAGGTCAG
GCGTTCGAGA CCAGCCTGGC CAACATGGTG AAACCCCGTC TCTACTAAAA ATACAAAAAT
TAGCCTGGTG TGGTGGCAGC CATCTGTAAT CCCAGTACTC AGGAGGCTGA GGCAGGGGAA
TCTCTTGAAC TTGGGAGGCA GAGGTTCAG TGAGCCAAGA TCACACCACA GCACTCCATC
CTGGGTGACA GAGCGAGACT CTGTCTCAA AAAAATAAAA AGGAAAAATAT
AATCAAGAAT ATTGACAGGT AACATTTATT CAACACTTAC TATGCACCAG GCAATACACT
AAGTGTTTTA CATGGATTAA CTCATTTAAT CTTAACAATA GCCCTATGAA GTCAGTGCTG
TTATTATCTC CACTTTATAG ATAAGGAAAC TGAAGTACAG AAAGGTCAAG TAGAGAAATG
GCCATGCTTG CATCTCAGT TTTTGAAGCA ACTGTTACAG GAATCTGGTG TGAGAAATGC
TCTAACAAAG TGTGAGTCAG GGGTTGGGAG GTACTGAGTC TGAGTTGGC AGTTGGGGAT

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FIGURE 16 (93)

GGAAGGATGG ATGAAGAAC A GCTTGACAGA GAAGCTGACA CTTGGCAACT CTGTGGGACC
TTGAAGGGTT AGAGGGACTT CACCAAAGAA ACTGGTGGTC AGGGAACGG GAGGGTCACG
GCAAGGAGGG AAAGGAAACT GTACCACAGC AGAGAGTCTG AAGCTACTAC AGTGTAGTTC
AGCGTATAAA GAATAATTAT TTTAAGGTAA ACTTATAACC TCATGCAAT ATAAATGAA
CACGTGTCAA AGATCTTATT TAATTTATTA ATTAATGAGG GAACCTGTAA GATGTTACAG
CCAGTTCAAA GGATAATTCA AATAAATCCA TGCACATATG TAGGCAATAA GGAATGCTGA
AATGAATTTA AAAGTAGATG TAAACTGATT TATCCACAGA GAAATAATCA GTTGCATTTC
ACATAACAAA ATTCAGTTGC TTTTCTACAG AAGGAATTGT TTGCATCATT ACCAATTTT
CTACAAC TAA CAGAAATTATA AAATAACTCA AACACAATGA AAGCAGATA TAACCCACAA
TGGTATGATA GATACAAATAT CCACATCCAG GATGTTTTTT TCTCATTTCA AAGTCTTTCA
CAAGTTTCC TGATAAGGGA GTGTCAATAA TACTGTATGG CAGGCAATAA GACTGGATGG

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FIGURE 16 (94)

ATGGTTGGG CCAGGTTTAA AGGGGTAATA AATGCCATGT AAAGGTATGT GCATACGTGTG
CAACATGTCG GGGGAATCTC AAATTATTGG TAGAGTATGT AGGAAACACT TGTGGGAGCT
TGTTAATAAA TTCAAATTCC CAGACCCAAC TCCTCAAGGG GTCTAATACA GTAGGTTTGG
AGTAAAGCCT GAAAATCTGC AATTGTGCAA AAAAAAACC CAGGTGATTC TGATACACTT
TGAGAAGCAC TGGTGGAACT AATAGTCACT GAACGTTTTT GAGCAGGGA GAAACCTGAG
GACGTCATG TTGCAGCAGT GAAACTTGA TTAGAAAGTAG GAGAAGATGC ATGGTCTTAA
AAGAA TGCAA AATGATGGCT AATATTGAG TGCTTATGAT GGGCCAGGG CTGTGCTAGG
CGCGTGGCAC ACATTCAATA CGATGGAAGC CTGTACCAGT CAGTATTAGT GGGGTATCTT
TAAGAGTGAC CAGAATTAA GGGGGTTTC ACCAAAGCCT GAGGACTGAG CCTCCTCATC
CTAAATTCAG ACACAATGCT GTACCTATGC ATTTGCCCTCC AGGCTGTTCC TGGGCCCTCCA
GGGACTGGCC CAGGCTCCTG ATAAATAGG ACTCCCAACA ACATAAAGCC TGGATTTTGG

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FIGURE 16 (95)

AACTTCCTGA ATGTTACTCA GGCTTTCTAG TAACTGTGGA GATCTGAATA ATAACACAAT
TCTAAGTTCC CCTACTCATA AAGCTGCTCA TCATTTAGAT GGGTAAAGC ACCTGAAATA
CAATGAGCAT CACTATTTTC ATTCAATCCAT GAAATGAACA TTCCGGGGAG ATCAGTAAGT
TGATGTATCA CCCTTGAAACA GGGCAAAATG AATACTCACC AGGAATATGT GGTATTTTAA
AAAGAAGGCA AAGGGAAGAA TAGTGGGGAT GGGCAAAA CTTTAAATAG ATTCCCCCAA
TCATATATGG CAATTGAAGA TAATTAAATT ATCATTTTAA TTGAGTAAGT ACTCATAGAG
CCCTCACTAT TTGAAAATGA ACTGCCCTCCT AATTGTTATT GTGCAAAATGT GATACATTAA
ACTTAAGCTA TTTTAAATAA ACATCCATT TCGGAAGCTG TAGTAGGTTT TCCCAGGTCA
GATTTGATAA GCCATAAAGA ACAAATGCCA ACTCCTATTT TTCTATGGTG CTGGGAAATA
AGAGAGAAAT GTGTAATTCA AAGCAATCAT TTAAATTTTAT CCAATAGCTT GATTCTCCTC
TCTCTTCTAG CCTTTTAGCT AAGCTGTTAC CAAGTAACCA CACTAGTTGG CTTGAGTCTT

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FIGURE 16 (96)

ACCACGTGTTT CCCTGACCCC ACAGTGGAGA GACTGCATCT GTTAAAGAGC AGTTATGTAA
CCATGGCTAT GCTGAGCTGG GATTCCCAAG GCTTAGGTTT TTTCTGTGAA TGACCTTCAC
CAAGACACCT GAGGTCTGTG TGGAAACCACA GGCTTGTCTAT CTCTAAGGCA GAGTTGATAA
TTCCATCTGT TTCTTGAGCC CACACTGAGA AAAAGATTAC ATGACTGCAG TTATTTGAAT
GCCTCATGGA AAGACGCTTT ATAAATATTA TAATTAATGT TATCATTAAG TAATGCTTCA
ATGCAGATCT TCCAAGTATA AATATCAGCT GAGTAAGAAG TCAATCTTCC CTGAAGCAAA
ATTGAAATTT GTAAATGCCA TTTCTGGGAG CTTATTTTGT AATACATGAT TCCAGAGTGT
CCATAACACA CACAATTGTC TTTTTTCCCC TACATGGGCT ATTTACAACA AAATTGGACT
TATAATGTTT ATTTCCAGGG ATGACTAGAA CTTTAATAAC AAACCTTGGG CCAGGCATAG
TGGCTCATGC CTATAATCAC AGCACTTCGG GAGGCTGAGG CTGGTAGATT ACTTGAGGCC
AGGAGTTTGA GAACAGCCTG GCCAACATGG CAAAACCCCTG TCTCTACTAA AAATATAAAA

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FIGURE 16 (97)

ATTAGCCGGG TGTGTGGCG CATGCCAGTA ATCCCAGTTA CTAAGTAGGC TGAGGTACGA
CAATCGCTGG AACCTGGGAG GCGGAGGTTG CAGTGAGCTG AGATTGCACT ACTGCACCTCC
AGCCTGGGTG ACAGAGAAAG ACTCTGTCTC AAAAAAAAAA AAAAAAAAAA ATAATAATAA
TAAACCCCTGA TGAAAGGTTT CTAAAAATGTT TTCACTCTAAT GGTTTTCTTG ACAATTAAAT
TTTCTATATA ATGTCAGTTC ATAAAAAAC TGAGAACGAC CACATGTCTAT ATCGACTGCT
TAAAGAAAA TACGTATATT TACAAACATA TACACGATAC TGTCTTTTGT CTGGTTAGTT
TAGAGGTTAG ATAAACTGCA GTATGTTGTA GTGGACAGAT CATAGAACTA GGAGTCAGGA
TGCTCTGGATT CCTAGGAAGC AATGAATAGG TTGCACGGTG CAGACCAGCA TCATGAGTAT
CCTCAGGGAG CTTGTTAGAA CTGCAGATCC TTTAACTCAT TGAATCAGAA TCCCTAGGTG
TGGGGCCCTG AAATCTGTAT TTTAGCAGGC TCTCTGGGAT TGTGATGTGC CTTAGAGTTT
GACAACCACT GGGTAGCTGA TCCTGACTTA GACTTATCAG GCATGTGATC TTGAACAAGT

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FIGURE 16 (98)

CACATAATCT CACTGAGTTC AGTTTTCTTA TGCTTAAAT AGGCCCAATA ATATCTATTT
CACATGGACT GCTTTGAGGA TTAGGCAAGA GATCTGTAAC AGACACTGTA GAACAGTGTC
TCTGGTCTAC AGCTGACCTT CCATAAATGG TAGTTGCCCTT GATCTCTGCT CTGCCACATA
ATAGCTGGTT AACTATGAGC AAGTAATTTA GTTCTTCTCA GTTTAGTTTC TTCACCTGTA
AAAGAAGGAA AATAACTGTT ATACTCAATT TCTGAAGTGG CTATAAAAT CAGTTTAAAT
TATGGGCATT GAAGCTCTTT GTACACTGTA TAAAGGACTGT ACATCTAAGG GATTAATGAG
ACCAGGCTTA TGATTTTAAG CATGGAGTAA ATAGTAACAC TGACTCTGTT CTATGAACCA
CATGGAAACT CTAAAGAATA TGCACATTTG AAACACAGGT ATCATCTGGG GAAGGTGATC
TGCTCACCCA AACCAGTTCA TGAACATCAA TCTCCAGTGG CGTGCTGGAG CTAGCTGTAC
CAGCTCATGA GGGCCAAATTG TTTTCATTTTT AGGAATTTTG TTTGCTGGTT AAAAATAGTC
ATTATTATAA ATTAAATTAT GTAAACAATA ATATTAGATA AAATAAGTTA AAATAAAAC

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FIGURE 16 (99)

AAAGGAAC TA ATTATCCCCA AACCTCTTCCC CACCTAATTA TTTTACTATC TGTGCCCTTGG
GATTATTAC ATTGATTTTA TCCATATGGT GACAATACTA TTCATATATA AATGGTGTGC
TTCTCTTCAT AACCTCTACAT AGCCTGATGT CAGGCTAGTA GCTTGAAATT GGCCACAGTG
GGAGTGTGAG CATTGTGACC ATGAGGCTTG GCCAAGGCTA CAAATCCAGA CTTTGTGTTT
TCCCTCCTGG AGAGCTGTCT GTTAAAAAT TACCAACACA CCACTGGTCT TACCTTTGTT
AATTACCAC AGTCCAGGT CTGACCCTAGA CTAGAAACC TGGATTGTC AGCAAGCTGA
GGATAGAGCC ATTATTTTA AGAAGGACTC ACATTACCCA AGTGCAAAGC CTGATATATA
CCTTCAGAA ATCAATTAT TAATTACAG TGAAGAAAGC CACCCACGG CATCCCCAG
GGGAAGGCAA AAAGAGCTAG TTGCACATTT TGAATGTTG ATGACATTAG GGTAAAGGTGA
CACAGAAAT CCAATTCCAC AACTGAGATA CCTGCTGCCT TAAGGAAGGG ACAGGCAAGT
CCTTGGGCAG GACCTTAGAT TGTCACTGTC CATCTTGCTC TAGGACTCTC CTTTCCAGGC

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FIGURE 16 (100)

ATGACGATGG CCAACTCTGT CCTCCTACCC TACTGATGGG ATTATCTTTT CTTGACACAT
GGCAATGCCT CCAATCAGAG GCTGGTAGCT ATTTTAAATC TTCAGGGCAG TATTTTCAA
AGGGAAGTTC ATGGACCATA TGCATCTGTA TCATTTAGAT GTATATTAAA AATGCTTAGT
CTTCCCCAGT TATACTAGAT CAGAATCTCT GTTGGTGGG CCCACGAATC GGTATTTTCA
ACAAATCACT AGGTAATTTC TGTATATACT ATAGTGTGAA GACCACTGCT TGAAGGTTTC
TTTGCCATATC TCCACTAAAT ATAAAAATA TTGACTTCTA GATTAACTC CCAAAGCACT
TGCATTTTAA AGTTTCTGGG GGCATTATAT TGTGGTACCC CTATACCACT CACACTCTAG
TCAGGAGGTA TATTATGGAC TGAATGTTTG TGTCCCTCCA AAACTCATAT GTTGAAGTCT
TAGCTTCCAA TGTGATAGTA TTAGGAGATG GTGCCTTCTG GAGGTAAAAT CAAGCCCCA
TGAATGGGAT TAGTGCCCTT AGAAAGAGAG CTCCTGTCCT GTCTTTCCAT CAATTGAAGA
TGCAGTGAGA AGCTGGTAGT CTTGCATCTG GAAGAGGGCC CTCACACAAC CTGATCATGC

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FIGURE 16 (101)

TGGCACCTGG TCTCAGACTT TCTGCCCTCCA GAACTATGAG ATGATAAATT TCTGTTGTTT
ATACCCACC CAGGCTACAA TATTAGGTG CTGCAAAGTA TTTGTGATTT TTGCCCTTTAC
TTTTTCAGGC AAAAAGTCA ATTACTTTTG TGCCAACCTA ATATTTTGT ATAGCAGCCC
GAACTAAGGC AAGGAGACT ACATCAGACA GTGTAGCTAT GTAAGTACAA ATGTATCCCT
GTTGAGGAAA ACTAAGTTCT AACCCCTGACT TCAGGCCAGT AGCCACCCTT TCAATCTCTT
TCATGAAGG ACCATTATCA TTATCACTGG TGGCAAAAAT AGAGGCACGA GAATGGAATT
TGCTTTTCTG TGAATCTCA GTGTATACAG ATTGAAGAGC AAGGGTTGC TTTCATCTCT
AAGAAGCAA AGTGAGTAC GACTGGCACA TTATCAGAGA AAGAATCAT CTAGCTCGGT
GGGTCTTAAC CAGAGTGAA TTTGACTCCA GGAACAGTT GGCAATGTCT GGAGACGTTT
TTATTTGTTA TAGCTGGGG ATGAGTGGGT GGGTTGCTAC TGGCATCTAG TGGGTGGAGA
CCAGAGATGC TGTAAACAT CCCGCAAAGC ACAGGACAGT CCCCAGAAC AAAGAAATTAT

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FIGURE 16 (102)

CTGGCCCCAA ATATCAATAG TGCCAAAGTT GAGAAACCTC ATTCTAGCTT CCTTTTCCCT
TCTACGTTCT AATCAACTGT TGTTCCTTCA GCATTAGGAT TCATCCAGCA GTCTCTTTCC
CCAGCAATTT GTTGAAATTT TTTTAAAAAT GGACTCATTT TAGTGTCA CAAGAAAAAT
ACATTACAG GAAAGGATGG GTCATTTTGT TTAATGATGT TTTGCCCTTC ACATAGCAAA
AGCTTAATAA AGTATTTTAA AATAAAATGG TGAATAGATC AAAACATTA TTTTCACATGT
GTTTAAATAA ATAACAGGAA GATGGCTATA TTATATAAAT TGTTCCTTGA TATGCTTGA
GTGGATCATC AAACACAAAC GTATCTACAT GCCTTTCTT GTGAATAGAT CTAATAATAA
CGCTCTTCTA AAAACAAATT AAATGGATAT TATTGCTGA GAATGTAATG CTTGTGTGAA
TAGAAGCCAG CCTGAATCC AAGCCCCCAG ATCTATTAA AGAATTGAA GAATGTCAGA
AAAGCACGTG GCTTCAAGGT TAATGTGTAA GACTCACAGA AACTTGAAAA ATCACTATGA
CTAAAAAGAA AGTATGAGCT CCCTGCATGC CTGTAAATG GAATGACAGC CAAAACCCAGT

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FIGURE 16 (103)

TAATTATAAA AACAGCTAAT TTAACAGGTT TTCAAATTGG TTTCCTTCTC CAAGTAGCAT
ATAGTCAATA ATCCTTAAAG AGAAAGCAAA GAAGGGGAAG CACTGAACCA AATTGCTTT
TTTGTAACCTG CTCAGCTCAA ATGCAGAGTT CTCTACCTGG AAATTGACTG CTTCATAGT
TTGATAGCCA CAGAGAGATG GGAACAGAAG GAGAGGTATA ATCCCAGACT TGATTCAGCT
ATAGAGAATG ACAATAGTGT CAGAGGCCCTT CCAACCAGAG CGACTCCATC TTGAATACGG
GCTGGGTAAA ACAGGGCTGA GACCTACTGG GCTGCATTCC CAGGAGGCTA AGCATTTCTAA
GTCACAGGAT GAGACAGGAG GTCAGCACAA GACCTTGCTG ATAAAACAGG TTGTAATAAA
GAAGCCAGCC AAAACCCACC AAAACCAAGA TGGCCATGAG AGTATCTGT GGTGGTCTC
ACTGCTCATT GTATGCTAAT TATAATGTAT TAGCATGTTA AAAGACACTC CCACCAGTGC
TATGACAGTT TACAGGTACA TTGGCAACTT CCGGAAGTTA CCTCTATGG TCTAAAAAGG
GGAGGAACCC TCACCTCCCA GAATTGCCCA CCCCTTTCTT GAAAAACTTG TGAATAATTC

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FIGURE 16 (104)

ACCCTTGTTT AGCATATAAT CAAGAAAGTAA CTGTAAGTAT CCTTAGGCCA GAAGCTCAGG
CCTACTGCTCT GAATGTGGAA TAGCCATTCT TTTATCCCTT ACTTTCTTAA TAAACTTGCT
TTCACCTTAC TGTATGGACT CCTGTGAAT TCTTCTTGC AAGAGATCCA AGAACTCTCT
CTTGGGGTCT GGATCAGGAC CTCCTTCCAG TAACAATAGT AGTAAGGGGT CAGGAGACT
GGACAAAGGA GTTAAAGAAG CCTTAGATAA AGGTCCTCA TCATTGTCAT AACATAAAAT
CATGGACTCC TAGAATTTTA TAGCTGATAG GATTAGAAAT TTCAAAAATC AATTTCATTA
ATTTTCATCT GCGAAAACAG ATGGCCAGAG AGGCCAAACA ATTTGTTAAG GAGCACTGAG
GGCAGACCAC ACTGGAACGC AAACCTCTTA GCAGAGTATA CAAGGCCCTT GATCTCCTCA
GTCAGAATGA ACTAGAGCTT TCCAGGGTAC CCTTCTGAC TGTTTAGCAT GTTTGCCAGT
CTGACTAATT TTGAAGTTGC TTAATAATCT GTCATTTCCA CTGTATCATA ATCTCCTCAT
TCATCTTCAA TCTCCAATGC CTTGAACTCA GTAAATGTTA GTTGAACAAA AGTAAATTGA

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FIGURE 16 (105)

ACCCAGAATT TCTGATCATA ATCTGGAGCA CTTTAAAATT GTCAGCTTAC TGGGAAACGG
GATAACATGT GATTGTGCTT TGATTTTTTT TTTCTCATAT GCTTTTCCCA CCTATAGATG
CTACACGAAT GTTTTAAAAA TCTGATATAA AAATTAAAAT TAAAAAATTA AAAAAGAAA
ATTTGATACA ATGCTACATT TAGAGTGTTG TGATTAGATT CCTTAAGTGT ATCATGGTGA
TCTCTACATC ACGTGGTGAT CAAATTGCTT TGGGTTTTAA CACATAACTG ACAAAGGCTT
GGGACATGT AAGATCCCAA ATACATTTTT ATTGATTTTT TTTTCTTGTT TGTCCCTCTTT
TAAATAACTT TTTTTTTGTTA TAAGAAATAAT TCATGTTTCAG TGGAGAAACC ATAGAAAATA
GTGACAAAGTG AAGGAATAAA TTTTAAAATGA CCCATAATG TACCATACAT TCTGATTTTT
TAAACGCTGA ACAAATTAGC CTTGGGTAAG TACCAGGAAT AGAGTGCAGC ATTGAAAGTT
AAAGTTTGGG GAAGGATAGC TGACTTAAGA AATTATCTAG TTAGACATTT TTTGATGGGG
TAATTTTGCA GATGACATTA GTGAGAGAAA GGACTTGCCA CTCTCACACA GCTAGTAGGG

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FIGURE 16 (106)

GTGTGGGAGG ATATTGAAC CAAGTTTCAA GTCTTCAGTG AAGAATCAAG GGAGAAGTTC
TAA AACCTAA CAATATCCCT CTGGATGGAC ATTTATTTTA TTA CTACAAT AAGCCACACG
GTGAGTCATA AGGAGCAATT CATTCCTTCTA ATATGCTCT ACTGTATTTA GAATCTGATA
AAGCCCCCTAT TAGAATTTCAT CTCCTTTAAGA ATAAAAGAAG CTGAGGAACT AAAGAGAGGG
TTGGAATAAT CCACTAATTA TATCCGTTAA GCTTCAGTTA CGCTAATAAG GAATATCACA
TGACTGTGGT GTGTGCTTGT TCTGAACAGT AAAGTACATG AGGAAAGATA AGATTCAGGG
CTGAAATGTC CTTCAGCATA TGTAGGTAGT GGTGATGAAA GTCATTAAAA GAAAAATTGA
TTGAGGTATT TTAGTAAACA AAAGAACTCA CCACTTACCC ATCAGGAAGT GTATTGTTAA
TGCAGTGCTG TTCAGCCCTTC TGGAAAGAAA GGTTCCTTCA TGCTTCCTC TTTAGCCCTAA
TTCTTATCCT GTCACCTTTC AGGCAAAATT AAAAAAAA AAAGATTGAA AACGATGCTC
CTATTTTATT TGCTTCAAAA GAAACAGGCT GTTGCATTGT GCTTGAACA GTTACTCTT

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FIGURE 16 (107)

GGCCTTGATG TAAGTGTGAA AGGAAGCCCA TGTAATTGAC TAGGCAGTAT CTGAAGAAGC
AGGAAATACA GTGTTAAGAA AATGAACAGG CATGAAAACC ATGGCTATTT GATAAAAGTA
AATAATTCT GCAGTTCACA TGTTCCTCAGC ATATTTTCTT TGATACTGAC TTGCTTAATA
TGACAAATAGC AGAACCATGG TAGCTTGTAG GCATTACTTT TCTTTTAATT TCTTTTACAT
TTTGAAATTTA CCAGCACTCA CATTGTATT ACTTTTGGGT TATACTGAGG ATCTATAACT
TATAGATCAA ATACCTGACA TATATATGCA TTCTCTGAAG TCTTAGGGCA GAACTAGAAC
ATTCTTGTGA ACATCAGTAT AAGATATTAA AATGGAAGTT TTGCCCTAAGA CTGAAGACAA
TAAAAATATC ATAGTCTGAA ATGAATGCCA GCACACCATA CAGGATTAA ATATCTATAC
ATATATATGT GTGTGTATTA TATATATTTA ATATATATCT GTGTGGGATA GGAAGAGGTA
GGGGGAAATC AGTTTACAA TTATTAAGTA TTTACCCCTT GACAAGAGTA TATATATTGG
AAATCAGTTG GAGAGTATTT TCAAAGATAA ATGTTAGTGT GCTATGAATG AATCCACCCC

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FIGURE 16 (108)

TACCACCACT GAGCAGGGT AGGAGAGGCC TGTGCTCCTC AAGCATAGTT GGAAAAGGAC
CTCAACAAGA CCACTTCAAG AGTCTAATGT GTGGAGACTG TTGCTTAGGG AGACCTTATG
GTCTAGCTTC TGA CTCACAG CTAAGTCAGG GAGACAGGTT GGCTGCTCTG ATCGTGGAGT
CCAAAAGATG GCCTGCACTG AAAAGCCCTCA TGAGTGTTGA CTTAGGGCTA GTCTAAGAGG
TCCCTGGAAG AAGAAACACT CAGTAGGAGA GAAGCTGGAG GTACCTTCAG TGCTGAATTG
GAACCTAGAT TCATTCCCC GTGGAGCAAA TTACATAGGA AAGATGCCCCA GTGATGGAGA
GTGGGGGTGT CTCTAACAAAT TACCCACCCA CCTGCCCCCA CCCCTAAGAA AAAGAAAATC
ACATACAACC AGTCAGCTGT AAACATATGC CGAGCCTAGT AAATCAGAT ACTAAGTTAC
CAGGGTACCT GGCAAGTAAG AACATTCCCTG ATTCCCTTCC CTCCTCTTCC TCTTTGCCCT
CCAACCTTAG TGGCTAGCAA GATGGGGAGA GGAGGAGAAG CTGTAAGTGG GGAAAAAAGA
GCAGCTTTCT CTCCTTTTCA GCTGCTGGAT TCTCCCTCAT CATAGGCCCTG AGCTGGGGAA

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FIGURE 16 (109)

TCAGGAAGAA GGATTCTTTT TAAAACTGAA GTAAACGTTAT CATTTAATTT TAAACATTT
TAAATTTGA CAATGTTGAG ATTAGATATA CTAATTATTA AACTAAGATT ATGTTTTGCA
GCTTGAAGTG ATAAGAAAAA CCTCTTATCT AAGAGCATCC AGGAAAGTCG GGGGTTTCCT
GAACATCCCTT TTAAATCCCTT TGGAAAGTCAG CTTTCAGAGA GGATTTAAAG TGTAGACTGG
GCCTTCAGAA ACTTGGTTAA TGTAGGGGTT TCCTATGCAG ACTTGGGAC TATACCTTGT
GTGGAAGAGA GAAAATAAGA TTATCTTACA TTTTTCCTCCAT TCCTTTTCA AAAAGAAAGC
TCAGCTAGCA TGAAGTTAA ATTCAAAACG TAATGGGTAT TATTTCGATA TTCAAATCTA
GTGCATATCA TGTAAGTACT GAATTATGGT ATTCATTATT TCAAATGACA AGCTGGATTT
TTTTTTCTTT CGAATTTAC AAATTAATTT TCCTTGGAAC CTTTGGGTTT GGGCTTTAAG
AGTTTAGGCT TTCATCACAA AGAGAGGACA GCCTTGAAGA TTAAAGTGTG TGGCTCTTCT
CAAGATGTTT TTAGTCCAGC AAAGGATTCT ATGCATATTT GGGCTTCCTT CTGTCTCATA

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FIGURE 16 (110)

ACCTGTATTT CTTGATATTC TATTTATATT CTGTAAGATT TTTTTTTTAA AGGAAAAATT
CTTCCATGGT TGAAGGACAT GTCAAAAATA GAGATACAG TTTTATATCA AAGGAAGTTT
CATGATATGA CTGTAGAAGC TCATTTGACT TAAGACACAT CATTTCCCTCA TGGAGTGTT
AAACAGATCT GTACAATAAG GTTGGCAATC TTTGTGTAAA ACAGTTTTTT TTCTCCTGCT
CTAAAGAAAG TGTATATTC AAAATGTGAA TGTGAGCAGT CAGAAAAATAG TATTTTTTTA
ACTTCGTTTT CAAAGTCCTC AAAAACCTGT ACCTAATCAT GAATTTTTTT TCCCACAGAT
TGTTTTCTCT TCTCCCTCCC AGAAACTTTG AAGTTTTTCT ACATGACACC AGGACCTATG
TCTTTTTTTA ATTACACAGA AATGAAAGAA AAAAAGTGTG TTGTATCGTT AACCAAATAT
ATGAAATCTT TAAGCTGTAT TTTTATTTTT AACTTTGTTT TGCAAAAGAGG CCATTCCTCT
TGGTAAATA ATTTGTTATT CACAGTTTCC TTGTCCCTCAT ATTATCAAGG GGAAAAATTGT
AGAAATTTA AAGGAAGCTC TAGGCAATGT TTTTCATCCCT GAATCTTTGG AGAGTTATAA

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FIGURE 16 (111)

AAACAAACAG ATTACTGAAC CTGTAAGAGA ACCAATCGTG AAGTCATTAC ATCTAAGCAT
AAGCAAAATC TCCTCTTGGA TCATTAAAGTT ATAGAAGAAA AGAAAGCCCTG CACTTTGAAA
TTTAAATAAA GCTTGGTAAC TTGTAAGTCA AACACGTAAA ATTTTACAAT TCAGGAATAT
CGATAGCAGT TGAGTTTAAT AGACTTCTCA CATCCAAAT TTAAAGCTTC CTTCTCTGTG
CTAATAGAGA TACAATAGCA GTAGGCGTTT AAGAAGAATG AATCAACAAT TTAAAACTAT
AATGTGTTTT TTATTCACTT CCCTTATTCA CATATATTG TTTTGTTTTG AGAAGGAGTT
CTGCTCTGTC GCCCAGGCAG GAGTGCTGTG GCACGATCTC AGCTCACCGC AACCTCTGCC
TCCCGGGTTC AAGCGATTCT CTTGCCCTCAG CCTCCTGAGT AGCTGCGATT ACAGGCGTGC
GCCAGCAACC CCGGCTAATT TTTGTATTTT TAGTAGAGAC AGGTTTTCAC CACGTTGGCC
AGGTTGGTCT CGAACCCCTG ATCTCAAGTG ATCAGCCCGC CTCGGCCTCC CAAAGTGCTG
GGATTACAGG CGTGAGCCAT CACTTCTGGC CCTTATTCGC ATACAATTTA AAAATCATCA

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FIGURE 16 (112)

CAGAAGGTTT GAAAGAAGGA AGGGGCAGAA AATTACCCTAC TTTTCCCTCTC CCCAGCGATC
TCCTTCAAAT CTGTGCCCTTT TCCTCAGGCC CAGGCCTCAA TTTACTGAGC AGTCACACCT
CACAGAGGA GGCTGGGCA ATCCACTCTT GGTACACAGGA AAGCCATTGA CCCTCCCACT
TCCTCTCCTC CACCTTGTC TCAACTCTTG ACTTTGGGT TGTGTTCTGT TCAAGTCCCTA
GGAAC TG GTT TCTTTATCA GGTAAAGTGA TTAGTTCTCT TCCCTCTAG TTGCTCTCAC
TCCCTGACTC TTGCCTTCTG TAACAACTGG AGACAACTCT TTCAAAACCA GCTCCAAGCC
CCAGACTTCT CTC TGGGCTT TAGTTCGTAA GGCAGGTGCC C TACTGAGTG AGCCTAGATC
AGACAGAAAC ATAGCTGTTG GCAATGATTT AGGTGAATTT CCTTCCATTG TTTTCTTAAT
ACCTTCTTTT TTTTGTAAAT ATAACCATGC ACATACACAC ATATTGAAT ATCCTGCTT
TTTATTTAAA ATGACAAATAG GTCCGGGAGT GGTGGCTCAT GCCGTAAATC CCAGCACTTT
GGGAGGCCGA GTGGGCAAT CACCTGAGGT CAGGAGTTCG AGACCAGCCT GGCCAACATG

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FIGURE 16 (113)

GTGAAACTCC ATCTCTACTA AAAATCAAAA ATTAGCCGGG CATGGTGGCA GGCTCCCAGC
TACTCAGGAG GCTGAGATGT GAAAATCGCT TGAACCCGGG AGGTAGAGGT TGCAGTGAGC
TGAGATCTTG CCATTGCACT CCAACCTGGG CAATAAGAGC GAAACTCCAT CTCATGGAAA
AAAAA AAAA AAAGACAGGA TAAACATCT AGATAGTCTC TATAATGGTC ATGATTAAAG
CAATAAAATA GTCTGAAATT GTCAATATAT ATTAATAATA ATTTATTGG CCATTCTGCC
AAGTAGCAGA CACCTGTCTAT TCTGCCCCACT CAGCACCTCT CTTTCTTTTA GGGAAATGCT
ACCCACTCTT TGCATGGGTT CTGGATGGAA CTGTTGATCA CAGTGTTTT ACTCCCCATT
TTGCCTCACC AGAGGTAGAC AGAAGACCCA AGCCAGGCCA GTTACACACA ATCTTCAGAT
AATTACCGTA TTGATCACAG TATCACCCA CTCAAGGCTT GGTGGAGAT GAGCAGAAGA
GACTAAAGCT GGGTCATTTT AATTAACACC TGTACCCCAA AGAAAGACTG TCAATGAGGC
TTTTATACCG ACACTCCTGG TTTCCATTCT TCCTGATGCC ATTCATTGA CGAACTACCC

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FIGURE 16 (114)

AATCTTTCCA ACAGTGTCTT TGGAAGAAAG ATAGTCAGAA AAGAAGATAG AGTTGTTTTC
TGTTCCTTGC AACCAAGGAA CTCATAATGA TAGACTTGTT GCTAGGCACT TTGGTTATTT
TTATTATCTT GAATACTTCT GTGATATACT TCTTTGTGCA TGCCCTGTTG TACGGATGTA
GCTTTTTATA TATTTTATAT AATTCTCAG AAGTGAATT ACTTAGTCAA AAGGTATGAA
CATTTTCTG ATTCTTAATA TAAATTGTGC AAATGCTTTT TAAGAGGATT ATACCAGTTT
ACATTTTGTG TTATATATAA CAGAAAGTAC TACTGAAAAA ATATTACAAA AATTGTCTC
TCGTTCAGG AGGACCTTGT AATAGATGAT AAAGTACTTG AAATAGGAAC ATAGAGCATT
TTCAGTTTAA AATAATTCA TTGGGTATT TACGGAATCC TTAGAATTAT GGCCAGACAT
TTATAGATGA TCTGTACCAA ACCTAGGTG GTTACATAAA TTGCTTATTC AACTGGCTTA
AATCTATAAT AGAAAGATGA CACTTACTGA ATGTTTAATA TACACTTTGT CAGGGGCTTT
GTATTATTCT ATGACATCTT CAAAATGACC CTACTTTCCT ATTTTATAAG TAAGGACAGG

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FIGURE 16 (115)

AAGGCTTCAA GAACATGACT AATTTTCCCA AGGGCTGTAC CAAAGCCAGA ACCCAAATCT
ATAAGGCTTT TAAACCTGCA TTCTAAACT GCATCTCGGC CATCTTATTC CTACAGAACT
TAAGGTTAGA AAGCAGATT GGAGTCCCAA TTTCACCACT TAGTAACCAG ACAAAC TTGA
GGAATTCACT CAACGTCCTT GAATCTTTCAT TTTCTAATCT TTAAAACTAA AACATAATA
CTTGCTCTAC CTATGTCCCTA AGATTTCGTG AGGCACATAG AGATAGTGTG GAAGAGTGCT
GTACAGATGT CAAGTGTTAG CGTGATTACT TAGATCCCCTG AACACCATGG ATGAATGTCT
CTGACTGCTA TTAGAGGTCA TAAAGAATAT TGGGGCCAGG TACATTGGCT TATTCCCTATA
ATGCCAGCAC TTTGGGAGCC TGAGACAGGA GGATCACTCG AGGCCACGAG TTCAAGACCG
GCCTGGGCAA CATAGTGAGA CCCCTTCTCT ACAAAAAAAA AAGCAGCCAC GTGTAGTGGC
ACACACCTGT AGTCCCACAT ACTCAGGAGG GTGAGTTGGG AGGATAACTT TAGTCCAGGA
GTTTCAAGGT GCAGTGAGCT GTGATTGCAC CACTGTACTC TAACCTGGAC AGCAGAGTGA

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FIGURE 16 (116)

GACCCCTGTCT CTAAAAAAA AGAAAAAAA ATAATAATAA TAAAGAAATAA TGGGGCCTTG
GGATACCCAC TCCTCTCTTT CTGCTCTGAG TTGTGAAGCA GTTGAGTTAC ATATGCATGT
CCAATGGATG AGGTTGAAAA TATCAACTGG ATTGGAATGT GGCTTACTTG CGTGGCCACA
ATGAGCTTCG TAACACTTCC TGACAGGGTG AGAAGACAAA CTTCCTCACC CAGTCACTGG
CAGAGCTGGA CACTCTGTGT CTCTCCCCACA GAACAACCTC TTACTGCATG GAGGTGGATG
AAAAAGTCAA CCGAGAACAG GCTACTCCAA AAAGCAGAGC ACCAAAGGCA CCAGCTGGTC
AGGTCCCCCT TCCTAAGTAA ACAATCACGT AATTCATTCTG GGACAAAGCC AGAGAGGTGG
TGTGGAGAAA GAGAGGGCAG TTTCCCTCCCA AGTTTTCCTT GGAATTCCTT ATGGGAATAT
GAGGTTAGG GGAATAAGAC TTCCCTTTAA CAGTGAAGAA TCCCCAGCTC TATTGGTAAT
AGGAAATCGC TTACAAGGAT CATGGGGAGT ATTCCTCAG CTCGTTCTGC CTCCCTACTTG
GCTGAGTGGA ATGGAACCAT CTGTGGCTGC TGCATATGAT ATTGTCAACT TTGTCAATCC

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FIGURE 16 (117)

ACACCCACTC CTTGACGCCC TACCATGTGG TCATAAGACT CCCTTTAAAG TGTTCCCTTTA
AAAAACA AAA TGTGTTTGT TTCTATAAAA TACAGCTCAA TGTGAGAAC CTTGTCTTGT
TTGCTCTCTG ATGTAACCCCT TTCACAATGT TTGGGCAGCT TATCTCTCT ATTTCCCTGT
AGGGTCCCAT CCAGGCCAAA GTGAGTGCCA GCCTCATTG GGCAGCAGAT GCCCTGTGGA
AGGGCAGGAG GAGACGAGAG CTAATTGTAA CTTTGTGATT AGCTGTCATG GATGCCCTGGT
CCTGTCAATA GCGCTCAATA AAGCCAGAAG GCCAAGCGTT CGCTTCTGCA TACTGATGTC
TGAGTCAGAT TTCTCAGTGC AGAAGGGCTT TCTAGGCAGT CAATTTTGA ATATTAGTCT
TGGTTCCTAA GTGGTTAAAA TCCCTAGCTG GTCTTTAATC TGAGCCTGGA GAATTTAGTT
ATGGCTGACA TTCTGCTGTG ATATTTTTC CCTCAATATA TATGTCTTTC CTCCATCTCT
TAGATCCCTG AATCATAGAG ATATATATGT TATATAATCA ACTGTCTCCA GTCTCTAAGA
GTGATAAGTA CACATTGTGT CAGGTTGAGG GGACAGGAGA ACTTCAAAA GCCTTTCTTG

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FIGURE 16 (118)

CCCCTTTTTC CTTCTCACTG CCTCCCACTA AGTCCAGCCA CTTATTATTC AGCTGACACT
ATCATCATGA CCATGAGGTC TTTTGGGGCT ACCCTGGTTC GGATCCTTCT GGAGGTTTGT
TGCTTAACTC TGTCTTCAGT CCTATGAGCT GCTTTTCAA TAAGTTTCTA TTTTGGCTAA
AGTTGGCCAG AATCTCCTTG TAACCAAAGA ACAATAAAA TACCAGCTTG CAATGTTCTA
TGTTGCTTCC ACCAAACTTA TGCAGCACTT CCTATCTAAT CCACCTACTA GTCTTTTTTT
TTTTTATTTT TTTTGAGACG GAGTCTCGCT CTGTTGCTCA GGATGGAGTG CAATGGTGCA
ATCTCGGCTC ACTGCAACCT CTGCCCTCCG GGTCAAGCA ATTCCCCGGC CTCAGCCTCC
TGAGTAGCTG GGA CTACAGG TGCA TGCCAC CACGTCCGGC TAATTTTGT ATTTAGGAG
AGAGAGGGTT TCACCATGTT GCCCAGGCTG GTCACGAACT CCTGAGCTCA GGCAATCCGC
CCTCCTCGGG CTCCCAAAGT GCTGGGATTA CAGGAGTGAG CCACCTCACC TGGCCCCGAC
CTACTAGTCT TTAGTGTTTG CTTCCCTTCTA TTGGGTAATT GTCTGTATTAT ATGCATGTCT

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FIGURE 16 (119)

TGTTTCCCTCA AATAAAATGT GGTCTTCTCA AGGGTATTGG CCCATGTTCT ATCCATCTGT
AGATATCACA GCACCTAGCA GTGTCTTTCA CAGAGGAAGT ACACAACTGG CATTATTGAT
TCATTGCTCC ATTTTTCCT TCTTTATCCC CAGCATTTCT CAATAATTTC AACATCTCC
ATTGGAGTAC CGGAGAAAGC AGGTAGCTTT ACTTGCAGCT ATGTTTCTAT CCCATAGTA
ACTAAAAGAG GACCCAGAGA AACATGTTTA AATGCTGTCC TGTTATCAGG ACCTCAGCCT
TCTGATGCTC CGTGGCTTGG GGGTTATTGC TTGATCATCT CCTCCCCAAC CTACACTGTG
TACCTATGCT AGTCTCTTCA TGAGGACTAA GCCCCATAGT AAAAGGGCTA GATAAATAGA
AAATCATTTT ATGTAATTAT AAGAAATGAGA ATACTGAGTA TTCTGGTGTT TGTTTAGGAT
AAGCACATCT TTATTTGTAT GAGAAAAAGA AAAAGAGAGT GAAAAATATA TTAACGTGCA
TATTGTTTCAG AACCCTTGGA TTGCAAGTGA CAGAAACTCA ATTCAAACCA ACGTAAGTCA
AAAGGAAAAT ATATTGGCTC ATGTAACCTT CTCACAGAGA GGCAGGATG GAAGGGGCTT

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FIGURE 16 (120)

TGGGAACAAG AGAATTGTTT TCAAAATCTA GGAATACTAG GATTAGTCCA GGATGGGTCA
CCTTCCTGTC CCTGAGGTGG TGGTAGCGAT GGTAGAGTCT TATGGGAGGA AAGAGTGTCAT
GTTAGGATGA AGTAGGGCT AAGCAAAACA GGGCAAGGGC CACTATATCA TGCTAAAAAT
GGTTTTTTTT GATGTCCTCC TTAATTTTAC AAATGCTTCC AACAAAGTAG CACACAGGAA
AAAGAACATA GGGACTCTAC TGGTGGGTGC TTTTATCTTA AGCCTTGTC TCGCTTTTCA
CAGCTTACTC ACTGCTTGTA CCTGAGGCCA TATGCCCTGT AAAAGCTTCT GCAGGGTTTC
TACTAAGCTG GGTCCCTTAT ATGGCTCTCT CCCATTCTG TTGCCCTCACT CTAGTGATCT
TTCTCTTTTC CTCACCTCTG GGACTGGTGG CTGTTTGAT GGACTGCCCT AGCTTTGCTT
TGGGTTTTTT CCTGGGGACA ATGTCTTCAG ATTATCCTAG ACCAAATAAA CTACAGCCAC
TGGGCCAGGC TCTTCCTCCT CCAACTGGAC CATGTTCCTCA GGGCTCTTCA CCTTAGTTTA
GGTCAAGCAT TCTTGCAAA AGAAAGGCCT AGTTAAACAAT AGACATCTTA GCAATTGATT

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FIGURE 16 (121)

CTTTTGACA TGTGTGAAGA TCTATTACACA TTTTGTAAAT AAAGCATTC CCTATGGAAA
CCAACACGAA CTAAGCTGCT CCTGGAATGC AGGGTGGCCT CCTCAATACA GGATGTTCTA
GAGAGCTGTA TTTTGGGCAC TTAACATATC TCCACTACTT AGGGCACAGC ACTGAAATTA
ACACCACTAA GTTGTGTCATG TCCATGTAGT TAGTCTCAGG CAGTGCAGCC TCAGGAGTGG
AACTGACCTC TTATGTGTGT CCAGCCTTTC TTCCCTCAGA AGTCAGCTGT GTTTTCTGCT
GACTCTCCAT AGGAACATCA GTCCTGAATC CTCAGACCAC CATCTGGAGT AGTAAGTGCT
CCTGACAGTC CTAGAAGTTG TCTACCGCTG GATCTCCAAA GCGTGTGACA CACCGTGAGA
GAGAAATGAG AAAGCTGGGC TCTTCAGGTA AATCTTGCTT TTTCACAAGC CCCCTAATT
TACTGCATAA TTATTTTGAA TTCACTGATA ATTTCTACAA TTTTCCCATA AGTCATCTAC
ACACAATACC CTCTCATGCA ACACTTGGCT TTGCTAATAC ATATCTATTA TGAGAGCTGT
GCTTCTTAAG CGTAAATGTT TTATATGCAC TAAGGCTCTT GGCTTACATA TAAAAGGGGT

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FIGURE 16 (122)

ATTGAGCAAT GTGATACAGA AGTCTTTTCT CCACAGGTCT CATATGTAAA GAATTCATTA
GATTGGCTGA AATAGACTGA TCTGTCCATT TCTCTGCTCA CTTATCATAA GGAAGTCATT
AGCTAAGGAA CAAAAACTAC AATCTATGTA ATTAGAAGAA CAAGCTGGTT TTGCTCAATA
TAAAAATAAG AAAAAGAAAC CATGTGAAAG TCAAAATATT TGTTAATCA GGTCATTGAG
AATCTATTAA AAAGTATTG AATTCTTTAT GATGAGAACT ATCTTGACTC AAGTGACAG
TGGTGAGCTT TTTGGCCCTGT GGTCCCCTACG TAGAAAGGAG GCTTTGTCAT AAAGTCTTAT
ATGGTACAGG TGCCAAGTTA AGTGCCCCAAG CTTGCTCTTA AAAGCATACT GGATTTTG

INTERNATIONAL SEARCH REPORT

International Application No.
PCT/AU 98/00352

A. CLASSIFICATION OF SUBJECT MATTER																						
Int Cl ⁶ : C12N 15/11, 15/79 A61K 48/00																						
According to International Patent Classification (IPC) or to both national classification and IPC																						
B. FIELDS SEARCHED																						
Minimum documentation searched (classification system followed by classification symbols) WPAT (see below) STN (CA - see below)																						
Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched MEDLINE (see below)																						
Electronic data base consulted during the international search (name of data base and, where practicable, search terms used) WPAT - (ARTIFICIAL CHROMOSOME# OR MINICHROMOSOME# OR MINI CHROMOSOME# OR MICRO CHROMOSOME# OR MICRO CHROMOSOME# OR YAC# OR MAC# OR HAC# OR CENTROMERE# OR NEO CENROMERE#) AND C12N-015/IC STN (CA and MEDLINE): CENTROMERE AND (ALPHA SATELLITE OR ALPHASATELLITE)																						
C. DOCUMENTS CONSIDERED TO BE RELEVANT																						
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.																				
PX	Human Molecular Genetics 6(8), pages 1195-1204 (1997) Depinet, T.T. et al "Characterization of neocentromeres in marker chromosomes lacking detectable alpha-satellite DNA." See whole document.	1-4, 11-17, 24-30, 37-39, 61-64, 71-74																				
PX	Genetic Counseling 8(4), pages 341-343 (1997) Petit, P. and Fryns, J.P. "Interstitial deletion 2P accompanied by marker chromosome formation of the deleted segment resulting in a stable acentric marker chromosome." See whole document.	1-39, 61-74																				
<input checked="" type="checkbox"/> Further documents are listed in the continuation of Box C <input type="checkbox"/> See patent family annex																						
<p>* Special categories of cited documents:</p> <table border="0"> <tr> <td>"A"</td> <td>document defining the general state of the art which is not considered to be of particular relevance</td> <td>"T"</td> <td>later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention</td> </tr> <tr> <td>"E"</td> <td>earlier document but published on or after the international filing date</td> <td>"X"</td> <td>document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone</td> </tr> <tr> <td>"L"</td> <td>document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)</td> <td>"Y"</td> <td>document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art</td> </tr> <tr> <td>"O"</td> <td>document referring to an oral disclosure, use, exhibition or other means</td> <td>"&"</td> <td>document member of the same patent family</td> </tr> <tr> <td>"P"</td> <td>document published prior to the international filing date but later than the priority date claimed</td> <td></td> <td></td> </tr> </table>			"A"	document defining the general state of the art which is not considered to be of particular relevance	"T"	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention	"E"	earlier document but published on or after the international filing date	"X"	document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone	"L"	document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"Y"	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art	"O"	document referring to an oral disclosure, use, exhibition or other means	"&"	document member of the same patent family	"P"	document published prior to the international filing date but later than the priority date claimed		
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Date of the actual completion of the international search 7 JULY 1998		Date of mailing of the international search report 14 JUL 1998																				
Name and mailing address of the ISA/AU AUSTRALIAN PATENT OFFICE PO BOX 200 WODEN ACT 2606 AUSTRALIA Facsimile No.: (02) 6285 3929		Authorized officer JIM CHAN Telephone No.: (02) 6283 2340																				

INTERNATIONAL SEARCH REPORT

International Application No.

PCT/AU 98/00352

C (Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
PX	Nature Genetics 16(2), pages 144-53 (1997) du Sart, D. et al "A functional neo-centromere formed through activation of a latent human centromere and consisting of non-alpha-satellite DNA." See whole document.	1-39, 61-74
X	Human Genetics 97, pages 453-6 (1996) Bukvic N. et al "An unusual dicentric Y chromosome with a functional centromere with no detectable alpha-satellite." See whole document.	1-4, 11-17, 24-30, 37-39, 61-64, 71-74
X	Cancer Genetics & Cytogenetics 39(1) pages 1-6 (1996) Abeliovich, D. et al "dup (109) lacking α -satellite DNA in bone marrow cells of patient with acute myeloid leukemia." See whole document.	1-6, 8-19, 21-32, 34-39, 61-66, 68-74
X	Proc. Natl. Acad. Sci. USA 93, pages 8512-17 (1996) Dawe, R.K. and Carde, W.Z. "Induction of centromeric activity in maize <i>suppressor of meiotic drive 1</i> ." See introduction and discussion.	1, 2, 15, 16, 61, 62
X	Trends In Genetics 11(9) pages 337-9 (1995) Brown, W. and Tyler-Smith, C. "Centromere Activation." See whole document.	1-74
X	Am. J. Human. Genet. 54, pages 877-83 (1994) Blennow, E. et al "Tetrasomy 15q: Two marker chromosomes with no detectable alpha-satellite DNA." See whole document.	1-4, 11-17, 24-30, 37-39, 61-64, 71-74
X	Am. J. Human. Genet. 55, pages 1202-8 (1994) Ohashi, H. et al "A stable acentric marker chromosome; possible existence of intercalary ancient centromere at distal 8p." See whole document	1-4, 11-17, 24-30, 37-39, 61-64, 71-74
X	Am. J. Human. Genet. 52 pages 1153-63 (1994) Voullaire, L. E. et al "A functional marker centromere with no detectable alpha-satellite III or CENP-B protein: activation of a latent centromere?" See whole document.	1-39, 61-74
A	WO A 97 16533 (THE REGENTS OF THE UNIVERSITY OF CALIFORNIA) 9 May 1997. See whole document.	1-74

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No.
PCT/AU 98/00352

This Annex lists the known "A" publication level patent family members relating to the patent documents cited in the above-mentioned international search report. The Australian Patent Office is in no way liable for these particulars which are merely given for the purpose of information.

Patent Document Cited in Search Report		Patent Family Member	
WO	9716533	US	9716533
			END OF ANNEX